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.5 16.4 204 22 AAE10920 Human gene 12 .5 8.6 617 21 AAY76048 Skin cell prot .5 8.6 617 22 AAB55987 Skin cell prot .5 8.6 617 22 AAB55987 Skin cell prot .6 8.6 667 22 AAU04957 Human Interle .6 4.6 864 12 AAW04184 Mouse interle .6 4.6 864 20 AAW92408 Murine IL-17R .6 4.6 864 21 AAY97130 Murine interle .6 864 21 AAY97180 Murine interle .6 864 21 AAB03806 Murine interle .6 864 22 AAB62060 Murine interle .6 864 22 AAB62060 Murine interle .6 864 28 AAW72748 Murine interle .6 864 28 AAW72748 Murine interle .6 864 29 AAW61272 Human interle	-	21	866	4.2	151.5	8
.5 16.4 204 22 AAE10920 .5 8.6 617 21 AAY76048 .5 8.6 617 22 AAB25987 .5 8.6 617 22 AAB35987 .6 8.6 617 22 AAB36127 .6 8.6 864 17 AAW32408 .6 864 18 864 21 AAY99935 .6 864 21 AAY99180 .6 864 21 AAY97130 .6 864 21 AAY97180 .6 864 21 AAB38060 .6 864 21 AAB38080 .6 864 22 AAB39180		20	866	4.2	151.5	7
.5 16.4 204 22 AAE10920 Human gene 12 .5 8.6 617 21 AAY76048 Murine skin cel .5 8.6 617 22 AAB55987 Skin cell prot .5 8.6 667 22 AAB55987 Human Interle .6 8.6 667 22 AAW04957 Human Interle .6 8.6 17 AAW04184 Murine interle .6 8.6 19 AAW04184 Murine II-17R .6 8.6 20 AAW92408 Murine II-17R .6 8.6 21 AAY97130 Murine interle .6 8.6 21 AAY97180 Murine interle .6 8.6 21 AAY97180 Murine interle .6 8.6 8.6 21 AAY97180 Murine interle .6 8.6 8.6 21 AAY97180 Murine interle .6 8.6 8.6 22 AAX97248 Murine interle .6 8.6 8.6 22 AAB52060 Murine II-17R .6 8.6 8.6 22 AAB52060 Murine interle .6 8.6 8.6 22 AAB52060 Murine interle .6 8.6 8.6 22 AAB52060 Murine II-17R .6 8.6 8.6 22 AAB52060 Murine II-17R .6 8.6 8.6 8.6 22 AAB52060 Murine II-17R .6 8.6 8.6 8.6 8.6 22 AAB52060 Murine II-17R .6 8.6 8.6 8.6 8.6 8.6 8.6 8.6 8.6 8.6 8		19	866	4.2	151.5	6
.5 16.4 204 22 AAE10920 Human gene 12 .5 8.6 617 21 AAY76048 Murine skin cel .5 8.6 617 22 AAB55987 Skin cell prot .5 8.6 617 22 AAB55987 Human Interle .6 8.6 667 22 AAW04957 Human Interle .6 8.6 19 AAW04957 Human Interle .6 8.6 19 AAW04184 Murine interle .6 8.6 19 AAW02408 Murine IL-17R .6 8.6 20 AAW92408 Murine IL-17R .6 8.6 21 AAY97130 Murine interle .6 8.6 21 AAY97180 Murine interle .6 8.6 21 AAY97180 Murine interle .6 8.6 21 AAB62060 Murine interle .6 8.6 22 AAY72748 Murine IL-17R .6 8.6 22 AAY72748 Murine Interle	μ.	17	866	4.2	151.5	S
.5 16.4 204 22 AAE10920 Human gene 12 .5 8.6 617 21 AAY56048 Murine skin ce .5 8.6 617 22 AAB55987 Skin cell prot .5 8.6 617 22 AAB55987 Human Interlet .67 4.6 864 17 AAW04184 Mouse interlet .67 4.6 864 19 AAW61271 Murine IL-17R .67 4.6 864 21 AAY99130 Murine IL-17R .67 4.6 864 21 AAY97180 Murine interlet .67 4.6 864 21 AAB603806 Murine interlet .67 4.6 864 21 AAB603806 Murine interlet .68 4.6 864 22 AAB62060 Murine interlet .69 4.6 864 22 AAB62060 Murine interlet .60 4.0 864 22 AAB62060 Murine interlet		22	864	4.6	167	
.5 16.4 204 22 AAE10920 Human gene 12 .5 8.6 617 21 AAY76048 Murine skin cel .5 8.6 617 22 AAB55987 Skin cell prot .5 8.6 617 22 AAB55987 Human Interle .6 8.6 667 22 AAU04957 Human Interle .6 8.6 19 AAW04184 Murine interle .6 4.6 864 19 AAW061271 Murine II-17R .6 864 20 AAW992408 Murine II-17R .6 864 21 AAY99130 Murine II-17R .6 864 21 AAY99130 Murine interle .6 864 21 AAY99180 Murine interle .6 864 21 AAY99180 Murine interle .6 864 21 AAB03806 Murine interle		22	864	4.6	167	ω
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5 16.4 204 22 AAE10920 Human gene 12 5 8.6 617 21 AAY76048 Murine skin ce 5 8.6 617 22 AAB55987 Skin cell prot 67 4.6 864 17 AAW04184 Mouse interlet 67 4.6 864 19 AAW61271 Mouse interlet 67 4.6 864 20 AAW92408 Murine IL-17R 67 4.6 864 21 AAY9935 Murine IL-17R 67 4.6 864 21 AAY97130 Murine IL-17R		21	864	4.6	167	
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5 16.4 204 22 AAE10920 Human gene 12 5 8.6 617 21 AAY76048 Murine skin cel 5 8.6 617 22 AAB55987 Skin cell prot 10 8.6 667 22 AAB55987 Human Interle 67 4.6 864 17 AAW04184 Murine interle 67 4.6 864 20 AAW92408 Murine Interle	IL-17R	21	864	4.6	167	9
5 16.4 204 22 AAE10920 5 8.6 617 21 AAY76048 5 8.6 617 22 AAB55987 10 8.6 667 22 AAB04957 67 4.6 864 17 AAW04184 67 4.6 864 19 AAW61271	IL-17R	20	864	4.6	167	œ
.5 16.4 204 22 AAE10920 .5 8.6 617 21 AAY76048 .5 8.6 617 22 AAB55987 10 8.6 667 22 AAU04957 67 4.6 864 17 AAW04184	Mouse interleuk	19	864	4.6	167	7
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	12	22	204	16.4	•	\sim

ALIGNMENTS

AAB61880 standard; Protein; 692 AA.

08-MAY-2001 (first entry)

Human cytokine receptor 2cytor14.

Cytokine receptor; 2cytor14; human; inflammation; rheumatoid arthritis; antiinflammatory; gene therapy; vaccine.

Burkhead SK, Pownder SL

Claim 2; Page 2; 112pp; English.

New polypeptide encoding a human cytokine receptor Zcytor14, for treating inflammation e.g. rheumatoid arthritis

colon;

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Query Match
Best Local S
Matches 457
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                                                                                                                                             RRILQEGGVVILLESPAAVAQCQQWLQLQTVEP----GPHDALAAWLSCVLPDFLQGRATG
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                                                                                                                     LQDFRSHQCMQLWNDDNMGSLWACPMDKYIHRRWVLVWLACLLLAAALFFFLLLKKDRRK 467
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Pred. No. 2.3e-214;
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08-NOV-2000;
01-DEC-2000;
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28-JUL-2000;
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02-JUN-2000;
                                                                                                                                  03-MAY-2000;
17-MAY-2000;
                                                                                                                                                                                                           04-APR-200
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30-MAR-2000;
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29-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                    WO200168848-A2
                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                        Human PRO
                                                                                                                                                                                                                                                                                                                                                                                                    18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                          AAU29322 standard; Protein; 705 AA
                                                                                                                                             25-APR
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                                                                                                                                                                                                                                                                                                                                                                 blood; chondrocyte cell;
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                                                                                                                                                                                                                                                                                                                                                                      pig;
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                                                                                                                                                                                                                                                                                                                                                               goat; rabbit; tumour necrosis factor alpha; TNF-alp
cyte cell; cell proliferation; cell differentiation;
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                                                                                                                                                                                                                                                                                                                                                                           tumour; cancer;
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                                                                                                                                                                                                                                                                                                                                                                           horse;
                                                                                                                                                                                                                                                                                                                                                                     rse; sheep;
TNF-alpha;
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(GETH) GENENTECH INC

Baker KP, Chen J, Pan J, Smith V, 1 Watanabe Désnoyers L, atanabe CK, Wood Goddard A, Godo ood WI, Zhang Z; Godowski PJ, Gurney AL;

2001-602746/68. DB; AAS46223.

Novel nucleic acids encoding PRO polypeptides, used to diagnose the presence of tumours, such as prostate and breast tumours, in mammals to screen for modulators of the compounds in mammals and

9322

N

Claim

11;

774pp;

English

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Matches
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                                                                                                                                                                                                                                                                                                                                                          LVPTRLQTELVLRCPQKTDCALRVRVVVHLAVHGHWAEPEE----AGKSDSELQESRNAS
                                                                                    KVQLQACSWADSLGPFKDDMLLVEMKTGLNNTSVCALEPSGCTPLPSMASTRAARLGEEL 407
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sgrlqeraeqvsralqpaldsyfhppgtpapg
                                                     SCVLPDFLQGRATGRYVGVYFDGLLHPDSVPSPFRVAPLFSLPTQLPAFLDALQGGCSTS
                                                                                                                                  gwlrllkqdvrsgaaarg-raalllysaddsgferlvgalasalcqlplrvavdlwsrre
                                                                                                                                                                             klqlqeclwadslgplkddvllletrgpqdnrslcalepsgctslpskastraarlgeyl
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                      AGRPADRVERVTQALRSALDSC - - TSSSEAPG
                                            scvlpdflqgrapgsyvgacfdrllhpdavpalfrtvpvftlpsqlpdflgalqqprapr
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Pred. No. 4.6e-213;
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                                 WO200146420-A2
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Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.

The PRO polypeptides and their associated nucleic acids can be used to detect the presence of a tumour in a mammal by comparing the level of cd expression of a PRO polypeptide in a test sample of cells from the animal and a control sample of normal cells, whereby a higher level of cd expression in the test sample indicates the presence of a tumour in the cd expression in the test sample indicates the presence of a tumour in the mammals include dogs, cats, cattle, horses, sheep, pigs, goats and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TNF) alpha release from human blood, when contacted with it. A specific polypeptide can be used to stimulate tumour differentiation of chondrocyte cells. The PRO cs. Susceptibility to tumour development, particularly adrenal, lung, colon, protate, prostate, rectal, cervical, or liver tumours, in mammalian subjects. The oligonucleotide probes specific for the PRO nucleic acids subjects. The oligonucleotide probes specific for the PRO nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for genetic analysis of individuals with genetic disorders
RESULT
AAUU4956
ID AAUU
XX AAUU
AC AAUU
CX AAUU
CX Huma
XX Huma
XX Huma
KW PRO2
KW rheu
KW alle
KW dege
XX Homo
XX Hom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; Interleukin-17 receptor; IL-17RH2; agonist; antag PRO20040; DNA 164625-2890; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; diabetes mellitus; allergic disease; asthma; demyelinating disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human Interleukin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU04956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU04956 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cartilaginous disorder; transplantation associated disease:
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                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 receptor,
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<u>##888888888888888</u>##

Sequence

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/note= "1700..705
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                                    696..701
                                                             692..697
                                                                                                                     phosphorylation
                                                                                                                                                 552..555
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                                               /note=
                                                                         /note-
                                                                                                                    /note= "cAMP/GMP-dependent protein
phosphorylation site".
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                                                                                                                                                                                                                                               391..394
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                                                                                                                                                                                   "Transmembrane domain"
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"N-myristoylation site"
                      "N-myristoylation site"
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                                                                      "N-myristoylation site"
                                                                                              "Glycosaminoglycan attachment site"
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Best Local S
Matches 459
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Gurney AL, L
Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-MAR-2000;
02-JUN-2000;
22-JUN-2000;
22-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-DEC-1999;
30-DEC-1999;
11-JAN-2000;
18-FEB-2000;
02-MAR-2000;
21-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, a demyelinating disease, an autoimmune or immune-mediated skin disease, contact dermatitis, an allergic disease e.g. food hypersensitivity, asthma, a transplantation associated disease, or a chronic inflammatory demyelinating polyneuropathy. Treating a degenerative cartilaginous disorder comprises administering a PRO1022 polypeptide agonist, or antagonist to the mammal. Numerous examples of the diseases and disorders are given in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  containing ant/agonists to the PRO polypeptides or individual components are useful for treating a mammal with an immune related disease, e.g. systemic upus erythematosus, rheumatoid arthritis, osteoarthritis, but only the property of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence is PRO20040 which is the human Interleukin 17 IL-17RH2, encoded by DNA 164625-2890. A composition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 10; Fig 14; 188pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel PRO polypeptides homologous to interleukin-17, useful for the diagnosis and treatment of immune related disease e.g. rheumatoid arthritis and diabetes - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         idiopathic inflammatory myopathy, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 - AUG
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                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                          1 MPVSWFLLSLALGRNPVVVSLERLMEPQDTARCSLGLSCHLWDGDVLCLPGSLQSAPGPV 60
                                                                                                                                                                                                                                 LVPTRLQTELVLRCPQKTDCALRVRVVVHLAVHGHWAEPEE----AGKSDSELQESRNAS 116
                                                    YQKELNLTQQLP------DGDNVLLTLDVSEEQDFSFLLYLRPVPDALKSLWYKNLT 227
                                                                                                            2001-451708/48.
)B; AAS09515.
                     yekelnhtqqlpalpwlnvsadgdnvhlvlnvseeqhfglslywnqvqgppkprwhknlt
                                                                                                                                                                                                                                                                                                  mpvpwfllslalgrspvvlslerlvgpqdathcspglscrlwdsdilclpgdivpapgpv 60
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Li H, Hillan KJ
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2000WO-US15264.
2000US-0213087.
2000US-0644848.
2000WO-US23328.
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2000US-0253646
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2000US-0175481.
2000WO-US04341.
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66.3%;
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lan KJ, Tumas D, Van Lookeren M,
PM, Wood WI, Yansura DG;
                                                                                                                                                                                                                                                                                                                                                                                                66;
                                                                                                                                                                                                                                                                                                                                                                                             Score 2339; DB 22;
Pred. No. 4.6e-213;
56; Mismatches 133;
                                                                                                                                                                                                                                                                                                                                                                                                Indels
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Vandlen RL;
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15-SEP-1999;
07-DEC-1999;
WPI; 2001-183260/18
                                           Eaton DL, F: Grimaldi CJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-MAR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; PRO protein; mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human PRO20040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB87606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB87606 standard;
                                                                                                                                                                                    25-APR-2000;
22-MAY-2000;
                                                                                                                                                                                                                                                       01-MAR-2000;
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18-FEB-2000;
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2000WO-US05601.
2000US-0187202.
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2000WO-US14042
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2000WO-US04342
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                                           Gurney
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99US-0170262.
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99WO-US21090
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                                                                   'n
                                           ΑL,
                                           Gerritsen ME,
Watanabe CK,
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                                           Goddard A,
Wood WI;
                                                                Godowski PJ;
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181 177 121

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Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is a human PRO polypeptide (secreted and transmembrane). The PRO protein, and PRO agonists, PRO antagonists or anti-PRO antibodies are useful for preparation of a medicament useful in the treatment of a condition which is responsive to the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO protein may also be employed as molecular weight markers for protein electrophoresis. The PRO coding sequence has applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eighty four nucleic acids encoding PRO polypeptides, useful in molecular biology, including use as hybridization probes, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chromosome and gene mapping.
                                                                                                                                                                                                                                                                 421
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                                  631 AGRPADRVERVTQALRSALDSC--TSSSEAPG 660
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                                                                                SCYLPDFLQGRATGRYYGYYFDGLLHPDSYPSPFRYAPLFSLPTQLPAFLDALQGGCSTS
                                                                                                                                                                                               gwlrllkqdvrsgaaarg-raalllysaddsgferlvgalasalcqlplrvavdlwsrre
                                                                                                                                                                                                                                                                                                                                 LVPTRLQTELVLRCPQKTDCALRVRVVVHLAVHGHWAEPEE----AGKSDSELQESRNAS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mpvpwfllslalgrspvvlslerlvgpqdathcspglscrlwdsdilclpgdlvpapgpv
                                                                scvlpdflggrapgsyvgacfdrllhpdavpalfrtvpvftlpsqlpdflgalqqprapr
                                                                                                                                                                LSAHGALAWFHHQRRRILQEGGVVILLFSPAAVAQCQQWLQLQTVEP----GPHDALAAWL
                                                                                                                                                                                                                                                                LQDFRSHQCMQLWNDDNMGSLWACPMDKYIHRRWVLVWLACLLLAAALFFFLLLKKDRRK
                                                                                                                                                                                                                                                                                                                                                  KVQLQACSWADSLGPFKDDMLLVEMKTGLNNTSVCALEPSGCTPLPSMASTRAARLGEEL
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Pred. No. 4.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proteins, polypeptides and peptides having Zcytor14 activity can be administered to a subject who lacks an adequate amount of this polypeptide, for treating inflammation and conditions such as rheumatoid arthritis. In contrast, Zcytor14 antagonists (e.g., anti-Zcytor14 antibodies) can be used to treat a subject who produces an excess of Zcytor14. Zcytor14 nucleotide sequences can also be used to provide Zcytor14 to a subject. The present sequence represents a chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention provides a new human cytokine receptor desinated Zcytor14. Zcytor14 can be expressed by standard recombinant methodology. The encoding nucleic acid is useful for detecting the expression of a Zcytor14 gene in a biological sample. Anti-Zcytor14 antibodies can be useful to screen biological samples in vitro for the presence of Zcytor14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polypeptide encoding a human cytokine receptor Zcytor14, treating inflammation e.g. rheumatoid arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUL-1999;
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                                                                                                                                            LQAQVVLSFQAYPIARCALLEVQVPADLVQPGQSVGSAVFDCFEASLGAEVQIWSYTKPR
                                                                                                                                                                                                                                                                                                                                     mpvpwfllslalgrspvvlslerlvgpqdathcspalscrlwdsdilclpgdivpapgpv
                                                           YQKELNLTQQLP---
                                                                                                                 lqaqvvlsf,qayptarcvllevqvpaalvqf,qsvgsvvydcfeaalgsevriwsytqpr
yekelnhtqqlpalpwlnvsadgdnvhlvlnvseeqhfglslywnqvqgppkprwhknlt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              705 AA;
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66.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 2339; DB 22;
Pred. No. 4.6e-213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English.
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                                 The invention provides a new human cytokine receptor desinated Zcytor14. Zcytor14 can be expressed by standard recombinant methodology. The encoding nucleic acid is useful for detecting the expression of a Zcytor14 gene in a biological sample. Anti-Zcytor14 antibodies can be used to screen biological samples in vitro for the presence of Zcytor14.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Chimeric Zcytor14 protein #3
                                                                                                                                                                                                                 Presnell SR,
           Proteins, polypeptides and peptides having Zcytor14 activity can administered to a subject who lacks an adequate amount of this
                                                                                                                     Claim 2; Page 107-109; 112pp;
                                                                                                                                                                                                                                                                    07-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                 Cytokine receptor;
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                                                                                                                                              polypeptide encoding a human cytokine receptor Zcytor14,
ating inflammation e.g. rheumatoid arthritis -
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                                                                                                                                                                                                                Burkhead SK,
                                                                                                                                                                                                                                                                    9908-0348854
 treating inflammation and conditions
                                                                                                                                                                                                                                                                                                                                                                                                     gene therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Zcytor14; human; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein; 675
                                                                                                                                                                                                                Pownder SL;
                                                                                                                     English
                                                                                                                                                                                                                                                                                                                                                                                                     vaccine
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such as rheumatoid
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447; Conserv
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Pred. No. 3.4e-207;
3; Mismatches 132;
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Cytokine receptor; Zcytor14; Chimeric Zcytor14 protein

human;

inflammation;

rheumatoid

08-MAY-2001 AAB61883 AAB61883

(first entry)

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standard;

Protein;

antiinflammatory; gene therapy; vaccine

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Matches 449
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LQDFRSHQCMQLWNDDNMGSLWACPMDKYIHRRWVLVWLACLLLAAALFFFLLLKKDRRK
                                                                                    ldapcslpaeaalcwrapggdpcqplvpplswenvtvd-
                                                                                                                                              gpqiitlnhtdlvpclciqvwplepdsvrtnicpfredprahqnlwqaarlrlltlqswl
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449; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 102-104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      688 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            62.8%; Score 2263.5; DB 22
64.9%; Pred. No. 6.7e-206;
Live 63; Mismatches 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112pp; English
                                                                                                                                                                                                                        -DGDNVLLTLDVSEEQDFSFLLYLRPVPDALKSLWYKNLT
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AAB61881
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                                            The invention provides a new human cytokine receptor desinated Zcytor14. Zcytor14 can be expressed by standard recombinant methodology. The encoding nucleic acid is useful for detacting the expression of a Zcytor14 gene in a biological sample. Anti-Zcytor14 antibodies can be used to screen biological samples in vitro for the presence of Zcytor14. Proteins, polypeptides and peptides having Zeytor14 activity can be administered to a subject who lacks an adequate amount of this polypeptide, for treating inflammation and conditions such as rheumatoid arthritis. In contrast, Zcytor14 antagonists (e.g. anti-Zcytor14 antibodies) can be used to treat a subject who produces an excess of Zcytor14 to a subject. The present sequence represents a variant of the human cytokine receptor Zcytor14, designated Zcytor14. This treat is a transfer of form of the receptor Scytor14, designated Zcytor14. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB61881 standard;
                                                                                                                                                                                                                                    Disclosure;
                                                                                                                                                                                                                                                         New polypeptide encoding a human cytokine receptor Zcytor14, treating inflammation e.g. rheumatoid arthritis -
                                                                                                                                                                                                                                                                                                  WPI; 2001-112618/12.
N-PSDB; AAC85029.
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                         amino acid residues
                                      variant is a
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                                      truncated form of
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                                      the receptor polypeptide and lacks
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Best Local
                                                                                                                                                                   Human; secreted protein; cancer; tumour; developmental abnormality; foetal deficiency; blood disorder; immune system disorder; inflammation; autoimmune disease; allergy; Alzheimer's disease; cognitive disorder; schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder; atheresclerosis; diabetes; cardiovascular disorder; kidney disorder; atheresclerosis; diabetes; cardiovascular disorder; kidney disorder;
                                                                                                                                                                                                                                                                                                                                                                                     AAY76143
                                                                                                                                                                                                                                                                              Human secreted protein encoded by gene 20
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                                                                                                                                                        digestive disorder;
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                                                                                                                                    therapy; chromosome
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                                                                                                   lomo sapiens
6-MAY-1999;
                                  8-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 wsytqpryekelnhtqqlpalpwlnvsadgdnvhlvlnvseeghfglslywnqvqgppkp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 eeprnaslqaqvvlsfqayptarcvllevqvpaalvqfgqsvgsvvydcfeaalgsevri
                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rwhknltgpqiitlnhtdlvpclciqvwplepdsvrtnicpfredprahqnlwqaarlrl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WSYTKPRYQKELNLTQQLP------DGDNVLLTLDVSEEQDFSFLLYLRPVPDALKS 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DLWSRRELSAHGALAWFHHQRRRILQEGGVVILLFSPAAVAQCQQWLQLQTVEP---GPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QGGCSTSAGRPADRVERVTQALRSALDSC--TSSSEAPG 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        \tt dafraslscvlpdflqgrapgsyvgacfdrllhpdavpalfrtvpvftlpsqlpdflgal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dlwsrrelsaggpvawfhagrrqtlqeggvvvllfspgavalcsewlqdgvsgpgahgph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LKKDRRK - - - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ltlqswlldapcslpaeaalcwrapggdpcqplvpplswenvtvd-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DALAAWLSCVLPDFLQGRATGRYVGVYFDGLLHPDSVPSPFRVAPLFSLPTQLPAFLDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qqpraprsgrlqeraeqvsralqpaldsyfhppgtpapg
                                                                                                                                                                                                                                                                                                                                                                                   standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                (first entry)
 99WO-US09847
                                                                                                                                                                                                                                                                                                                                                                                     Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51.48;
                                                                                                                                        endocrine disorder; infection;
3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----AARGSRTALLLHSADGAGYERLVGALASALSQMPLRVAV 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1851.5; DB 22
Pred. No. 7.7e-167;
2; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                       309
                                                                                                                                                                                                                                                                                                                                                                                       ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 47;
                                                                                                                                                          AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 575;
                                                                                                                                                            leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                400
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                                                                                                                                                                                                                                                                                               AA265250 to AA265350 represent 97 isolated human secreted protein genes. CC AAY76124 to AAY76223 are the secreted proteins encoded by the 97 human CC genes. The gene encoding this protein was found to be on chromosome 3. CC The genes and their corresponding secreted polypeptides are consistent or gene therapy. Also pathological conditions. CC e.g. by protein or gene therapy. Also pathological conditions can be CC diagnosed by determining the amount of the new polypeptides in a sample CC core by determining the presence of mutations in the new genes. Specific CC uses are described for each of the 97 genes, based on which tissues they CC diagnosis or treatment of cancer, tumours, developing products for the CC diagnosis or treatment of cancer, tumours, developmental abnormalities and foetal deficiencies, blood disorders, diseases of the immune system. CC disorders, schizophrenia, arthritis, asthma, psoriasis, sepsis, skin CC disorders, digestive/endocrine disorders, infections and AIDS. The collypeptides are also useful for identifying their binding partners.

The sequences shown in AAY76224 to AAY76424 represent fragments of the
                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-MAY-1998;
18-MAY-1998;
18-MAY-1998;
18-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-MAY-1998;
12-MAY-1998;
12-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ruben SM,
Olsen HS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; Page 372-373; 475pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated human genes and the secreted polypeptides they encode, useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-MAY-1998;
18-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAZ65269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-062296/05
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                                                                                                                                                                                                                                                            Sequence
                           121
                                                    117
 177
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                                                                                19
                                                                                                           61
                                                                                                                                                                 'n
                                                                                                                                      -
                      YOKELNLTQQLP----
                                                                                                                                                                                            192;
                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                         proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Florence K,
Shi Y, Your
                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Endress
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0085094.
98US-0085105.
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98US-0085925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0085924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0085923.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Young PE,
                                                                                                                                                                                                         26.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ni J, Rosen CA, Carter
1g PE, Wei F, Brewer LA,
                                                                                                                                                                                              20;
                                                                                                                                                                                                         Score 958.5; DB 21; Pred. No. 2.4e-82;
                                                                                                                                                                                            Mismatches
    -DGDNVLLTLDVSEEQDFSFLLYLR 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carter
                                                                                                                                                                                              56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; KC, MUULL,
, Soppet DR;
                                                                                                                                                                                                                       Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Moore PA;
                                                                                                                                                                                               29;
                                                                                                                                                                                               Gaps
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central nervous system; virtuelde; anti-HIV; fungicide; anti-mutagen; dardiovascular; anti-nemic; anti-nemic; fungicide; anti-mutagen; fardiovascular; anti-nemic; anti-aggregant; haemostatic; vulnerary; entidiabetic; cytostatic; neuroprotective; anti-delegate; anti-asthmatic; entidiabetic; cytostatic; neuroprotective; anti-depressant; nootropic; enti-parkinsonian; and immunostimulant. The proteins and polynucleotides encoding them can be used in gene therapy, anti-sense therapy and vaccine production, The proteins and polynucleotides are useful for screening for algorists or antagonists of a protein and for the treatment and diagnosis elemantoid arthritis, septic shock, pancreatitis, cardiac dysfunction, neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal effections, autoimmunity, genetic diseases, haematopoietic disorders, ottoporosis, severe combined immunodeficiency, eczema, altergic strombers, bacters, altergic strombers, disease, parkinson's disease courted constitutions depression,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAH99166 to AAH99904 encode the human proteins given in AAM25225 to AAM25963. The proteins can have activities based on the tissues and cells they are expressed in, such as: antiinflammatory; antirheumatintiarthritic; immunosuppressive; antibacterial; endocrine; cardian; central nervous system; virucide; anti-HIV; fungicide; antimutagen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-457603/49
N-PSDB; AAH99805.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-DEC-1999; 99US-0471275
21-JAN-2000; 2000US-0488725
25-APR-2000; 2000US-0552317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neuroprotective; antidepressant; nootropic; antiparkinsonian; infection; immunostimulant; gene therapy; antisense therapy; vaccine; inflammation; antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis; cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity; genetic disease; haematopoietic disorder; platelet disorder; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            laim 20; Page 283; 1217pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                isolated human polynucleotides encoding treatment and diagnosis of e.g. cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-DEC-2000; 2000WO-US35017.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thrombocytopaenia; osteoporosis; severe combined immunodeficiency; allergic rhinitis; diabetes; multiple sclerosis; depression; Alzheimer's disease; Parkinson's disease; neurodegenerative disord
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic; neuroprotective; antideprocessant neuroprotective; antideprotective; antideprotecti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antiaggregant; haemostatic; vulnerary; antiulcer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antibacterial; endocrine; cardiant; central nervous system; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antiinflammatory; antirheumatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM25864 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001
    teoporosis, severe combined immunodeficiency, eczema, initis, asthma, diabetes, cancer, multiple sclerosis, zheimer's disease, Parkinson's disease, neurodegenerat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 qvqqppkprwhknltqpqiitlnhtdlvpclciqvwplepdsvrrtsapsgrtp-ah 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drmanac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ID NO:1379.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             332 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibacterial; endocrine; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polypeptides, useful for ulcers and HIV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neurodegenerative disorder
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This invention relates to nucleic acid sequences AAF93744 - AAF93916 which encode human secretory or membrane proteins represented by AAB88419. Included in the invention are primers AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate CDNA sequences of the invention. The invention also includes methods
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<u>ਲ਼ਲ਼ਲ਼ਲ਼ਲ਼ਲ਼ਲ਼ਲ਼ਲ਼ਲ਼ਲ਼ਲ਼ਲ਼ਲ਼ਲ਼ਫ਼ਫ਼ਫ਼ਫ਼ਫ਼ਫ਼ਫ਼ਫ਼ਫ਼ਫ਼ਖ਼ਫ਼ਖ਼ਖ਼ਫ਼ਫ਼ਫ਼ਫ਼ਫ਼ਫ਼ਫ਼ੑੑਜ਼ੑਲ਼ੑਲ਼ੑਲ਼ੑਲ਼</u>

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AAB88448
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                            Nucleic acids encoding secretory proteins/membrane proteins, useful gene therapy or as candidate target molecules in drug development -
 Claim 1; SEQ ID 264; 609pp + CD
                                                                                WPI; 2001-093989/11.
N-PSDB; AAF93875.
                                                                                                                                                               (HELI-) HELIX
                                                                                                                                                                                               02-MAY-2000;
                                                                                                                                                                                                              08-JUL-1999;
11-JAN-2000;
                                                                                                                                                                                                                                                           07-JUL-2000; | 2000EP-0114090.
                                                                                                                                                                                                                                                                                             10-JAN-2001
                                                                                                                                                                                                                                                                                                                           EP1067182-A2
                                                                                                                                                                                                                                                                                                                                                                                         Human; secretory protein; membrane protein; vaccine; rheumatoid arthritis; diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Human membrane or secretory protein clone PSEC0233.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB88448 standard; Protein; 267 AA
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                                                                                                                               Isogai T,
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2000JP-0118775.
2000JP-0183766.
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                                                                                                                                                               RES INST
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Pred. No. 3.7e-7
ROM; English.
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                                                                                                                            Hayashi K;
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directed against the proteins,

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sequences, which can be used in vaccines. The polynucleotide sequences

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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (e.g. polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples. They may also be used to study the expression and function of secretory proteins/membrane polypeptides and their role in metabolism. The polypeptides may be used as antigens in the production of antibodies against them and in assays to identify modulators (agonists and antagonists) of expression and activity. The antibodies and antagonists may also be used as therapeutic agents to down regulate expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of the polypeptides in samples (e.g. by enzyme linked immunosorbant assay (ELISA). Examples of diseases which may be treated include rheumatoid
diabetes mellitus; arrhythmia; wound healing; ischaemic lesion; AIDS; Acquired Immune Deficiency Syndrome; virucide; hepatotropic; vasotrop autoimmune disorder; inflammation; cardiovascular disorder; hair loss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnosis of diseases associated with inappropriate secretory protein/membrane protein expression. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays
                                                                                                       Human; immune system-related protein; allergy; rheumatoid arthritis;
                                                                                                                                                      Human gene 12 encoded immune system-related protein HADEX14.
                                                                                                                                                                                                         18-DEC-2001 (first entry)
                                                                                                                                                                                                                                                              AAE10920
                                                                                                                                                                                                                                                                                                           AAE10920 standard; Protein; 204 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                can be used in gene therapy. The polynucleotide sequences and the
                                                                                  cancer; Gaucher's disease; viral hepatitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                     241 rpppsqvhshcrpmpv--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 lqaqvvlsfqayptarcvllevqvpaalvqfgqsvgsvvydcfeaalgsevriwsytqpr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 LQAQVVLSFQAYPIARCALLEVQVPADLVQPGQSVGSAVFDCFEASLGAEVQIWSYTKPR 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       228 GPQNITL-NHTDLVPCLCIQVWSLEPDSERVEFCPFREDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    177 YQKELNLTQQLP-----DGDNYLLTLDVSEEQDFSFLLYLRPYPDALKSLWYKNLT 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lapthlqtelvlrcqketdcdlclrvavhlavhghweepedeekfggaadsgveeprnas 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          267 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                          gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 267;
                                                                          cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27;
  hair loss;
                             vasotropic;
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lomo sapiens food preservative.

)Omain

omain

/label= Immunogenic_epitope 151..168

168

Immunogenic_epitope

ocation/Qualifiers

wound healing; cell proliferation; skin aging; endocrine disorder;

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disorders, autoimmune disorders (Theumatola aluminus, automatory disorders (allergies), immunodeficiencies (AIDS), inflammatory disorders (conserved disorders), infectious diseases (e.g., viral hepatitis), complement continuity disorders (allergies), infectious diseases (e.g., viral hepatitis), complement continuity disorders (activation disorders diseases, neoplastic disorders (cancer), hyperproliferative disorders (Gaucher's disease), disorders (cassociated with neovascularisation, diseases at the cellular level, cassociated with neovascularisation, wound healing and epithelial cell proliferation, endocrine disorders (diabetes mellitus) and cell proliferation, endocrine disorders (diabetes mellitus) and cell proliferation disorders (diabetes mellitus) and consumption of the proventing hair loss, skin aging due to sunburn, to modulate mammalian characteristics, to change a mammal's mental or complysical state, or as a food additive or preservative. Immune-system celated DNA is useful in gene therapy, for chromosome identification, to tradiation hybrid mapping, long range restriction mapping and in forensic radiation hybrid mapping, long range restriction mapping and in forensic
   AAY76048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 122; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to human immune system-related protein and their DNA. Human immune-system related protein and DNA are useful for preventing, treating on ameliorating a medical condition in a mammalian subject, for diagnosing, preventing or treating immune system-associated disorders, autoimmune disorders (rheumatoid arthritis), inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated immune system-related polypeptide useful for treating rheumatoid arthritis, AIDS, allergy, cancer, Gaucher's disease, diabetes mellitus, arrhythmia, wound healing, ischemic lesions and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-MAR-2000;
11-AUG-2000;
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AAY76048 standard; Protein; 617 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           477 LLHSADGAGYERLVGALASALSOMPLRVAVDLWSRRELSAHGALAWFHHQRRRILQEGGV 536
                                                                                                                                                                       181 hppgtpapg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
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                                                                                                                                                                                                                                                                                                                           Hilbert D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAD18278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Endress GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-187873P.
2000US-224367P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16.4%; Score 591.5; DB 22; 64.6%; Pred. No. 1e-47; tive 21; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ruben SM;
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                                                                                                                                                                                                                                                                                                                                                                                                        cancer cells, to modulate angiogenesis and tumour vascularisation, to modulate skin inflammation, to modulate epithelial cell growth and to inhibit binding of HIV-I to leukocytes. The invention may also be used to treat growth and developmental defects, skin wounds and hair follicle disorders. Sequences AAY75942-Y76133 represent polypeptides encoded by cDNA sequences derived from several mouse, rat or human skin cell types. Sequences AAY75942-Y75947, AAY76020-Y76021, AAY76094-Y76104 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Skin; dermal papilla; keratinocyte; neonatal foreskin fibroblast; embryonic skin cell; keratinocyte stem cell; transit amplifying cell secreted; transmembrane; inflammation; cancer; neurological disease; angiogenesis; tumour vascularisation; growth disorder; developmental disorder; skin wound; hair follicle disorder;
                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                     AAY76119 are proteins with an N-terminal signal sequence, indicatin that they are secreted. Sequences AAY75986-Y75989, AAY76061-Y76071, AAY76106-Y76109 and AAY76121-Y76122 are proteins with one or more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and mouse embryonic skin, keratinocyte stem cells and transit amplifying cells. Polypeptides of the invention may be used to treat inflammation, cancer and neurological diseases. The proteins may be used to stimulate the growth and motility of keratinocytes, to inhibit the growth of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dermai papilla, human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel polynucleotides useful for the treatment of various including wounds and cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-APR-1998;
09-NOV-1998;
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                                                                     qhnqmvmaltlrcplkleaslcwrqdpltpcetl----pnataqesegwyilenvdlh
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pqlcfkfs-fensshvecphqsgslpswtvsmdt-qaqqltlhfssrtyatfsaawsdpg
                                        PNLCVQVSTWEKVQLQAC--
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                                                                                                                                                                                                                                                                                                                                              transmembrane domains
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98US-0188930.
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                                                                                                                                                                                                                                     8.6%;
25.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to novel nucleic acid sequences derived from rat
keratinocytes and neonatal foreskin fibroblasts,
kin, keratinocyte stem cells and transit amplifying
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                                                                                                                                                                                                               Score 310.5; DB 21.
Pred. No. 3.1e-20;
5; Mismatches 208;
                                  -SWADSLGPFKDDMLLVEMKTGLNNTSVCALEPSG
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RESULT 14
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                                The present sequence is a polypeptide which is expressed in mammalian skin cells. The polypeptide is useful for stimulating keratinocyte growth and motility, inhibiting the growth of cancer cells, modulating angiogenesis, inhibiting angiogenesis and vascularisation of tumours, modulating skin inflammation, stimulating the growth of epithelial cells, inhibiting the binding of human immunodeficiency virus (HIV)-1 to leukocytes, and treating inflammatory disease, cancer and neurological diseases. The polynucleotide can be used as a marker, in the identification of genetic disorders, and for the design of
                                                                                                                                                                                       New isolated polynucleotide used in the ident disorders and encoding polypeptides used for disease, cancer and neurological diseases.
                          oligonucleotides
                                                                                                                                                                                   Claim 4; Page
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                                                                                                                                                                                                                                                                                   WPI; 2001-007495/01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nootropic; | neuroprotective; vulnerary; is
keratinocyte growth stimulation; cancer;
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                        expression
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                                                                                                                                                                                                                                                                                                                            Human; Interleukin-17 receptor; IL-17RH3; agonist; antagonist; PRO9877; DNA 119502-2789; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; diabetes mellitus;
                                         Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                494 ASALSOM----PLRVAVDLWSRRELSAHGALAWFHHORRRILQEGGVVILLFSPAAVAQCQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         441 WVLV-----WLACLLLAAALFFFLLLKKDRRKAARGSRTALLLHSADGAGYERLVGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   283 PG---VWQLDAPCCLPGKVTLCWQAPDQSPCQPLVPPVPQKNATVNEPQDFQLVAG---H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183 kivsgghtvdlpyefllpcmcieasylqedtvrrkkcpfqswpeaygsdfwqsirftdys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                224 KNLTGPQNITLNHTDLVPCLCIQVWSLEPDSERVEFCPFREDPGAH-RNLWHIARLRVLS 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SLPTQLPAFLDALQGGCSTSA-----GRPADRVERVTQA----LRSALDSCTSSSEAP 659
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/note= "17....
347..351
/note= "Asn is N-glycosylated"
                                                                                                /note= "cAMP/GMP-dependent protein kinase
phosphorylation site"
318..322
                                                                                                                                                                                                                              Location/Qualifiers 1..23
                                                                                                                                          /note= "N-myristoylation site"
                                                                                  /note-
                                                                                                                                                                                  /label= Mature_IL_17RH3
                                                                                                                                                                                                               /label Signal_peptide
                                                                      22..329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.6%;
25.7%;
                                                                                "Asn is N-glycosylated
                                                   "Tyrosine kinase phosphorylation site"
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Pred. No. 3.1e-20;
                                                                                                                                                                                                                                                                                                                                                                                           IL-17RH3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches 208;
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      Query Match
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Gurney ;
                                                                                                                                                                                                                                                                   containing
                                                                                                                                                                                                                                                                                                                              Claim 10;
                                                                                                                                                                                                                                                                                                                                                         arthritis
                                                                                                                                                                                                                                                                                                                                                                       diagnosis
                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Watanabe CK,
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28-NOV-2000;
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degenerative cartilaginous disorder comprises administering a PRO1031 PRO1122 polypeptide agonist, or antagonist to the mammal. Numerous examples of the diseases and disorders are given in the specification.
                                                                                                                                                                                                                                                                                                         are useful for treating a mammal with an immune related disease, e systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis; juvenile chronic arthritis, a spondylogathropathy, systemic sclerosidiopathic inflammatory myopathy, Sjogren's syndrome, systemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence is PRO9877 which is the human Interleukin 17 receptor, IL-17RH3, encoded by DNA 119502-2789. A composition
                                                                                                                                       hypersensitivity, asthma, a transplantation associated disease, or a chronic inflammatory demyelinating polyneuropathy. Treating a
                                                                                                                                                                                                vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes melatus, immune-mediated disease, a demyelinating disease, an autoimmune or immune-mediated disease, contact dermatitis, an allergic disease e.g. food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAS09516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001 451708/48
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Li H, Hillan KJ, Tumas D, Van Look

CK, Williams PM, Wood WI, Yansura DG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polypeptides homologous to interleukin-17, useful for the and treatment of immune related disease e.g. rheumatoid and diabetes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fig 16; 188pp;
                                                                                                                                                                                                                                                                                                                                                                                                                           encoded by DNA 119502-2789. A composition ant/agonists to the PRO polypeptides or individual components
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/note= "Eukaryotic cobalbumin-binding
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phosphorylation site"
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fumas D, Van Lookeren M,
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2: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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US-09-022-253-10
US-09-022-259-10
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US-09-022-259-10
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US-09-188-930-125
US-09-188-930-125
US-08-444-5318-28
US-08-4488-546A-28
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US-09-188-930-30
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 303
LENGTH: 617
TYPE: PRT
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Best Local Similarity
Matches 123; Conserv
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Onrust, Rene
TITLE OF INVENTION: Compositions Isolated
TITLE OF INVENTION: and Methods For Their
FILE REFERENCE: 11000.1011c1
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              494 ASALSOM --- PLRVAVDLWSRRELSAHGALAWFHHORRRILQEGGVVILLESPAAVAQCO 550
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                                                                                                                                                                                                               337 PNLCVQVSTWEKVQLQAC------SWADSLGPEKDDMLLVEMKTGLNNTSVCALEPSG
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                                                                                     WVLV--
                                                                                                                                                   C---TPLPSMASTRAARLGEELLQD-----FRSHQCMQLWNDDNMGSLWACPMDKYIHRR 440
                                                  WKHVLCPDDAPYPTQLLL-------RSLGSGRTRPVLLLHAADSEAQRRLVGAL
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                                                                                  ---WLACLLLAAALFFFLLLKKDRRKAARGSRTALLLHSADGAGYERLVGAL 493
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US-09-261-907-2
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KNLTGPQNITLNSER 256	Query Match 4.6%; Score 167; DB 2; Length 864; Best Local Similarity 20.3%; Pred. No. 1.1e-08; Matches 105; Conservative 62; Mismatches 167; Indels 184; Gaps 25;	TELECOMMUNICATION INFORMATIO TELEPHONE: (206)587-0430 TELEPAX: (206) INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 864 amino acids TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: protein 08-620-694A-2	FICATION: 435 PLICATION DATA: ATION NUMBER: USSN 08/41 PLICATION 08/41 PLICATION: 435 PLICATION: 435 PACHICLE ANNE PERKINS, PARTICLA ANNE PERKINS, PARTICLA ANNE PARTICUMBER: 34,695 NOS TOWNER: 34,695	CATION NUMBER G DATE: 21 P IFICATION: (PPLICATION D) CATION NUMBER G DATE: 7 AN	STATE: WAS COUNTRY: USA COUNTRY: USA ZIP: 98101 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: Apple Power Macintosh OPERATING SYSTEM: Apple Operating System 7.5.5 SOFTWARE: Microsoft Word for Apple, Version 6.0.1 CURRENT APPLICATION DATA:	SULT 2 108-620-694A-2 108-620-694A-2 sequence 2. Application US/08620694A patent No. 5869286 GENERAL INFORMATION: APPLICANT: Yao, Zhengbin APPLICANT: Spriggs, Melanie APPLICANT: Forslow, William TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17 NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS: ADDRESSEE: Immunex Corporation STREET: 51 University Street	449 AELLRTALGGGRDVIVDLWEGTHVARIGPLPWLWAARERVAREQGTVLLLWNCAGPS 505 551 QWLQLQTVEPGPHDALAAWLSCVLPDFLQGRATGRYVGVYFDGLLHPDSVPSPFRVAPLF 610

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RESULT 3
US-09-022-255-1
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Patent No.
INFORMATION FOR SEQ ID NO:
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER! Apple Power Macintosh

OPERATING SYSTEM: Apple Operating System 7.5.5

SOFTWARE! Microsoft Word for Apple, Version 6.(

CURRENT APPLICATION DATA:

CURRENT APPLICATION UMBER: US/09/022,255
                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (206)587-0430
                                                                                                                                    FILING DATE: 23 MARCH 19
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: | D. SPATTIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   491 PDFKRPACFGTYVVCYFSGICSERDVPDLFNITSRYPL 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              575 PDFLQGRATGRYVGVYFDGLLHPDSVPSPFRVAPLFSL 612
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                                                     REFERENCE/DOCKET NUMBER: 261
                                                                                                                                                                                                                                    APPLICATION NUMBER: USSN 08/620,694
FILING DATE: 21 MARCH 1996
APPLICATION NUMBER: USSN 08/538,765
                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                     FILING DATE:
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                                                                                                               Perkins, Patricia Anne
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Fanslow, William
VENTION: No. 6072033el Receptor That Binds IL-17
                      (206)
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                                                                                                                                                                                                                     7 AUGUST 1995
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S-09-022-696-2
Sequence 2, Application
Patent No. 6072037
GENEEAL INFORMATION:
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1S-09-022-255-2
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est Local Similarity
                                                                                                         COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
OPERATING SYSTEM: Apple Operating System 6.0.1
                                                                                                                                                                                                                                                                                                                                 APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6072037el
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                 SOFTWARE: MICROSOFT WORD for Apple, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,696
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    438 MVESNSKIIILCSRGTQAKWKAILGWAEPAVQLRCDHW-----KPA-GDLFTAAMNMIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            257 -- VEFCPFREDPGAHRNLWHIARLR-VLSPG-----VWQLDAPCCLPGKVTLCWQAPDQ 307
                                                                                                                                                                                                                         COUNTRY: UZIP: 98101
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                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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51 University Street
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RESULT 5
US-08-978-773-2
Sequence 2, Application US/08978773
Patent No. 6083906
GENERAL INFORMATION:
APPLICANT: Troutt, Anthony
TITLE OF INVENTION: Method of Re-
NUMBER OF SEQUENCES: 4
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Best Local Similarity 20.3%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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NAME: Perkins, Patricia Ann
REGISTRATION NUMBER: 34,695
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APPLICATION NUMBER: US
FILING DATE: 23 MARCH
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                                                                                                                                                                                                                                                     575 PDFLQGRATGRYVGVYFDGLLHPDSVPSPFRVAPLFSb-6T2
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                                                                                                                                                                                                                             PDFKRPACFGTYVVCYFSGICSERDVPDLFNITSRYPL 528
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Method of Regulating Nitric Oxide Production
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Gaps

25;

171

--PVADY 318

287 386 230

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Othery Match: 4.6
Best Local Similarity 20.3
Matches 105; Conservative
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8-978-773-2
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                                                                                530
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575 PDFLQGRATGRYVGVYFDGLLHPDSVPSPFRVAPLFSL 612
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                                                                                                                                                                                                                                                                                                               387
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                                                                                                                                                                                                                                                                        288 SSCLNDCLRHAVTVPCPVISNTTVPK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 KNLTPSSPKNIYINLSVSSTQHGELVPVLHVE-WTLQTDASILYLEGAELSVLQLNTNER 124
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OPERATING SYSTEM: Apple Operat
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CITY: Seattle
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                                                                                                             RPRKVWIVYSADHPLYVEVVLKFAQFLITACGTEVALDLLEEQVISEVGVMTWVSRQKQE 437
                                                                                                                                                 --RTALLLHSADGAGYERLVGALASAL-SQMPLRVAVDLWSRRELSAHGALAWFHHQRRR 529
                                                                                                                                                                                       I-PLWVYGLITLIAILLVGSVIVLIICMTWRLSGADQEKHGDDSKINGILPVADLTPPPL
                                    MVESNSKIIILCSRGTQAKWKAILGWAEPAVQLRCDHW-----KPA-GDLFTAAMNMIL
                                                                                                                                                                                                                                  IHRRWV--LVWLACLLLAAALFFFL--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      864 amino acids
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27 NOVEMBER 1996
                                                                                                                                                                                                                                                                                                           --TPLPSMASTRAARLGEELLQDFRSHQCMQLWNDDNMGSLWACPMDKY 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Apple Operating System 7.5.5 ft Word for PowerMacintosh, V
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Pred. No. 1.1e-08;
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                                                                          PAAVAQCQQWLQLQTVEPGPHDALAAWLSCVL
                                                                                                                                                                                                                                  --LLKKDRRKAARGS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 864;
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                                                                                                                                                                                                                                                                                                                                                                                     ----CA----LEP-- 386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --- IPDG 171
                                                                                                                                                                                                                                                                    -PVADY 318
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Best Local Similarity
                                                                                                                                                                                                                                        Matches 105;
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APPLICANT: Yao, 2
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/620,694
FILING DATE: 21-MARCH-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: USSN 0
FILING DATE: 23 MARCH 1995
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                                   172
                                                                    308
                                                                                                                               257 --VEFCPFREDPGAHRNLWHIARLR-VLSPG-----VWQLDAPCCLPGKVTLCWQAPDQ 307
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364 KDDMLLVEMKTGLNNTSV-
                                                                                                                                                                APPLICATION NUMBER: FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Perkins, Patricia Anne REGISTRATION NUMBER: 34,695
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: USSN 0 FILING DATE: 7 AUGUST 1995
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                               DPNHKSKIIFVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNEST-PY
                                                                    SPCQP-
                                                                                                 LCVKF-QFLSMLQHHRKRWRFSFSHFVVDPGQEYEVTVHHLPKP
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                                                               -LVPPVPQKNATVNEPQDFQLVAGHPNLCVQVSTWEKVQLQACSWADSLGPF 363
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                                                                                                                                                                                                                                                     4.6%;
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                                                                                                                                                                                                                                ; Score 167; DB 3; Length 864;
; Pred. No. Lae-08;
62; Mismatches 167; Indels 184; Gaps
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--LEP-- 386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENERAL INFORMATION:
                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 864 amino acids
TYPE: amino acid
                                                                                                                          FORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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                                                         TOPOLOGY:
                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                     NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 23 MA
                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
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                           ULE TYPE:
260-2
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51 University Street
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Fanslow, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SYSTEM: Apple Operating System 7.5.5
Microsoft Word for Apple, Version 6.
                                                                                                                                                         (206)587-0430
                                       protein
                                                                                                                                                                                                                                                                            23 MARCH 1995
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US-09-022-259-2
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Matches
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Best Local Similarity
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                                                                                      438 MVESNSKIIILCSRGTQAKWKAILGWAEPAVQLRCDHW-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  308 SPCQP ----LVPPVPQKNATVNEPQDFQLVAGHPNLCVQVSTWEKVQLQACSWADSLGPF 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125 LCVKF QFLSMLQHHRKRWRFSFSHFVVDPGQEYEVTVHHLPKP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    257 -- VEFCPFREDPGAHRNLWHIARLR-VLSPG------ VWQLDAPCCLPGKVTLCWQAPDQ 307
PDFKRPACEGTYVVCYFSGICSERDVPDLFNITSRYPL 528
                                        PDFLQGRATGRYVGVYFDGLLHPDSVPSPFRVAPLFSL 612
                                                                                                                              ILQEGGVVILLES----
                                                                                                                                                                                                                                                           I-PLWYGLITLIAILLYGSVIVLIICMTWRLSGADQEKHGDDSKINGILPVADLTPPPL
                                                                                                                                                                                                                                                                                                                                                    SSCLNDCLRHAVTVPCPVISNTTVPK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DPNHKSKIIFVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNEST-PY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KNLTPSSPKNIYINLSVSSTQHGELVPVLHVE-WTLQTDASILYLEGAELSVLQLNTNER 124
                                                                                                                                                                                                                --RTALLLHSADGAGYERLVGALASAL-SQMPLRVAVDLWSRRELSAHGALAWFHHQRRR 529
                                                                                                                                                                                                                                                                                                      IHRRWV -- LVWLACLLLAAALFFFL-----LLKKDRRKAARGS--
                                                                                                                                                                                                                                                                                                                                                                                               SGC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                          --TPLPSMASTRAARLGEELLODFRSHOCMOLWNDDNMGSLWACPMDKY 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.6%; Score 167; DB 3;
20.3%; Pred. No. 1.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                            -PAAVAQCQQWLQLQTVEPGPHDALAAWLSCVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 864;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -CA----LEP--
                                                                                                                                                                                                                                                                                                                                                 -PVADY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --IPDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -SER 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                      490
                                                                                                                                                                       437
                                                                                                                                                                                                                                                           377
                                                                                                                                                                                                                                                                                                      472
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Sequence 2, Applic Patent No. 6191104 GENERAL INFORMATION: APPLICANT: | YAO, AMENUAL APPLICANT: | Spriggs, Melanie | APPLICANT: | Fanslow, William | ADDRESSEE Application US/09022259 Immunex Corporation
51 University Street

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy STREET: 51 Uni COUNTRY: 98101 WA USA Floppy disk

ř

COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA: CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: APPLICATION NUMBER: FILING DATE: us/09/022,259

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SOULT 9
09-022-257-2
Sequence 2, Application US/09022257
Patent No. 6197525
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 4.6%;
Best Local Similarity 20.3%;
Matches 105; Conservative 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: protein 09-022-259-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                           575
                                                                                                                                                                                                                                                                                                                                                                                                                            438 MVESNSKIIILCSRGTQAKWKAILGWAEPAVQLRCDHW-----KPA-GDLFTAAMNMIL 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     378 RPRKVWIVYSADHPLIVEVVLKFAQFLITACGTEVALDLLEEQVISEVGVMTWVSRQKQE 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 473 --RTALLLHSADGAGYERLVGALASAL-SQMPLRVAVDLWSRRELSAHGALAWFHHQRRR 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             319 I-PLWYYGLITLIAILLYGSVIVLIICMTWRLSGADQEKHGDDSKINGILPVADLTPPPL 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 864 amino acids
                                                                                                                                                                                                                                                                                                                                       491 PDFKRPACFGTYVVCYFSGICSERDVPDLFNITSRYPL 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               530 ILQEGGVVILLFS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          437 IHRRWY--LVWLACLLLAAALFFFL-----LLKKDRRKAARGS--
                                             TITLE OF INVENTION: NO DUMBER OF SEQUENCES: 10 ORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             288 SSCLNDCLRHAVTVPCPVISNTTVPK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                387 SGC-----TPLPSMASTRAARLGEELLQDFRSHQCMQLWNDDNMGSLWACPMDKY 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              231 Q---VILLESFSDSENHSCFDVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFF 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      172 DPNHKSKIIFVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNEST-PY 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 308 SPCQP----LVPPVPQKNATVNEPQDFQLVAGHPNLCVQVSTWEKVQLQACSWADSLGPF 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125 LCVKF-QFLSMLQHHRKRWRFSFSHFVVDPGQEYEVTVHHLPKP------IPDG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         257 --VEFCPFREDPGAHRNLWHIARLR-VLSPG-----VWQLDAPCCLPGKVTLCWQAPDQ 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        224 KNLT--GPQNITLN------HTDLVPCLCIQVWSLEPD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     364 KDDMLLVEMKTGLNNTSV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia
  ADDRESSEE:
STREET: 5
                                                                                                                                                             PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 KNLTPSSPKNIYINLSVSSTOHGELVPVLHVE-WTLQTDASILYLEGAELSVLQLNTNER 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Perkins, Patricia Ann
REGISTRATION NUMBER: 34,695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                    PDFLQGRATGRYVGVYFDGLLHPDSVPSPFRVAPLFSL 612
E: Immunex Corporation
51 University Street
                                                                                                             Spriggs, Melanie
Fanslow, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (206)
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                                                                                                                                                           Zhengbin
                                                                                     6197525el Receptor That Binds IL-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 167; DB 4;
; Pred. No. 1.1e-08;
62; Mismatches 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----PAAVAQCQQWLQLQTVEPGPHDALAAWLSCVL 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2617-в
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 864;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 184; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----SER 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---CA----LEP-- 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---PVADY 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             472
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\$2.00 \$2.0
160 226 207 207 271 248 331 365 266 385 296 445 385 296 4480 387 480 387 480 539 539 539 539 539 539 539 539 539 539
226 207 207 207 207 208 248 331 331 345 266 445 385 296 4480 387 480 387 480 539 539 539 539 539 539 539 539 539 539

12

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Query Match
Best Local Similarity
Matches 142; Conserv
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SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein 19-022-255-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                            445 YLCSRGTRAKWQALLGRGAPVRLRCDHGKPVGDLFTAAMMILPDFKRPACFGTYVVCYF
                                                                                                                                                                                                                                                                                                                                 480
                                                                                                                                                                                                                                                                                                                                                                                 327
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NAME: Perkins, Patricia
555 GDNYLRSPGGRQLRAALD 572
                                                                                  505 SEVSCDGDVPDLFGAAPRYPLMDRFEEVYFRIQDLEMFQPG-
                                                                                                                              592 DGLLHPDSVPSPFRVAPLFSLPTQLPAF-----LDALQGGCSTSAGRPADRVERVTQ-- 643
                                                                                                                                                                                                                           539 LLFSPAAVAQCQQWL-----QLQTVEPGP-HDALAAWLSCVLPDFLQGRATGRYVGVYF 591
                                                                                                                                                                                                                                                                                     385
                                                                                                                                                                                                                                                                                                                                                                                                                    445 WLACLLLAAALFFFLLLKKDRRKAARGS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    296 RHSATVSCPEMPDT----PEPIPDY-----MPLW---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         385 EPSGCTPLPSMASTRAARLGEELLQDFRSHQCMQLWNDDNMGSLWACPMDKYIHRRWVLV 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     331 Q-----LVAGHPNLCVQVSTWEKVQLQACSWADSLGPFKDDMLLVEMKTGLNNTSVCAL 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  271 NLWHIARLRVLSPGVWQLDAPCCLPGKVTLCWQAPDQSPCQPLVPPVPQKNATVNEPQDF 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             248 НМННІ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            226 LTGPQNITLNHTDLVPCLCIQVWSLEPDSERVEFC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160 TVHHLPKPIPDGD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 --- NLTQQLPDGDNVLLTLDVSEEQDFSFLLYLRPVPD------ALKSLWYKN 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104 ----ASILYLEGAELSVLQLNTNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEV 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 EAGKSDSELQESRNASLQAQVVLSF----QAYPIARCALLEVQVPADLVQPGQSVGSAVF 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       157 DCFEASL----GAEVQI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55 SAPGP-----VLVP----TRIQTELVLRCPQKTDCALRVRVVVHLAVHGHWAEPE 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 AVPGPLLGLLLLLLGVLAPGGASLRLLDHRALVCSQP---GLNCTVKNSTCLDDSWIHPR 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                                                                                                    SADHPLYVDVVLKFAQFLLTACGTEVALDLLEEQAISEAGVMTWVGRQKQEMVESNSKII
                                                                                                                                                                                                                                                                                                                       SADGAGYERLYGALAS-ALSOMPLRVAYDLWSRRELSAHGALAWFHHORRRILQEGGVVI 538
                                                                                                                                                                                                                                                                                                                                                                     GISILLYGSVI--LLIVCHTWRLAGPGSEKYSDDTKYTDGLPAADLIPPPLKPRKVWIIY 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HORSNVTLTLRNLKGCCR----HOVQIQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----NLTPSSPKDLQIQLHFAHTQQGDLFPVAH---IEWTLQTD----
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                                              --ALRSALD 650
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19.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 151.5; DB 3; ; Pred. No. 5.4e-07; 73; Mismatches 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2617-в
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----PF-----FSSCLND----CL 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -PAPR-----PEEF 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 317; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 866;
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                                                                                     RMHRVGELS
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Db	QY .	물 5	Db Db	Qy	đ	Qy	DЪ	Qy	Quer Best Matc	0S-09	٠. ٠.	٠. ٠		 !			•• ••	••	٠. ٠.	٠		٠. ٠.	•••	٠. ٠.	•••		٠. ،		٠. ٠	٠.,	٠. ٠.		٠.		٠. ٠.	٠. ٠.	; pa	us-o
207	226	160	104	157	67	101	10	55	7 5	9-022-696-	MOLEC	TYPE:	SEQUE	INFORMATION	TEL	TELEC	REGIS	ATTOR	CLA	APPI	CLA	FIL	PRIOR	CLA	APP	CURRENT	OPE	MED	COMPUTER	COUN	STATE	STR	CORRE	TITLE (APPLI	APPLI	Patent No	09-022-6
I7	LTGPQNIT	: : : : TVHHLPKP	AS	DCFEASL		EAGKSD	AVPGPL	SAPGP-	Match .ocal Simi			1	QUENCE CH	RMATION F	TELEPHONE:	REFERENCE,	T R	ATTORNEY/AGENT	FILING DA CLASSIFIC	LICATI	SSIFIC	FILING DATE	•	FILING DATE: CLASSIFICATI	APPLICATION	SOFTWARE:	RATING	IUM TY	TER RE	TRY:	 El	ET:	GNO	R OF I	APPLICANT:	()	1, 10,	596-
-		HLPKPIPDGDPNHQSKNFLVPDC	ILYLEGA		-NLTPS	EAGKSDSELQESRNASLQAQVVLS			ilarity Conser	10	'n	amino acid		FOR SEO	(206	REFERENCE/DOCKET			FILING DATE: 23 CLASSIFICATION:	APPLICATION NUMBER:	CLASSIFICATION:	TE:	APPLICATION	FILING DATE: CLASSIFICATION:	ON NUM	APPLICATION DATA:	SYSTE	MEDIUM TYPE: Floppy	READABLE	USA	WA WA	51	•	SEQUENCES:	2	ANT: Yao, Z	Applicat 072037	:
	DLVPCLC)	ELSVIC	GAEVQI	SPKDLQ1	ADJSANS	TGVLAF	VLVP-	19. vative		ear protein	id	RISTICS	I NO	5)587-04	INFORMAT	S, Patricia NUMBER: 34	INFORMATION:	MARC)	DATE:		DATA:		NUMBER: (M: Api		FORM:		٠	University	SS			: Zhengbin	nor	
VETL	LNHTDLVPCLCIQVWSLEPDSERVEFC	OHNA	YLEGAELSVLQLNTNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEV		NLTPSSPKDLQIQLHFAHTQQGDLFPVAH-	12)	GGASLR		2%; 2%; 73			•		10.)587-0430	ER: 261	34,695		1 1995	USSN 08		08/620,			us/09/022,696	H	le :					Str		. 6072037e1	Melanie William	5	05/0902269	,
;	EPDSER	PNHOSKNEL-	LCVRFE	. !	TQQGDL	QA	LLDHRA	TRLQTELVLRCPÖRTDCALRVRVVVHLAVHGHWAEPE	Score 151 Pred. No. ; Mismat							17-в	O			/410,5		694	١		22,696	d for Apple	rating	+			•	eet	•				696	
/ VSFTLWN	VEFC	VPI	FLSKLRI		FPVAH-	QAYPIARCALLEVQVPADLVQPGQSVGSAVF	LVCSOP	LRCPOR	151.5; D No. 5.4e-									٠		35.							System		٠					Receptor	٠		·	
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                                                             TELEFAX: (206)
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple PowerMacintosh
OPERATING SYSTEM: Apple Operating System 7.5
SOFTWARE: Microsoft Word for PowerMacintosh,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENERAL INFORMATION: APPLICANT: Troutt
                                                                                                                                                                                                                                              CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                               EQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                               ELECOMMUNICATION INFORMATION
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FILING DATE: 27 NOVEMBER 1996
CLASSIFICATION: 530
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                                                                                                                             REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 26
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                                                                                               TELEPHONE:
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                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Seattle
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51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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                                                                                                 (206)587-0430
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                                                                                                                 Sequence 10, Appli
Patent No. 6096305
                                                                                               GENERAL INFORMATION:
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Best Local Similarity
                            APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6096
CORRESPONDENCE ADDRESS:
                 TUMBER OF SEQUENCES:
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                                                                                                                                  Application US/09022253
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Pred. No. 5.4e-07;
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                            Receptor That Binds IL-17
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PFILING DATE: 21-MARCH: 1996 APPLICATION NUMBER: USSN 08/538,765 FILING DATE: 7 AGGUST 1995 CLASSIFICATION NUMBER: USSN 08/410,535. PRIOR APPLICATION NUMBER: 34,695 APPLICATION NUMBER: 34,695 FILING DATE: 23 MARCH 1995 CLASSIFICATION NUMBER: 34,695 REFERENCE/DOCKET NUMBER: 36,695 REFERENCE/DOCKET NUMBER: 37,895 REFERENCE/DOCKET NUMBER: 36,695 REFERENCE/DOCKET NUMBER: 37,895 REFERENCE/DOCKET NUMBER: 36,695 REFERENCE/DOCKET NUMBER: 37,895 REFERENCE/DOCKET NUMBER: 36,695 REFEREN
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US-09-022-260-10 process
GY: 1in
; LENGTH: 866 amino acids
CHARACTERISTICS:
; INFORMATION FOR SEQ ID NO: 10:
; TELECOMMUNICATION INFORMATION:
TRATION NUMBER: 34,695
NAME: Perkins, Patricia Anne
0
FILING DATE: 23 MARCH 1995
TION DATA:
CLASSIFICATION:
PPLICATION NUMB
CATION DATA:
; FILING DATE:
APPLICATION NUMBER
SYSTEM: Apple Operating System 7.5.5
; MEDIUM TYPE: Floppy disk
₽,
; COUNTRY: USA
::
STREET: 51 University Street
Immunex Cor
NUMBER OF SEQUENCES: 10
OF INVENTION:
; APPLICANT: Spriggs, Melanie APPLICANT: Fanslow, William
CANT: Yao, Zhen
<u>.</u> °
equence 1
ESULT 15
Db 555 GDNYLRSPGGRQLRAALD 572
Db 505 SEVSCOGDVPDLFGAAPRYPLMDRFEEVYFRIQDLEMFQPGRMHRVGELS 554
QY 592 DGLLHPDSVPSPFRVAPLFSLPTQLPAFLDALQGGCSTSAGRPADRVERVTQ 643
LCSRGTRAKWQALLGRGAPVRLRCDHGKPVGDLFTAAMNMILP
Qy 539 LLFSPÅAVAQCQQWLQLQTVEPGP-HDALAAWLSCVLPDFLQGRATGRYVGVVF 591
Db 385 SADHPLYVDVYLKFAQFILTACGTEVALDLLEEQAISEAGVMTWVGRQKQEMVESNSKII 444
QY 480 SADGAĞYERLVGALAS-ALSQMPLRVAYDLMSRRELSAHGALAWFHHQRRRILQEGGVVI 538
Db 327 GISILLVGSVILLIVCMTWRLAGPGSEKYSDDTKYTDGLPAADLIPPPLKPRKVWIIY 384
QY 445 WLACLILAAALFFFLLLKKDRRKAARGSTALLH 479
Db 296 RHSATVSCPEMPDTPEPIPDYMPLWVYWPIT 326
QY 385 EPSGCTPLPSMASTRAARLGEELLQDFRSHQCMQLWNDDNMGSLWACPMDKYIHRRWVLV 444

Similarity 2; Conserv 3; Conserv 3; Conserv 3; Conserv 3; Conserv 4; SUSELQESRN 1 1 1 1 1 1 1 1 1 1	4 6 4 6 4 6 4	8 5	- AA	₽ ¥	- - - ₹	-a-k	0:≪-				
1.5; DB 3; Length 866; 1.5.4e-07; 1.5.4e-07; 1.5.4e-07; 1.5.4e-07; 1.6.4e-07; 1.7.5ches 206; Indels 317; Gaps 34; 2CPQKTDCALRVRVVVHLAVHGHWAEPE 100 1	Query Match 4.2%; Score 151.5; DB 3; Length 866; Best Local Similarity 19.2%; Pred. No. 5.4e-07; Matches 142; Conservative 73; Mismatches 206; Indels 317; Gaps 55 SAPGPVLVPTRLQTELVLRCPQKTDCALRVRVVVHLAVHGHWARPE 100 10 AVPGPLLGLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDDSWIHPR 66 101 EAGKSDSELQESRNASLQAQVVLSFQAYPIARCALLEVQVPADLVQPGQSVGSAVF 156 67NLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTD	NLTQQLPDGDNVLLTLDVSEEQDFSFLLYLRPVPDALKSLWYKN	LTGPQNITLNHTDLVPCLCIQVWSLEPDSERVEFCPFREDPGAHR	NLWHIARLRVLSPGVWQLDAPCCLPGKVTLCWQAPDQSPCQPLVPPVPQKNATVNEPQDE::	QLVAGHPNLCVQVSTWEKVQLQACSWADSLGPFKDDMLLVEMKTGLNNTSVCAL	EPSGCTPLPSMASTRAARLGEELLQDFRSHQCMQLWNDDNMGSLWACPMDKYIHRRWVLV	WLACLLAAALEFFLLLKKDRRKAARGSRTALLH:	SADGAGYERLVGALAS-ALSQMPLRVAVDLWSRRELSAHGALAWFHHQRRRILQEGGVVI	LLESPAAVAQCQQWLQLQTVEPGP-HDALAAWLSCVLPDFLQGRATGRYVGVYF	DGLLHPDSVPSPERVAPLESLPTQLPAFLDALQGGCSTSAGRPADRVERVTQ	GDNYLRSPGGRQLRAALD

rch completed: September 28, 2002, 19:40:27

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Maximum Match 100%
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Q9bx84 homo sapien
Q55775
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Q9y497 homo sapien
Q9ry89 deinococcus
Q94903 flaveria pr
Q9uj61 homo sapien
  Q9r612 agrobacteri
Q9pbh5 xylella fa
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Best Local Similarity 94.7%;
Matches 463; Conservative
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Strausberg R;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases
EMBL; BC004759; AAH04759.1; -
Hypothetical protein.
SEQUENCE 567 AA; 62798 MW; Claaab79E2006BlD CRC64;
                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 62.8 KDA PROTEIN.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Bukaryota; Metazoa; Rodentia; Sciurognathi; Muridae
                                                                                                                                                                                                                                                                                                                                                                                Q99J43
Q99J43;
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Q98SW6
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Q9VTY5
3 Q98ST1
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Q68870
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Q9UBZ5
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Q43297
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Q24495
                                                                                                                                                               0;
                                                                                                                                                            Score 2471; DB 11;
Pred. No. 7.3e-214;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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          DGDNVLLTLDVSEEQDFSFLLYLRPVPD
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Length 567;
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09n2h7 sus scrofa
096dn2 homo sapien
068870 hepatitis c
014775 homo sapien
09nsj3 homo sapien
092530 hepatitis c
092529 hepatitis c
094902 flaveria pr
09jkw7 mus musculu
09d2v7 mus musculu
091vb4 mus musculu
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Q9nxr9 homo sapien
Q9def4 xenopus lae
Q98sw6 xenopus lae
Q08907 mus musculu
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Q81258 hepatitis c
Q9vty5 drosophila
Q98st1 gallus gall
Q9u2s3 caenorhabdi
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Q9unc9 homo sapien
Q9ubz5 homo sapien
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Q24495 drosophila
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Best Local Similarity
Matches 339; Conserv
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01-JUN-2001
01-JUN-2001
01-DEC-2001
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SEQUENCE 538 AA; 59127 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE-ENDOMETRIAL ADENOCARCINOMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 59.1 KDA PROTEIN.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9BR97
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                                                                                                                                                                                                                 LQAQVVLSFQAYPIARCALLEVQVPADLVQPGQSVGSAVFDCFEASLGAEVQIWSYTKPR
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                                                                                                                                                                                                                                                                                                                                                                     MPVSWFLLSLALGRNPVVVSLERLMEPQDTARCSLGLSCHLWDGDVLCLPGSLQSAPGPV 60
LDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSE
                 LDAPCCLPGKYTLCWQAPDQSPCQPLYPPYPQKNATYNEPQDFQLVAGHPNLCVQVSTWE
                                                                                 GPQNITLNHTDLVPCLCIQVWSLEPDSERVEFCPFREDPGAHRNLWHIARLRVLSPGVWQ
                                                                                                                                                     YQKELNLTQQLP-----DGDNVLLTLDVSEEQDFSFLLYLRPVPDALKSLWYKNLT
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                                                               GPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWL
                                                                                                                               YEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLT
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Pred. No. 6.5;
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01-NOV-1996
01-DEC-2001
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Immunity 3:811-821(1995).
EMBL; U31993; AAC52357.1; -.
MGD; MGI:107399; I117r.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
MCBI_TaxID=|0090;
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RPRKVWINYSADHPLYVEVVLKFAQFLITACGTEVALDLLEEQVISEVGVMTWVSRQKQE 437
                                    --RTALLLHSADGAGYERLYGALASAL-SQMPLRVAVDLWSRRELSAHGALAWFHHQRRR 529
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Last annotation update)
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Pred. No. 4.3e-06;
2; Mismatches 167;
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SHOCMOLWNDDNMGSLWACPMDKYIHRRWVLV	271 NLWHIARLRVLSPGVWQLDAPCCLPGKVTLCWQAPDQSPCQPLVPPVPQKNATVNEPQDF 330 ::	ASILYLEGAELSVLQLNTNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDDDQEYEVNLTQQLPLDGAELSVLQLNTNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDDDQEYEV	101 EAGKSDSELQESRNASLQAQVVLSFQAYPIARCALLEVQVPADLVQPGQSVGSAVF 156 67NLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTD	Ouery Match 4.2%; Score 151.5; DB 4; Length 866; Best Local Similarity 19.2%; Pred. No. 0.00011; Best Local Similarity 19.2%;	v; 88AF626A83F3FF70 CRC64	Eukaryola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606; [1] SEQUENCE FROM N.A. MEDLINE-9803583; PubMed=9367539; MEDLINE-9803583; PubMed=9367539; Yao Z., Spriggs M.K., Derry J.M.J., Strockbine L., Park L.S., VandenBos T., Zappone J., Painter S.L., Armitage R.J.; "Molecular characterization of the human interleukin (II)-17	PRSULT 4 A 3844 PRELIMINARY; PRT; 866 AA. C 043844; PRELIMINARY; PRT; 866 AA. C 04	530 ILQEGGVVILLES
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HMHHI	182NLTQQLPDGDNVLLTLDVSEEQDFSFLLYLREVPD	EAGKSDSELQESRNASLQAQVVLSFQAYPIARCALLEVQVPADLVQPGQSVGSAVF	Best Local Similarity 19.2%; Pred. No. 0.00011; Matches 142; Conservative 73; Mismatches 206; Indels 317; Gaps 75 SAPGP	Etted (JUL-2001) to the BC011624; AAH11624.1; ttor. 866 AA; 96131 A	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID-9606; [1] SEQUENCE FROM N.A. TISSUE-GTERUS, AND LEIOMYOSARCOMA;	5 36F46; 96F46; 1-DEC-2001 1-DEC-2001 1-DEC-2001 1-DEC-2001 1-DEC-2001 1-DEC-2001	592 DGLLHPDSYPSPFRYAPLFSLPTQLPAFLDALQGGCSTSAGRPADRYERYTQ 643 505 SEVSCDGDVPDLFGAAPRYPLMDRFEEVYFRIQDLEMFQPGRMHRVGELS 554 644ALRSALD 650 11:11 555 GDNYLRSPGGRQLRAALD 572	480 SADGAGYERLVGALAS-ALSQMPLRVAVDLWSRRELSAHGALAWFHHQRRRILQEGGVVI 538

	90 LAVHGHWAEPEEAGKSDSELQESRNASLQAQVVLSFQAYPIARCALLEVQVPADL 144 : :	_o_4
33;	uery Match 3.2%; Score 114.5; DB 16; Length 1013; est Local Similarity 20:4%; Pred. No. 0.28; etches 143; Conservative 75; Mismatches 232; Indels 251; Gaps	¥ 8 5
	SMART; SM00487; DEXDC; 1. SMART; SM00490; HELICC; 1. ATP-binding; Complete proteome; Helicase. SEQUENCE 1013 AA; 111629 MW; 601FDF1DB5CA8EF1 CRC64;	
	InterPro; IPR001410; DEAD. InterPro; IPR001650; Helicase_C. InterPro; IPR00135; SNF2_N. Pfam; PF00271; helicase_C; 1. Pfam; PF00176; SNF2_N; 1.	א'א א א'יא
	93:537-544(1998) LARITY: TO HELIC 021924; CAA17284 ist: Rv2101: -	א'א'ח'די
	kelton S., Squares S., Squares R., Whitehead S., Barrell B.G.; y of Mycobacterium tuberculosis from t	H-H D.P
	R., Devlin K., Feltwell T., Gentles S., Hamlin N., Y T., Jagels K., Krogh A., McLean J., Moule S., Murp S., Osborne J., Quail M.A., Rajandream M.A., Rogers	ששש
•	· H 7	アットで
	Mycobacterium tuberculosis, Mycobacterium tuberculosis, Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium, NCBI_TaxID=1773; [1] SEQUENCE FROM N.A.	\$2×000
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                                                                                                                                                                                                                                                                       Q9BX84;
01-JUN-2001
01-JUN-2001
01-OCT-2001
Ryazanova L.V., Pavur K.S., Petrov A.N., "Novel type of signaling molecules: prote to ion channels.";
                                                                                                                       MEDLINE-99147092; PubMed=10021370;
Ryazanov A.G., Pavur K.S., Dorovko
                                        TISSUE-KIDNEY;
                                                                     Curr. Biol.
                                                                                             "Alpha-kinases: a new class of protein kinases with a novel catalytic domain.";
                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
                                                                                                                                                                                                                                                       01-JUN-2001 (Tremblrel. 17,
01-JUN-2001 (Tremblrel. 17,
01-OCT-2001 (Tremblrel. 18,
CHANNEL-KINASE 2.
                                                                                                                      Ryazanov A.G.,
                                                                                                                                                  TISSUE-KIDNEY;
                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                         NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              KPTGRKTTAEILALAASHPDDVDTPLEVTAV-----RADGWLGDLLAGAAAASLQPLDPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QWLQLQTVE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IHRRWV|----LVWLACLLLAAALFFFLLLKKDRRKAARGSRTALLLHSADGAGYERLVGA 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VCALEPSGCTPLPSMASTRAARLGEELLQDFRSHQCM----QLWNDDNMGSLWACPMDKY 436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --RRWLDRPQELLLTELGRASRIFPELV-----PALRTACPSGLELDADGA--YRFLSG
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                                                                                9:R43-R45(1999).
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                                                                                                                                                                                                     Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----PGPHDALAAWLSCVLP----
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                                                                                                                       Dorovkov M.V.;
                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                             Craniata; Vertebrata; I
Catarrhinia Hominidae;
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             A.N., Dorovkov M.V., Ryazanov A.G., protein kinases covalently linked
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                                                                                                                                                                                                                  Euteleostomi;
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Hest Local Similarity 19.6
                                             055225;
01-JUN-1998 (
01-JUN-1998)
01-DEC-2001
   Mus musculus (Mouse)
Eukaryota; Metazoa;
                                      OTOGELIN
                                                                                           055225
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InterPro; IPR002111; Cat_channel_TrpL.
pfam; PF00020; ion_trans; 1.
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EMBL; AF350881; AAK31202.1; -.
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                                                                                                                                                                AAWLSCVLPDFLQGRATGRYYGYYFDGLLHPDSVPSPFRVAPLF 610
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                                                                                                                                                                                                                                                                                                                        SEEEYSKNWFTVSKFSHTGVEPYIHQ-KMKTKEIGQCAIQISDYLKQSHQDLSKNSLWNS
                                                                                                                                                                                        MDGGLRKAMRVVSTWSEDD---ILKPGQVFIVKSFLPEVVRTWHKIFQESTV-----
                                                                                                                                                                                                                                                                               RSTNLNRNSLLKSSIGVDKISASLKSPQEPHHHYSAI---
                                                                                                                                                                                                                                                                                                                                                                   ----VKAKMLT----KDRRLSKKKKNTQGLQVPIIT-----VNACSQSDQLNPEPGENSI 1607
                                                                                                                                                                                                                                                                                                                                                                                         LVPPVPQKNATVNEPQDFQLVAGHPN---LCVQVSTWEKVQLQACSWADSLGPFKDDMLL
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                                                                                                                                             ---LHLCLREIQQQRAAQKL--IYTFNQVKPQTIPYTPRELEVF
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                                              (TrEMBLrel.) (TrEMBLrel.) (TrEMBLrel.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2012 AA;
                                                                                          PRELIMINARY;
                                                                                                                                                                                                          -AWFHHQRRRILQEGGV-VILLFSPAAVAQCQQWLQLQTVEPGPHDAL
   Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             230493 MW;
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                                              90,
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                                          Last sequence update)
                                                                    Created)
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Pred. No. 1.
   Craniata;
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 Vertebrata;
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 Euteleostomi;
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Query Match 3.18;
Best Local Similarity 20.88;
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STRAIN-972H;
Lyne M., Rajandream M.A., Bu
Submitted (MAR-1998) to the
EMBL; AL022304; CAA18417.1;
                                                                                                       Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
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                                                              SEQUENCE FROM N.A.
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PROSITE; PŚ01225; CTCK_2; 1.
SEQUENCE | 2910 AA; 313410 MW; 7270FC61A23264CI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00041; CT; 1.
SMART; SM00214; VWC; 1.
SMART; SM00216; VWD; 4.
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NCBI_TaxID=10090;
[1]
                                                                                              NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                 416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  214 VPDALKSLWYKNLTGPQNITLNHTDLVPCLCIQVWSLEPDS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                         TSVCALEPSGC----TPLPSMASTRA-----ARLGEELLQDFRSHQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EDPGAHRNLWHIARLRVLSPGVWQLDAPCCLPGKVTLCWQAPDQSPCQPLVPPVPQKNAT 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ITHFQEDSCCPSYSCECDPGLC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Natl! Acad. Sci. U.S.A. 94:14450-14455(1997).
U96411; AAB96561.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR001007; VWFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR002086; Aldehyde_dehydr
IPR000359; Cys_knot.
IPR002919; TIL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PR001846; Vwd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A glycoprotein
                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---RFGEVILLQP----TEDPCCL-GSVCVC----NQTLCEGLAPTCRPGHSL 2510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Otog.
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                                                                                                                                                                                                                                                                                                                                                  2631
                                                                                                                                                                                                                                                                                                                                                                              434
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specific
                Barrell B.G., Badcock K., Chu
he EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 110; DB Pred. No. 3.1;
                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sciurognathi;
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fic to the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7270FC61A23264CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -CCQQQCQAPDTIIPVDLDCPGPRPESCP-- 2469
                                                                                                                                                                                                                                                          361 AA
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acellular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 2910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REDQILIEGRIG---
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membranes
                               Churcher
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Query Match
Best Local S
Matches 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9Y4G7
                                                                                                                                    SEQUENCE
                                                                                                                                                  SMART; SM00089; PKD; PROSITE; PS50093; PKI
                                                                                                                                                                 InterPro; Irnver, 3. Pfam; PF00801; PKD; 3.
                                                                                                                                                                                                 code for large proteins in vitro.
DNA Res. 4:141-150(1997).
EMBL; AB002317; BAA20777.1; -.
InterPro; IPR006501; PKD_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9Y4G7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
SEQUENCE 361 AA; 40144 MW; A62A7E4E8EFBE70A CRC64;
                                                                                                                                                                                                                                                                                                             Wagase T., Ishikawa K., Nakajima D., Ohira M., Seki N., Miyajima N.,
Panaka A., Kotani H., Nomura N., Ohara O.;
                                                                                                                                                                                                                                                                                                                                               IEDLINE=97349984; PubMed=9205841;
                                                                                                                                                                                                                                                                                                                                                                                                                           CBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CIAA03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (IAA0319 PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             349 VQLQACSWADSLGPFKDDMLLVEMKTGLNNTSVCALEPSGCTPLPSMASTRAA
                                                                                                                                                                                                                                                                       Prediction of the coding sequences of unidentified human genes. Vere complete sequences of 100 new cDNA clones from brain which can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               103 RPGTQHWPFSW--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 238 DLVPCLCIQVWSLEPDSE---RVEFCPFREDPGAHRNLWHIARLRVLSPGVWQLDAPCCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 YLSFQAYPIARCALLEVQYPADLVQPGQSVGSAVFDCFEASLGAEVQIWSYTKPRYQKEL
     44 GDVLCLPGSLQ--
                                                                                                                                                                                                                                                                                                                                                                                     QUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 VPTRLQTELVLRCPQKTDCALRVRVVVHLAVHGHWAEPEEAGKSDSELQESRNASLQAQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --LPS----TLHPHGAALMEVTMTGFAQNDG---NDWKINRV-----TWRLEEHM--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TLCYGTPEGG-----ISPSKPEVLKFPLQLKRAAIPSPDTI----HKRIFPPTNLVANIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PGKVTLCWQAPDQSPCQP-----LVPPVPQKNATVNEPQDFQLVAGHPNLCVQVSTWEK 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NLTQQLPDGDNVLLTLDVSEEQDFSFLLYLR----PVPDALKSLWYKNLTGPQNITLNHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KVHTLKLQLIKRI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PLKLALPRSTTPKDPARCTLDIR---MESPPLVFLGSPETSSGALASGILKLTILHQPFI 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PVVVSLERLMEPQDTARCSLGLSCHLWDGDVLCLPGSLQSAPG-------PVL
                                           ; 88
                                                          Similarity
                                                                                                                                  1072 AA;
                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                  PKD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QFSCQPCERHRDLVKPRPIEEKRILSTQDLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata;
Primates;
                                                       3.0%;
                                                                                                                               117742 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.0%; Score 108.5; D
20.3%; Pred. No. 0.24;
ive 53; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----TVLHPAI-SHCS----ACAGSKEVLQTWDLAANTTY 102
---SAPGPVLVPTRLQTELVLRCPQKTDCALRVRVVVHLA
                                       50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                       Score 108.5;
Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                       Mismatches
                                                                                                                           C8020284C4D3B67C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1072 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----LFPGSLPASVSN-RYIKLEYYLEA 136
                                                                        DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133;
                                       139;
                                                                        Length 1072;
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                                     Indels 133;
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                                                                                                                                                                                                                                                                                        genes. VII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       401
                                    Gaps
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                                    18;
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                                                                                                                                                                                            Query Match
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01-MAY-2000
01-MAR-2001
                                                                                                                                                                                                                                                                EMBL; AE001869; AAF09658.1; TIGR; DR0061; ~.
                                                                                                                                                                                                                                                                                                                                                   MAKATOVA K.S., Aravind L., Daly M.J., Winton K.W., 1
Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O.,
Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-20036896; PubMed-10567266; Milte O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson M.C., Richardson D.L., Dodson R.J., Haft D.H., Gwinn M.L., Pamphile W., Crosby M., Shen M., Woffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D
                                                                                                                                                                                                                                          Hypothetical SEQUENCE 4
                                                                                                                                                                                                                                                                                                      "Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.";
Science 286:1571-1577(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-R1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Thermus/Deinococcus group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Deinococcus radiodurans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DR0061.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9RY89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9RY89
                                                                                                                            213 PVP----DALKSLWYKNLTGPQNITLNHTDLVPCLCIQVWSLEPDSERVEFCPFREDPGAH 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               483
287 QLDAPCCLPGKVTLCWQAPDQSPCQPLVPPVPQKNATVNEPQDFQLVAGHPNLCVQVSTW 346
                                                                  270 RNLWHIARLR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     312 PLVPPVPQKNATVNEPQ---DFQLVAGHPNLCVQVSTWEKVQLQACSWADSLGPFKDD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          255
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                                    74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92
                                                                                                                                                                              Local Similarity
                             ALFAQLAAIRQRGGSPHERAQLEEVLRAGAGPQSALRADPRERPLLREAAQRIRRWLARR
                                                                                             PVPGAGDVLVSLGNSEVVRQLARTLGDLLLLPGGAAQVWQA---LDRVEDDPFPPQPGDD 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SVDSPVLRLSNLDPGNYSFRLTVTDSDGATNSTTAALIVNNAVDYPPVAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----TLPLTSALIDGSQSTDDTEIVSYH------WEEIN-----GPFIEEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENAFGEGFVNVTVKPARRVNLPPVA---VVSPQLQEL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ERV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KAFVAPAPPVETTYNYEW-NLISHPTDYQGEIKQGHKQTLNLSQL--SVGLYVFKVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FSFLLYLRPVPDALKSLWYKNLTGPQNI-----TLNHTDLVPCLCIQVWSLEPDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STEHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QSVGSAVFDCFEA----SLGAEVQIWSYTKPRYQKELNLTQQLPDGDNVLLTLDVSEEQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -SGEVLEKEKA----SQLQEQSSNSSGKEVLMPSHSLPPASLELSSVTVEKSPVLTVTPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VHGHWAEPEEAGKSDSELQESRNASLQAQVVLSFQAYPIARCALLEVQV----PADLVQPG 148
                                                                                                                                                              118;
                                                                                                                                                                                                                              1 protein; Complete proteome.
478 AA; 51231 MW; 5E74CDEBBBBBA5C95 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel.
(TrEMBLrel.
L 51.2 KDA PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EFCPFREDPGAHRNLWHIARLRVLSPGVWQLDAPCCLPGKVTLCWQAPDQSPCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PTPPTSAAPSESTPSELPISPTTAPRTVKELTVSA----GDNLIITLPDNEVEL
                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                           3.0%;
23.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13,
16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -MLLVEMKTGLNNTSVCALEPSGCTPLPSMAS 397
                                                                                                                                                              38;
                                                                                                                                                                         Score 106.5; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                -VLSPGV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Deinococcales; Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               478
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                                                                                                                                                                                     DB-16;
                                                                                                                                                          184; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              update)
                                                                                                                                                                                        Length 478;
                                                                                                                                                                                                                                                                                                                                                                  Venter J.C.,
                                                                                                                                                          169;
                                                                                                                                                                                                                                                                                                                                                                                   R.D.,
                                                                                                                                                         Gaps
                                                             286
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23;

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Query Match
Best Local S
Matches 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q94G03;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE CYTOSOLIC NADP-MALIC ENZYME (EC 1.1.1.40).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lai L.B., Nelson T.; "Expression of the cytosolic NADP-malic enzyme genes in Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.EMBL; AF288920; AAK83073.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oxidoreductase.
SEQUENCE 589 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids II; Asterales; Asteraceae; Asteroideae; Helenieae; Flaveria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q94G03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Flaveria pringlei.
                                                                                                                               106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID-4226;
                                         139
                                                                                   303
                                                                                                                                                                         243
                                                                                                                                                                                                                                                                                                                                         135 LLEVQVPADLVQPGQSVGSAVFDCFEASLGAEVQI---WS-----YT----KPRYQKELN 182
                                                                                                                                                                                                                                                                 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      347
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                                                                                                                                                                                                                                                                                                             S
                                                                   QAPDQSPCQPLVPPVPQKNATV-NEPQDFQLVAGHPNLCVQV-STWEKVQLQACSWADSL
                                                                                                                          RYVAMMELEERNERLFY
                                                                                                                                                           LCIQVWSLEPDSERVEFCPFREDPGAHRNLWHIARLRVLSPGVWQLDAPCCLPGKVTLCW 302
                                                                                                                                                                                                                                                   LTQQLPDGDNVLLTLDVSEEQDFSFLLYLRPVPDALKSLWYKNLTGPQNITLNHTDLVPC
                                                                                                                                                                                                                     FTER----
                                                                                                                                                                                                                                                                                               LKQMKEGESVVDPSSAVGGGVDDVYGEDRASEDQLITPWTVSVASGYTLLRDPHHNKGLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VFPLGPDPLEVRLPGDRLLTLRPDYRAEL 428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LSCVLPDFLQGRATGRYVGVYFDGLLHPDSVPSPFRVA---PLFSL---PTQLPA---FL 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASGQVAFAQTPAECLAAARRSLQRLEPLLGRFSPAQVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AHGALAWEH------HQRRRILQEGGVVILLESPAAVAQCQQWLQLQTVEEPGPHDALAAW 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EKVQLQACSWADSLGPFKDDMLLVEMKTG--LNNTSVCALEPSGCTPLPSMASTRAARLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADAAQTRHLARLAALGRACALLLLPAEQHGRLRLARTLARRLRGDP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LARAPGOLPGTVPAHSVLYAQEEASALSAPAAGDGLTLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EELLQDFRSHQCMQLWNDDNMGSLWACPMDKYIHRRWVLVWLACLLLAAALFFFLLLKKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QGLRL---SWR-SLGP--NWQLLVQDETSQPVSGGQLALLRPD---
                                                                                                                                                                                                                                                                                                                                                                                              al Similarity 17.8
106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -QLFLTVGGQQLQVLFSGD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -- RRKAARGSRTALLLHSADGAGYERLVGALASALSQMPLRVAVDLWSRRELS
                                PTVGEACQKYGSIFKRPQGLYISLKEKGKILEVLRNWPERNIQVIVVTDG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65124 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -HYAAQVQQAAEHAASAAEPLREAATDPLVGREAGPPVLPATGHFI
                                                                                                                                                                                                                                                                                                                                                                                                                 3.0%;
                                                                                                                                                                                                       ERDSHYLRGLLPPAVATQELQEKKLM--QNIRSYEVPL--H 105
                                                                                                                                                                                                                                                                                                                                                                                            70;
                                                                                                                                                                                                                                                                                                                                                                                                               Score 106.5; D
Pred. No. 0.71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AB3A6FB01BBEF95A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  649
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                                                                                                                        KLLIDNVEEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 10;
                                                                                                                                                                                                                                                                                                                                                                                            182;
                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -LP--ASER-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----YVLLRRR 250
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                                                                                                                                      Matches
                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                 Protease;
SEQUENCE
                                                                                                                                                                                                                                                                                 PROSITE; PS50209; CARD; 1.

PROSITE; PS00678; WD_REPEATS_1; UNKNOWNSPROSITE; PS50082; WD_REPEATS_2; 9.

PROSITE; PS50294; WD_REPEATS_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO0364; DISEASERSIST.
PRINTS; PRO0320; GPROTEINBRPT.
SMART; SM00320; WD40; 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00400; WD40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Piam; PF00931; NB-ARC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00619; CARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
      129
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                                                                                        DCALRVRVVVHLAVHGH-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EQAYTWTQGRAIFSSGSPFDPYEYNGNL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LHSAD-
                                                                                                                                    al Similarity
112; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -QQWLQLQTV-
PIARCALLEVQVPADLV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR001680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR001315; CARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR000767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -GAGYERLVGALASALSQMPLRVA-VDLW---
                                                                                                                                                                                                                                              epeat; WD
1248 AA;
                                                                                                                                    Conservative
                                                                                                                                                      3.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disease_resist.
NB-ARC.
                                                                                                                                                                                                                                              repeat.
141728 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WD40.
                                                                                                                                    64;
                                                                                                                               Score 106.5;
Pred. No. 2;
64; Mismatches
  -QPGQSVGSAVFD--
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LGAGEAGTGIAELIALEISTKANIPIDEARKKIWLVDSKGLIVSSRKETLQHFKKPWAHE
                                                                                                                                                                                                                                                                                                                                                          DDEFY IGLROKRATGKEYYDLLEEFMSAVKQNYGEKVLVQFEDFANHNAFELLAKYRTSH
                                                                                    HEPLSTLLDAVKAIKPSVLIGTSGVGQTFTQNVVEAMAAFNERPLIMALSNPTSQAECTA
                                                                                                                                                                                                                                                                                                           --WNDDNMGSLWACPMDKYIHRRWYLVWLACLLLAAALFFFLLLKKDRRKAARGSRTALL 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ERILGLGDLGCQGMGIPVGKLALYTALGGVRPSACLPITIDVGTNNQKLL
                                       EPGPHDALAAWLSCVLPDFLQGRATGRYVGVYFDGL
                                                                                                                                                                                                                                                                    ----ASVVLAGLVASLKLL-----GGSLADHTFLF
                                                                                                                                                                                                                                                                                                                                                                                                  -GEELL---QDFRSHQCMQL-----
                                                                                                                                ·QRRRILQEGGVVILLFSPAAVAQC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TSVCALEPSGCTPLPSMASTRAARL-
--FIPGQANNAYI---FPGL
                                                                                                                                                                                                                       SRRELSAHGALAWFHH
497
                                          594
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Hahn C., Duerkop H., Stein H.;
"Sequence of Apaf-1 in L 428.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS 11 WD REPEATS (TRP-ASP DOMAINS)
EMBL; AJ243009; CAB55585.1;
-- HSSP; O14727; 1CY5. Q9UJ61 PRELIMINARY; PRT; 1248 AA.
Q9UJ61;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
APOPTOTIC PROTEASE ACTIVATING FACTOR 1. Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo. update)

DDA7285E6D5C8F37 CRC64; ľ

537 DCAVSENFQEFLSLNGHLLGRQPFPNIVQLGLCEPETSEVYQQAKLQAKQEVDNGMLYLE 596 -WAEPEEAGKSDSELQE-SRNASLQA-QVVLSFQAY-- 128 DB 4; 188; Length 1248; Indels 221; Gaps

27;

CFEASLG

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93XR9
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                                                                                                          Best Loc
Matches
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01-DEC-2001
01-DEC-2001
                                                                                                                                                                                  "Identification of mRNA transcripts differentially expre response to high salinity by means of differential displemangrove plant, Brugulera gymnorrhiza."; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AB061795; BAB55653.1; -
SEQUENCE 756 AA; 84482 MW; 1597F3D46C3E0809 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                Bruguiera gymnorrhiza.

Bruguiera gymnorrhiza.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid

eurosids []; Malpighiales; Rhizophoraceae; Bruguiera.
                                                                                                                                                                                                                                                                                              Banzai T., Hershkovits G., Katcoff D.J., Hanagata N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q93XR9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q93XR9
                                                                                                                                                                                                                                                                                       Karube
                                                                                                                                                                                                                                                                                                                     TISSUE-LEAF;
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=39984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BG55 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            893
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                                                                                                                           Local
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                                       VVDRIERLFPNIEASRPRCRLGI-----EVLCLLNDALDRAKQVLQYCSESSKLYLAL
                                                                  VVVSLERIMEPQDTA--RCSIGLSCHLWDGDVICLPGSLQSAPGPVLVPTRLQTELVL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DGAGYERLVGALASALSQMPLRVAVDLWSRRELSAHGALAWFHHQRRRILQEGGVVILLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DDNMGSLWACPMDKYIHRRWYLVWLACLLLAAALFFFLLLKKDRRKAARGSRTALLLHSA 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WINKKNITNLSCLVVRPHTDAVYHACFSEDGQRIASCGADKTLQVFKAETGEKLLEIKAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPAAVAQCQQWLQLQTVEPGPHDAL--AAWLSCVLPDFLQGRATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NVKQFFLNLEDPQEDM---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PVPQKNATVNEPQDFQLVAGHPNLCVQVSTWEKVQLQACSW-ADS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SVNHCRFSPDD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RVEFCPFREDPGAHRNLWHIARLRVLSPGVWQLDAPCCLPGKVTLCWQAPDQSPCQPLVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TDSRSKVADCRG----HLSWV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IHTSGLLGEIHTGHHSTIQYCDFSPQNHLAVVAL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FKDDMLLVEMKTGLNNT-SVCALEPSGCTPLPSMASTRAARLGEELLQDFRSHQCMQLWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TLDVSEEQDFSFLLYLRPVPDALKSLWYKNLTGPQNITLNHTDLVPCLCIQVWSLEPDSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EDEVLCCAFSTDDRFIATCSVDKKVKIWNSMTGELVHTYDEHSEQVNCCHFTNSSHHLLL
                                                                                                             140;
                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [ (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
RCPQKTDC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -LTSSDDQ----TIRLWETKKVCKNSAV-MLKQEVDVVFQENEVMVL--
                                                                                                          itive
                                                                                                                       2.9%;
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19,
             --ALRVRVVVHLA--
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                                                                                                                                                                                                                                                                                                                                                                              Rhizophoraceae;
                                                                                                        92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                       Score 106; DB Pred. No. 1.1;
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                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                              Bruguiera
                                                                                                                                      10;
                                                                                                                                     Length 756;
                                                                                                        Indels
                                                                                                                                                                                                                                                 expressed display in
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             VHGHWAEPEEAGK
                                                                                                                                                                                                                                                                                                 Dubinsky
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                                                                                                     Gaps
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SEQUENCE FAVOR.

STRAIN-MARFE 301001;

MEDLINE 98193120; PubMed 9524202;

SUZUKİ K., Ohta N., Hattori Y., Uraji M., Katoh A., Yoshida K.;

SUZUKİ K., Ohta N., Hattori Y., Uraji M., Katoh A., Yoshida K.;

"Novel structural difference between nopaline and octopine tyg

gene:construction of genetic and physical map and sequencing of

gene:construction of gene clusters of a new Ti plasmid pTi-SAKURA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000
01-MAY-2000
01-DEC-2001
                                                                                                                                                                                                                                                                                                               STRAIN-MAFF301001;
MEDLINE-20184752; Pubmed-10721727;
Suzuki K., Hattori Y., Uraji M., Ohta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19, TIORF47 PROTEIN.
                                                                                                                                                                                                                                                    Katoh A., Yoshida K.;
"Complete nucleotide sequence of a plant tumor-inducing
Gene 242:331-336(2000).
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rhizobiaceae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmid pTi SAKURA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Agrobacterium tumefaciens
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Biochim. Biophys. Acta 1396:1-7(1998).

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Best Local Similarity

Matches 115; Conserv
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InterPro; IPRUVUV--
Pfam; pF00271; helicase_C; ...
PRINTS; PR00507; N12N6WTERASE; UNKNOWN_1.
PROSITE; PS00092; N6_WTASE; UNKNOWN_1.
PROSITE; PS00092; N6_WTASE; D18M0; ODD679?
412 RSHQCMQL--WNDD--NMGSLWACPMDKYIHRRWVLVWLACLLLAAALFFFLLLKKDRRK 467
                                           682 VAEAAAALDPYYNRNVTAL--AGVQPVDLRPSDITARLGAPWIPAADVVAFVKEMMGTDI
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Uraji M., Suzuki K.,
"Genome structure of
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STRAIN-MAFF301001;
Ohta N., Suzuki K., Hattori Y., Uraji M., Katoh A., Yoshida K.;
"Genome structure of pTi-SAKURA (III): Characteristics of T-DNA.";
Nucleic Acids Symp. Ser. 39:185-186(1998).
                                                                                369 LVEMKTGLN----NTSVCALEPSGCTPLPSMASTRAARLG----
                                                                                                                           622 LAVVLNERGRVDLDHIAELLHRDPDDVVAELGSAIFRDPADGSWQMADAYLSGPVRDKLK 681
                                                                                                                                                                                                            587 E-----DYDLENDTAKPGAIF-----TERVISPPAPPV------ITSAADA 621
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InterPro; IPR002296; N12N6_mtfra
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MSSP; P14385; 2
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N6_Mtase.
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; Pred. No. 3.4;
66; Mismatches 159; Indels 25
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                                                                                                                                                                                                                                                                                             homo sapien
  RESULT
PTPO_RAT
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                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Q64612;
EMBL; L36884; AAA63911.1; HSSP; P18052; 1YFO.
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LPH_RAT	SG2N_MOUSE	ICA1_MOUSE	TYO3_RAT	KATB_SCHPO	MUCM_RABIT	MUC_RABIT	YEHY_ECOLI	EPPL_HUMAN	LMA5_HUMAN	HAIR_HUMAN	NFX1_HUMAN
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	N: BY PARATHYROID CYTOPLASMIC DOMA	JM.			THE BASAL FORTION OF THE SEMINIFEROUS TUBULE. DEVELOPMENTAL STAGE: UP-REGULATED IN DIFFERENTIATING	TISSUE SPECIFICITY: BONE	OSTEOBLASTS, BUT NOT DETECTABLE AT OTHER STAGES.	••	LOCATION:	+ phosphate	ASSOCIATED WITH DIFFERENTIATION IN BONE AND TESTIS	PHOSPHATASE ACTIVITY IS 5.6.	ASSOCIATED WITH DIFFERENTIATION IN HOME AND	FUNCTION: MAY FUNCTION IN SIGNALING PATHWAYS DURING	Biol. Chem. 269:30659-30667(1994).	associated with b	"Identification of a hormonally requilated protein	Olmsted E.A., Skrobacz	MEDLINE=95074080; PubMed=7527035	sarcoma:	FROM N.A.	0116;	theria; Rodentia;		Rattus norvegicus (Rat).	(OST-PTP)	(Rel. 38, Last ar	35, Last		STANDARD;	
	HORMONE AND C	A CONTRACTOR DO	IDS REMAIN BOT	OWN-REGULATED	EGULATED IN DI	AND TESTIS. IN THE LATTER,	CTABLE AT OTH	RESUMED ALTER	Type I membrane protein.	in tyrosine pl	IATION IN BON	.6.	TATION IN BONI	SIGNALING PAT	7(1994).	one and testic	lv requilated :	obacz B.M., Mourey	035;				Sciurogna	Craniata;		ine phosphata	Last annotation update)	sequence update)	7	PRT; 1711 AA.	
	INDUCTION: BY PARATHYROID HORMONE ANT CYCLIC AMP ANALOGS. PTM: THE CYTOPLASMIC DOMAIN CONTAINS POTENTIAL PHOSPHORYLATION SITES	THE STREET STREET	TEN WITHIN THE SEBTOIT	MINERALI	TEFERENTIATING CULTURES OF	THE LATTER, RESTRICTED TO	DETECTABLE AT OTHER STAGES.	A PRESUMED ALTERNATE TRANSCRIPT OF 4.8-5.0	orotein.	CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein	AND TESTIS.	THE PERSON OF PERSON	HENCELL			phosphatase associated with bone and testicular differentiation. ":	protein tyrosine	ourey R.J., Davis A.R.,		•	•		Muridae; Murinae; Rattus.	Vertebrata; Euteleostomi;		se precursor (EC 3.1.3.48)					

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Query Match 3.2

Best Local Similarity 20.7

Matches 150; Conservative
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CARBOHYD
CARBOHYD
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PRINTS; PRO0700; PRTYPHPHTASE.
SMART; SM00060; FN3; 6.
SMART; SM00194; PTPC; 1.
SMART; SM00112; PTPC_DSPC; 1.
                                       435 PSGATHVIFCGLVPGAHYRVDIASSTGDISQSISG-----YTSPLPPQSLEV-----
                                                                                                  392 AALPREVPGARL---WLDGLEASK-----QPGRRALLYSD---
                                                                                                                                                       333 DGYYLKLSGPMESTSTLGPEECNAVFPGP-LPPGHYTLQLKYLAGPYDAWVEGSTWLAES 391
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Pfam; PF00102; Y_phosphatase; 1.
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                                                                                                                                                                               43 DGDVLCLPGSLQSA------PGPVLVPTRLQTEL-VLRCPQK-----TDC
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TYR_PHOSPHATASE_2;
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FN_III.
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FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 4.
FIBRONECTIN TYPE-III 5.
FIBRONECTIN TYPE-III 6.
FIBRONECTIN TYPE-III 7.
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PROTEIN-TYROSINE PHOSPHATASE 2.
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MEDLINE-19138495; Pubmed-1840592; MEDLINE-91358495; Pubmed-1840592; Overbergh L.; Torrekens S., van Leuven F., van den Berghe H.; "Molecular characterization of the muringhlobulins."; J. Biol. Chem. 266:16903-16910(1991). -i- FUNCTION: A PROTEINASE ACTIVATES THE INHIBITOR BY SPECIFIC PROTEOLYSIS IN THE BAIT REGION, WHICH, BY MUKNOWN MECHANISM LEADS TO REACTION AT THE CYSTEINYL-GLUTAMYL INTERNAL THIOL ESTIE SITE AND TO A CONFORMATIONAL CHANGE, WHEREBY THE PROTEINASE IS TRAPPED AND/OR COVALENTLY BOUND TO THE INHIBITOR. WHILE IN THE TETRAMERIC PROTEINASE INHIBITORS STERIC INHIBITION IS SUFFICIEN STRONG, MONOMERIC FORMS NEED A COVALENT LINKAGE BETWEEN THE ACTIVATED GLUTAMYL RESIDUE OF THE ORIGINAL THIOL ESTER AND A TERMINAL MAINO GROUP OF A LYSINE OR ANOTHER NUCLEOPHILIC GROUP THE PROTEINASE, FOR INHIBITION TO BE EFFECTIVE. -!- SIBLILARITY: TO OPHER PROTEINS OF THE ALPHA-MACROGLOBULIN FAMILY INCLUDING COMPLEMENT COMPONENTS C3, C4, AND C5.	M2_MOUSE A2M2_MOUSE A2M2_MOUSE A2M2_MOUSE A2M2_MOUSE A2M2_MOUSE P28666; 01-DEC-1992 (Rel. 24, Greated) 01-DEC-1992 (Rel. 24, Last sequence updated) 01-NOV-1997 (Rel. 35, Last annotation updated) Murinoglobulin 2 precursor (MuG2). Mug OR MUG-2. Mug musculus (Mouse) Eukaryota; Metazoa; Chordata; Craniata; 1 Mammalia; Eutheria; Rodentia; Sciurognatl NCBI_TaxID-1090; [1] SEQUENCE FROM N.A.	537 VILLESPAAVAQCQQMLQLQTVEPGP-HDALAAWLS	375 GLNNTSVCALEPSGCTPLPSMASTRAARLGEELLQDFRSHQCMQLWNDDNMGSLWACPMD :	482 237 TDLVPCLCIQVWSLEPDSERVEFCPFREDBGARNILMH 111
er on		579 864 627 920	434 718 7490 765 536 825	532 274 592 314 646 646 374

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InterPro; IPR001599; Alpha_2_macroglobln
Pfam; PF00207; AAM; 2.
Pfam; PF01835; A2M_N; 1.
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MGD; MGI:99836; Mug2.
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PIR; B41185; B41185.
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                                                                                                                         YKNLTGPQNITLNHTDLVP-------CLCIQVWSLEPDSERVEFCPFREDPGAHR--
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                                                        EDMDLKAFTNLKIKLPKICFDSAPMSGPRGKFDLAFSSEVSGTLQKGSSKRPQPEEPPRE
                                                                             ---NLWHIARLRVLSPGVWQLDAPCCLP-GKVTLCWQAPDQSPCQ-----PLVPPVPQK
                                                                                                                                                                   LGAEVQIWSYTKPRYQKELNLTQQLPDGDNVLLTLDVSEEQDESFLLYLRPVPDALKSLW
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AHRNIWHIARLRVLSPGVWQLDAPCCLPGKVTLCWQAPDQSPCQPLVPPVPQ-KNATVNE
                                                                                      AEVQIWSYTKPRYQKELNLTQQLPDGDNVLLTLDVSEEQDFSFLLYLRPVPDALKSLWYK 224
                                    NLTGPQNITUNHTDLV---
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                      -LTTPETVLTGHTEKIYSLREHPLAADVLASSSYDLTIRIWDLQARTEQLRL
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PROSITE; PS00678; WD_REPEATS_1; 1.
PROSITE; PS50082; WD_REPEATS_2; 2.
PROSITE; PS50294; WD_REPEATS_REGION;
                                                                                                                                                                                                                                                                                                                       InterPro; IPR001680; WD40. Pfam; PF00400; WD40; 3. SMART; SM00320; WD40; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Muralikrishna T., Begum Z., Swamy C.V., Khar A.;
"Molecular cloning and characterization of a tumor rejection antigen
from rat histiocytoma, AR-5.";
DNA Cell Biol. 17:603-612(1998).
-!- SIMILARITY: CONTAINS AT LEAST 4 WD REPEATS (TRP-ASP DOMAINS).
-!- SIMILARITY: BELONGS TO THE CORONIN FAMILY OF WD-REPEAT PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
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15-JUL-1998 (Rel. 36, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation updat
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Sciurognathi; Muridae;
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of a tumor rejection antigen
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SEQUENCE OF 810-864 AND 866-883 FROM N.A. Roberts D.L., Dalgleish R., Cohen G.M., MacFa The mammalian CED4 homologue, APAF1, exists
                                                                                                                                                               DNA Res. 4:307-313(1997).
                                                                                                                                                                                                                                                                             -prediction
                                                                                                                                                                                                                                                                                                              Ishikawa K.-I., Nagase T., Nakajima D.,
Miyajima N., Tanaka A., Kotani H., Nomus
                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-98116655; PubMed-9455477;
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SEQUENCE OF 385-1248 FROM N.A. (ISOFORM 1).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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INSSUE=Peripheral blood, Heart, and Cervical carcinoma;

AEDLINE=99373149; PubMed=10441495

Inches 99373149; PubMed=10441495
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4EDLINE=97410306; PubMed=9267021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aleh A., Srinivasula S.M., Acharya S., Fishel I Cytochrome c and dATP-mediated oligomerization rerequisite for procaspase 9 activation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OOU H., Henzel W.J., Liu X., Lutschg A., Wang X.; Apaf-1, a human protein homologous to C. elegans n cytochrome c-dependent activation of caspase-3 [ell 90:405-413(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EDLINE-99292765; PubMed-10364241;
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A., Kotani H., Nomura N., Ohara O.,
coding sequences of unidentified human genes.
from brain which code for large proteins in
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Yoo H.-S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-20047184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRUCTURE BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (1.3 ANGSTROMS) OF 1-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Moroni M.C., Hickman E.S., Denchi E.L., Caprara Cecconi F., Mueller H., Helin K.; Papfara is a transcriptional target for E2F and Nat. Cell Biol. 3:552-558(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21283226; PubMed=11389439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APAF-1-MEDIÁTED OLIGOMERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cloning of variant Apafl.";
Submitted (MAR-2000) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human cells.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INDUCTION BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATP.

SUBUNIT: Monomer. Oligomerizes upon binding of cytochrome c addrp. Oligomeric Apaf-1 and pro-caspase-9 bind to each other their respective NH2-terminal CARD domains and consecutively mature caspase-9 is released from the complex.

SUBCELLULAR LOCATION: Cytoplasmic.

ALTERNATIVE PRODUCTS: 5 isoforms; 1/Apaf-1XL (shown here), 2, 11 3/Apaf-1S. 4/Apaf-1M and 5/Apaf-1XS; are produced by
                                                                                                                                                                                                                                                                                                                                                                                     INDUCTION: By E2F and p53 in apoptotic neurons. SIMILARITY: CONTAINS 1 CARD DOMAIN. SIMILARITY: CONTAINS 13 MD REPEARS (TRP-ASP DOM SIMILARITY: CONTAINS 1 NB-ARC DOMAIN.
                                                                                                                                                                                                                                                                                                                                        CAUTION: Ref.7 sequence differs from that shown due to frameshift in position 109.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE SPECIFICITY: Ubiquitous. Highest levels of expression in adult spleen and peripheral blood leukocytes, and in fetal brain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1L, 3/Apaf-1S, 4/Apaf-1M and 5/Apaf-1XS; alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: Oligomeric Apaf-1 mediates the cytochrome autocatalytic activation of pro-caspase 9 (Apaf-3), activation of caspase-3 and apoptosis. This activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: Oligomeric Apaf-1 autocatalytic activation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          kidney and
                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the Empression Birinformatics and the Empression Birinformatics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lee J.-W.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1-138 FROM N.A. (
J.-W., Ohr H.-H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Apaf-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NMR OF 1-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E2F AND P53
                                                                                 AAC51678.1;
CAB55579.1;
CAB55580.1;
CAB55580.1;
CAB55581.1;
CAB55582.1;
CAB55583.1;
CAB55584.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lung.
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    EMBL/GenBank/DDBJ
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, Kim D.-U., Chung
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is of
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InterPro; IPR001680; WD40.
Pfam; PF00619; CARD; 1.
Pfam; PF00931; NB-ARC; 1.
Pfam; PF00400; WD40; 11.
PRINTS; PR00320; GPROTEINBRPT.
SMART; SM00320; WD40; 10.
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PROSITE; PS00678; WD_REPEATS_1; 4.

PROSITE; PS50082; WD_REPEATS_2; 9.

PROSITE; PS50294; WD_REPEATS_REGION;
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L; AJ243009; CAB55585.1; -...
L; AJ243010; CAB55586.1; -...
L; AJ243011; CAB55587.1; -...
L; AJ243041; CAB55588.1; -...
L; AJ243040; CAB55588.1; -...
L; AF143979; AAD58344.1; -...
L; AF149794; AAD58044.1; -...
L; AB007873; BAA24843.1; -...
L; AJ133643; CAB65086.1; -...
L; AJ133644; CAB65086.1; -...
L; AJ133645; CAB65087.1; -...
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1CWW; 21-JAN-00
602233; -.
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1001
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877
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575
866
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                                                                                                                                                                                                                                  E -> ETLGFESKK (IN ISOFORM 5).

MISSING (IN ISOFORM 3, ISOFORM 5).

ISOFORM 5).

MISSING (IN ISOFORM 5).

S -> P (IN REF. 7).

G -> C (IN REF. 2, CAB55586).

I -> T (IN REF. 2, CAB55586).

Y -> H (IN REF. 2, CAB55586).
                                                                                                                                                                                                                                                                                                                                                                                            WD 1.
WD 2.
WD 3.
WD 4.
WD 5.
WD 6.
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WD 9.
WD 11.
WD 11.
WD 13.
POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                 MISSING (IN ISOFORM 2 AND ISOFORM 3).
E -> ETLGFESKK (IN ISOFORM 5).
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ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARD
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CAB55584)
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CAB55587)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                "The complete sequence of perlecan, a basement membrane heparan sulfate proteoglycan, reveals extensive similarity with laminin chain, low density lipoprotein-receptor, and the neural cell additional control of the chain, low density lipoprotein-receptor, and the neural cell additional control of the complete sequence of perlecan, a basement membrane heparan sulfate proteon.
                                                                                                                                         SEQUENCE FROM N.A. TISSUE-Melanoma; MEDLINE-92078153;
                                                                                                                                                                                                                                                                                                                                             PGBM_MOUSE
Q05793;
SEQUENCE OF 940-1601 AND 1870-2600 FROM N.A., MEDLINE-89034110; PubMed-2972708;
                                                                                                              MEDLINE-92078153; PubMed-1744087;
NOOnan D.M., Fulle A., Valente P., Cai S.,
Yamada Y., Hassell J.R.;
                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Basement membrane-specific heparan sulfate proteoglycan core
protein precursor (HSPG) (Perlecan) (PLC)
                                          J. Biol. Chem. 266:22939-22947(1991).
                                                         molecule.";
                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; MCBI_TaxID=10090;
                                                                                                                                                                                                                                                          HSPG2
                                                                                                                                                                                                                                               Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPAAVAQCQQWLQLQTVEPGPHDAL--AAWLSCVLPDFLQGRATG 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DGAGYERLVGALASALSOMPLRVAVDLWSRRELSAHGALAWFHHQRRRILQEGGVVILLF
                                                                                                                                                                                                                                                                                                                                                                                                                             ---AVDHIRR-LQLINGRTGQIDYLTEAQVSCCCLSPHLQYIAFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DDNMGSLWACPMDKYIHRRWYLVWLACLLLAAALFFFLLLKKDRRKAARGSRTALLLHSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DGSSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TLDVSEEQDFSFLLYLRPVPDALKSLWYKNLTGPQNITLNHTDLVPCLCIQVWSLEPDSE 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EDEVLCCAFSTDDRFIATCSVDKKVKIWNSMTGELVHTYDEHSEQVNCCHFTNSSHHLLL 716
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SVNHCRFSPDD---
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Sciurognashi; Muridae; Murinae; Mus
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Pred. No. 2.
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             PARTIAL SEQUENCE
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PROSITE: PS01186;
PROSITE: PS01186;
PROSITE: PS01286;
PROSITE: PS50025;
PROSITE: PS50129;
PROSITE: PS50024;
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SMART; S
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1. SUBCELLULAR LOCATION: EXCLAGED 1111ar.

1. SUBCELLULAR LOCATION: EXCLAGED 1111ar.

1. PIM: SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES.

1. PIM: CONTAINS THREE HEPARAN SULFATE CHAINS AS WELL AS N-LINKED AND O-LLINKED OLIGOSACCHARIDES.

1. SIMILARITY: CONTAINS 4 LDL-RECEPTOR CLASS A DOMAINS.

1. SIMILARITY: CONTAINS 10.5 LAMININ EGF-LIKE DOMAINS.

1. SIMILARITY: CONTAINS 3 LAMININ DOMAINS IV.

1. SIMILARITY: CONTAINS 3 LAMININ G-LIKE C2-TYPE DOMAINS.

1. SIMILARITY: CONTAINS 3 LAMININ G-LIKE DOMAINS.

1. SIMILARITY: CONTAINS 1 EGF-LIKE DOMAINS.

1. SIMILARITY: CONTAINS 1 SEA DOMAIN.
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J. Biol. Chem. 263:16379-16387(1988).

-I- FUNCTION: THIS PROTEIN IS AN INTEGRAL COMPONENT OF BASEMENT MEMBRANES. IT IS RESPONSIBLE FOR THE FIXED NEGATIVE ELECTROSTATIC CHARGE AND IS INVOLVED IN THE CHARGE-SELECTIVE ULTRAFILTRATION PROPERTIES. IT INTERACTS WITH OTHER BASEMENT MEMBRANE COMPONENTS SUCH AS LAMINIA AND COLLAGEN TYPE IV AND SERVES AS AN ATTACHMENT SUBSTRATE FOR CELLS:
SUBSTRATE FOR CELLS:
SUBBUNIT: PURIFIED PERLECAN HAS A STRONG TENDENCY TO AGGREGATE IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an
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BL; J04054; AAA39899.1; -.
BL; J04055; AAA39912.1; -.
SP; Q07954; ICR8.
D; MGI:96257; Hspg2.
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m; PD003031; Lamlinim;
p D003031; Lamlinim;
p SM00180; EGF_Lam; 7.
sM00101; EGF_11ke; 6.
sM00408; IGC2; 14.
sM00192; LDLa; 4.
sM00281; LamB; 3.
                                                             SM002UU; 544,
; PS00022; EGF_1; 8.
;; PS01186; EGF_2; 5.
8; PS01248; LAMINI_TYPE_EGF; 1.
E; PS0025; LAM_G_DOMAIN; 3.
E; PS01209; LDLRA_1; 4.
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SM00200;
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IPR001438; EGF_II.
IPR003006; Ig_MHC.
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; EGF_Lam; 7.
; EGF_like; 6.
; IGc2; 14.
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                                                                                                                                                                                    LamG; 3
SEA; 1
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Laminin_B.
Laminin_EGF.
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       rane; Proteoglycan; Repeat; Glycoprotein;
nin EGF-like domain; Immunoglobulin domai
EGF-like domain.
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LAMININ G-LIKE 3.

HEPARAN SULFATE (POTENTIAL).

HEPARAN SULFATE (POTENTIAL).

HEPARAN SULFATE (POTENTIAL).

MEDIATES MOTOR NEURON ATTACHMENT
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LDL-RECEPTOR CLASS A 2
LDL-RECEPTOR CLASS A 3
LDL-RECEPTOR CLASS A 4
IG-LIKE C2-TYPE DOMAIN
   EGF-LIKE.
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BASEMENT MEMBRANE-SPECIFIC HEPARAN
DEOTEOGLYCAN CORE PROTEIN.
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IN EOR-LIKE 1 (C-TERMINAL).

IN EGF-LIKE 2.

IN EGF-LIKE 3.

IN EGF-LIKE 4 (INCOMPLETE).

IN EGF-LIKE 5 (N-TERMINAL).

IN EGF-LIKE 5 (N-TERMINAL).

IN EGF-LIKE 5 (C-TERMINAL).

IN EGF-LIKE 6.

IN EGF-LIKE 6.

IN EGF-LIKE 7.

IN EGF-LIKE 9 (N-TERMINAL).

IN EGF-LIKE 9 (N-TERMINAL).

IN EGF-LIKE 10.

IN EGF-LIKE 10.

IN EGF-LIKE 11.

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Q9NXO2; Q9BVN5; (
16-OCT-2001 (Rel
16-OCT-2001 (Rel
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(Rel. 40, Last sequence upd
(Rel. 41, Last annotation u
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     InterPro; IPR000767; Disease_resist.
InterPro; IPR003592; LRR_out.
InterPro; IPR003592; LRR_DAPIN.
PRINTS; PR00364; DISEASERSIST.
SMART; SM00370; LRR; 7.
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EMBL; AF310106; AAG30289.1; -
EMBL; AK000517; BAA91223.1; -
EMBL; AK025952; BAB15233.1; -
EMBL; AK000784; BAA91377.1; ALT_INIT.
EMBL; BC003592; AAH03592.1; -
EMBL; BC001039; AAH01039.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a content of the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.
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-- FUNCTION: May be implicated in apoptosis (By similarity).

-- COFACTOR: Binds ATP (By similarity).

-- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

-- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; and produced by alternative splicing.

-- SIMILARITY: CONTAINS 1 DAPIN DOMAIN.

-- SIMILARITY: CONTAINS 1 NACHT DOMAIN.

-- SIMILARITY: CONTAINS 9 LEGCINE-RICH REPEATS (LRR).
                                                                                                                                                PROSITE; PS50824; DAPIN; PROSITE; PS50837; NACHT;
                                                                                                                                                                                                                                                                                                                                                                                                                            or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Kidney epithelium, and Colon; Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashii Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka : Nakamura Y., Isogai T., Sugano S.; "NEDO human cDNA sequencing project."; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                Alternative
                                                                                                                               Apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg
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"The pyrin domain: a possible member of timplicated in apoptosis and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Lung, and Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Curr. Biol.
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MEDLINE=21169419; PubMed=11270363;
Bertin J., DiStefano P.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NACHT-, LRR-
protein 1):
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MEDLINE=21148093; PubMed=11250163;
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domain: a novel motif found
                                                                                                                            ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                            email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Differ. 7:1273-1274(2000).
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possible member of the
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DAPIN.
NACHT.
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LRR 4.
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Catarrhini;
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i; Hominidae; Homo.
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                           DCC_HUMAN STANDARW,
P43146;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41)
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                                                                                                                                                                                                 DNMGSLWACPMDKYIHRRWYLVWL
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  ns (Human)
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 Chordata;
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Pred. No. 4.
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 Craniata; Vertebrata;
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NG (IN REF. 1)
E (IN REF. 4)
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                                       (Colorectal cancer
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                                                                                                                                                                                                                                                                                                                                                                                    -LCEQIASDTCHLQRVV----FKNI
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                                     suppressor).
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EMBL;
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                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement '-
                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  metastasis.";
Cancer Res. | 54:3007-3010(1994).
-!- FUNCTION: IMPLICATED AS A TUMOR SUPPRESSOR
-!- SUBCELLULAR LOCATION: Type I membrane prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 107-472 FROM.N.A. (SCRAMBELD EXONS).
MEDLINE-91121517; PubMed-1991322;
Nigro J.M., Cho K.R., Fearon E.R., Kern S.E., Ru
Oliner J.D., Kinzler K.W., Vogelstein B.;
"Scrambled exons.";
                                                                                                                                                                                                                      or send an
                                                                                                                                                                                                                                           entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENE STRUCTURE, AND VARIANTS CARCINOMA HIS-1375.
MEDLINE=94245241; PubMed=8188295;
Cho K.R., Oliner J.D., Simons J.W., Hedrick L., Fearor Preisinger A.C., Hedge P., Silverman G.A., Vogelstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-750 FROM N.A.
SEQUENCE OF 1-750 FROM N.A.
MEDLINE-90100559; PubMed-2294591;
Fearon E.R., Cho K.R., Nigro J.M., Kern
Ruppert J.M., Hamilton S.R., Preisinger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- SUBCELLULAR LOCATION: Type I membrane protein.
-i- TISSUE SPECIFICITY: FOUND IN ANONS OF THE CENTRAL AND PERIPHERAL NERVOUS SYSTEM AND IN DIFFERENTIATED CELL TYPES OF THE INTESTINE.
-i- DISEASE; COLORECTAL TUMORS THAT LOST THEIR CAPACITY TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Miyake S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANT CARCINOMA THR-168, AND VARIANT GLY-201
MEDLINE-94243823; PubMed-8187090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Miyake S., Nagai K., Yoshino K., Oto M., "Point mutations and allelic deletion of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genomics 19:525-531(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  carcinomas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Identification of a chromosome colorectal cancers.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human esophageal squamous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The DCC gene: structural analysis and mutations in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 247|:49-56(1990).
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NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POINT MUTATIONS MAY CAUSE BOTH LYMPHATIC AND HEMATOGENOUS METASTASIS OF OESOPHAGEAL SQUAMOUS CELL CARCINOMAS. SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. DC
                                                                                                                                                                                                                                                                                                                                                                                               SIMILARİTY: CONTAINS 4 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS SIMILARİTY: CONTAINS 6 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                            ; M32292; AAA35751.1;
M32286; AAA52174.1;
M32288; AAA52175.1;
M32290; AAA52176.1;
M32290; AAA52177.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DIFFERENTIATE INTO MUCUS PRODUCING CELLS UNIFORMLY LACK EXPRESSION. INACTIVATION OF DCC DUE TO ALLELIC DELETION
                                           M63696;
M63700;
                                                                                                                                                                           X76132; CAA53735.1;
                                                                                                                                                                                                                                              and this statement is not removed. requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                      email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8:1174-1183(1994).
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AAA52178.
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AAA52180.
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                                                                                                                                                                                                                                         license agreement
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                                                                                                                                                                                                                                    http://www.isb-sib.ch/announce/
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Thomas
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G., Kinzler !
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Query Match
Best Local Similarity
Matches 125; Conserv
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InterPro; IPR003962; FnIII_repeat.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003600; Ig_like.
             239
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                                                                                                                  126 QAYPIARCALLEVQVPADLVQPGQSVGSAVFDCFEASLGAEVQIWSYT-KPRYQKELNLT 184
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; A54100; A54100.
; A40098; A40098.
; A38442; A38442.
                                                                                                                                              VLLDCSAESDRGVPVIKWKKDGIHLAL------GMDERKQQLSNGSLLIQNILHS 105
                                                           QQLPD-----GDNVLLTLDVSEEQDFSFLLYLRPVPDALKSLWYKNLTGPQNITLNHTD-
                                                                                              RHH--
                                                                                                                                                                          LVLRCPQKTDCALRV----RVVVHLAVHGHWAEPEEAGKSDSELQESRNASLQAQVVLSF 125
                                      SQTESVTAFMGDTVLLKCEVIGE
        --- LVPCLCIQVWSLEPDSERVEFCPFR-
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A54100.
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                                                                                       -KPDE----GLYQC-EASLGDSGSIISRTAKVAVAGPLRFL 143
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                                                                                                                                                                                                                      Score 100; DB 1;
Pred. No. 6.9;
                                                                                                                                                                                                                                                                                  MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN 1.
IG-LIKE C2-TYPE DOMAIN 2.
IG-LIKE C2-TYPE DOMAIN 3.
IG-LIKE C2-TYPE DOMAIN 3.
IG-LIKE C2-TYPE DOMAIN 4.
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 4.
FIBRONECTIN TYPE-III 5.
FIBRONECTIN TYPE-III 5.
FIBRONECTIN TYPE-III 6.
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MISSING (IN REF. 3).
MISSING (IN REF. 3).
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P -> H (IN A COLORECTAL CARCINOMA)
/FTId=VAR_003911.
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                                  -PMPTI----HWQKN----QQDLTPIPGDS
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                                                                                                                                                                                                           183;
                                                                                                                                                                                                                                    Length 1447;
       EDPGAHRNLWHI - - - -
                                                                                                                                                                                                         Indels 322;
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(POTENTIAL).
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(POTENTIAL).
CARCINOMA).
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P21333;
01-MAY-1991
SEQUENCE OF 1658-1772 FROM N.A. MEDLINE-93357748; PubMed=7689010; Maestrini E., Patrosso C., Mancini Repetto M., Villa A., Frattini A.,
                                                                                    "Long-range sequence analysis in xq28: candidate genes in 219.4 kb of high GC G6PD loci.";
                                                                                                                                SEQUENCE FROM N.A.

MEDLINE-96311563; PubMed-8733135;

Chen E.Y., Zollo M., Mazzarella R.A., Ciccodicola A., Chen Chen E.Y., Zollo M., Burough F.W., Ripetto M., Schlessinger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HUMAN
                                                                       Hum. Mol. Genet. 5:659-668(1996)
                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND PARTIAL SEQUENCE MEDLINE-90361737; PubMed-2391361;
                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                           "Human endothelial actin-binding protein (ABP-280, filamin): a |molecular leaf spring.";
                                                                                                                                                                                                                                                            Kwiatkowski|D.J.,
                                                                                                                                                                                                                                                                            Gorlin J.B.
                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                        FLN1 OR FLN
                                                                                                                                                                                                                                                                                                                                                                                                                    Endothelial
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16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                     (Filamin 1)
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                                                                                                                                                                                                                 Cell Biol. 111:1089-1105(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSADGAGYERLVGALASALSQMPLR------VAVDLWSRRELSAHGALAWFHHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WNDDNMGSLWACPMDKYIHRRWVLVWLACLLLAAALEFFLLLKKDRRKAARGS-RTALLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NVVAIEGKDAVLECCVSGYPPPSFTWLRGEEVIQLRSKKYSLLGGSNLLISNVTDDDSGM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---QKNATVNEPQDFQLVAGHPNLCVQVSTWEKVQLQACSWADSLGPFKDD----MLLVE
                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 18, Last sequence update)
(Rel. 40, Last annotation update)
actin-binding protein (ABP-280) (Nonmuscle filamin)
                                                                                                                                                                                                                                                                                                                                                                                                  (Alpha-filamín).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 18, Created)
                                                                                                                                                                                                                                                            Yamin R., Egan S., Stewart & Stossel T.P.,
D.J., Hartwig J.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -WRPPAE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---ATGRYVGVYFDGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -QPIKVA-TQPELQVPGPVENLQAVSTSPTSILITWEP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -ARLRYLSPGVWQLDAPCCLPGKVTLCWQAPD-QSPCQPLVPPVP-
                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              581
M., Rivella S., Rocchi M. Zoppe M., Vezzoni P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2647 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -LPSMASTRAARLGEELLODFRSHQCMQL
                                                                                                thirteen known and six DNA between the RCP/GC
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                                                                                                                                                                                                                                             nonmuscle
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42;

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EMBL; X53416; CAA37495.1; -.
EMBL; L44140; AAA92644.1; -.
EMBL; X70082; CAA49687.1; -.
EMBL; X70085; CAA49690.1; -.
P1R; A37098; A37098.
HSSP; P13466; 1KSR.
MIM; 300017; -.
 REPEAT
REPEAT
REPEAT
DOMAIN
REPEAT
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00033; CH; 2.

PROSITE; PS00019; ACTININ_1; 1.

PROSITE; PS00020; ACTININ_2; 1.

PROSITE; PS00021; CH; 2.

PROSITE; PS50194; FILAMIN_REPEAT; 24.

ACTIN-binding; Phosphorylation; Repeat.

ACTIN-BINDING (HEAD).
                                                                                                         REPEAT
REPEAT
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DOMAIN
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-i- FUNCTION: PROMOTES ORTHOGONAL BRANCHING OF ACTIN FILAMENTS AND LINKS ACTIN FILAMENTS TO MEMBRANE GLYCOPROTEINS.

-i- SUBUNIT: HOMODIMER. INTERACTS WITH CYMSP.

-i- SUBUNIT: HOMODIMER. INTERACTS WITH CYMSP.

-i- SUBCELLULAR LOCATION: PERIPHERAL CYTOPLASM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                       REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                          REPEAT
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Pfam; PF00630; Filamin; 24.
SMART; SM00033; CH; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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InterPro; IPR001715; Calponin_hom.
InterPro; IPR001298; Filamin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Toniolo D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTIVATION.

SIMILARITY: THE ACTIN-BINDING DOMAIN IS OF A TYPE FOUND IN MANY ACTIN-BINDING PROTEINS (SUCH AS ACTININ, DYSTROPHIN, FIMBRIN, ABP-120, ABP-180, OR BETA-FODRIN).

ABP-120, ABP-180, OR BETA-FODRIN).

SIMILARITY: CONTAINS 2 CALPONIN-HOMOLOGY (CH) DOMAINS.

SIMILARITY: CONTAINS 24 FILAMIN REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTM: PHOSPHORYLATION EXTENT CHANGES IN RESPONSE TO CELL
     1540
1649
1771
1779
1861
1951
2042
2132
2233
2327
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1062
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2646
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1539
1636
1740
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1061
1154
1249
                                                                                                                                                                                                      FILAMIN 1.
FILAMIN 2.
FILAMIN 4.
FILAMIN 5.
FILAMIN 5.
FILAMIN 6.
FILAMIN 7.
FILAMIN 10.
FILAMIN 11.
FILAMIN 11.
FILAMIN 11.
FILAMIN 12.
FILAMIN 13.
FILAMIN 14.
FILAMIN 15.
                                                  FILAMIN 16.
FILAMIN 17.
FILAMIN 18.
FILAMIN 19.
FILAMIN 20.
FILAMIN 21.
FILAMIN 22.
FILAMIN 23.
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HINGE 2
FILAMIN 24.
SELF-ASSOCIATION SITE, TAIL.
                                                                                                                                                                                             HINGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Usage
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RESULT W70T_M ID AC AC AC AC AC AC AC AC AC AC AC AC AC	Оу	Db Qy	0 V Q G	04 04 04 09 09 09 09 09 09 09 09 09 09 09 09 09	0y 0y 0y 0y	FT SQ SQ Na
9 OUSE 707_MOUSE 9D2V7; 1-MAR-2002 1-MAR-2002 1-MAR-2002 1-MAR-2002 0 kDa WD-r 0 kDa WD-r ukaryota; anmalia; E CCBI_TaxID=	572 CVLP 030 VVRFLP 628 STSAGR 081SAGS	90 22 DVDIID 19 ALA 81 EKVDVG	12 RSHQC 29 66	.620 KIECDD 283 PGVWQL :: 680 PGLEKT 318 PQKNAT : 740 PVKHTA 368 LLVEMK	22 VLSFQA : 37 VYGFEY 73 TKPRYC : 84PGLE 33 TLNHTE	T SITE T MOD_RES T CONFLICT T CONFLICT SEQUENCE D SEQUENCE Ouery Match Best Local Sim Matches 145;
STANDARD; PRT; 922 AA. [Rel. 41, Created] [Rel. 41, Last sequence update] [Rel. 41, Last annotation update] [Rel. 41, Last annotation update] [Rel. 41, Last annotation of the sequence update] [Rel. 41, Last annotation update] [Rel. 41, Last annotation update] [Rel. 41, Last sequence update] [Rel. 41, Last sequence update] [Rel. 41, Last sequence update] [Rel. 41, Created] [Rel. 41, Created] [Rel. 41, Created] [Rel. 41, Created] [Rel. 41, Created] [Rel. 41, Last sequence update] [Rel. 41, Last sequence up	PDFLQGRATGRY-VGVYFDGLLHPDSVPSPFR-VAPLFSLPTQLPAFLDALQGGC 62	VGALASALSQMPLRVAVDLWSRRELSAHG 51	QUANDDNMGSLWACPMDKYIHRRWVLWHLAC : : : NDNDTFTVKYTPR	KGDGSCDVRYWPQEAGEYAVHVLCNSEDIRLSPFMADIRDAPQDFHPDRVKARG 6 DAPCCLPGKVTLCWQAPDQSPCQ	YPIARCALLEVOVPADLVQPGOSVGSAVFDCFEASLGAEVQIWSY 1	1761 1762 CLEAVAGE (BY CALPAIN). 1 1 BLOCKED. 1772 1772 A -> G (IN REF. 3). 2634 2634 H -> D (IN REF. 2). 2647 AA; 280759 MW; 6C1A07041DFA3D42 CRC64; 11arity 20.6%; Pred. No. 17; 11arity 20.6%; Pred. No. 17; 11conservative 76; Mismatches 197; Indels 285; Gap
•	980	10 10 129	51 55 28	79 17 39 39 67 77 71	72 83 32 19	ČA .

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Matches 101; Conserv
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SEQUENCE
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REPEAT
177 YOKELNLTQQLPDG--DNVLLTLD--VSBEQDESFLLYLRPV-PDALKSLWYKNLTGPQN 231
                                                                                                                  517 -GEVAVLELQKPGRLPDTALPTLQNGTAVMDLVWDPFDPHRLAVAGEDARIRLW----- 569
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PROSITE; PS50082; WD_REPEATS_2; 4.
PROSITE; PS50294; WD_REPEATS_REGION;
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Nature 409:685-690(2001).
-I- SIMILARITY: CONTAINS 8 WD REPEATS (TRP-ASP DOMAINS).
-I- SIMILARITY: BELONGS TO THE CORONIN FAMILY OF WD-REPEAT PROTEINS.
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Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                130 IARCALLEVQVPADL-----VQPGQSVGSAVFDCFE-----ASLGAEVQIWSYTKPR 176
                                                                                                                                                                                                                                                                                          492 LTTPGESDGFCANRLRVAVPLLSSG---
                                                                                                                                                                                                                                                                                                                                                                                                                                              451 IGTSPSQRSLQSLLGPSCKFRHTQGSLLHR-DSHITNLKG--
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r L., Washio T.,
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; PF000066; notch; 3.
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INTS; PF00010; EGFLOOD.
INTS; SM00179; EGF_CA; 19
SMART; SM00179; EGF_CA; 19
SMART; SM00104; NL; 3.
PROSITE; PS00004; NLX_F
PROSITE; PS50088; ANK_F
PROSITE; PS50098; ANK_F
PROSITE; PS00010; ASX_PROSITE; PS00012; EGF
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P00740; IEDM.
ZDB-GENE-990415-173;
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97; ANK_REP_REGION; 1.
10; ASX_HYDROXYL; 23.
22; EGF_1; 34.
86; EGF_2; 28.
87; EGF_CA; 22.
87; Neurogenesis; Repeat; P.
Signal; Glycoprotein.
           : Asx_hydroxyl.
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NAR-2002 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Description of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the c
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                          Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: IMPLICATED AS A TUMOR SUPPRESSOR GENE.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- ALTERNATIVE PRODUCTS: TWO FORMS OF THE PROTEIN ARE PRODUCED THE SAME GENE BY THE USE OF ALTERNATIVE INITIATION SITES. A FORM WHICH IS EXPRESSED ONLY IN THE EMBRYO IS PRODUCED BY
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Mammalia; Eutheria;
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                                                                                                                                                  Coper H.M.;
                                                                                                                                                                                                                Cooper H.M., Armes P., Britto J., Gad J., Wilks A.F.;
"Cloning of the mouse homologue of the deleted in colorectal cancer
gene (mDCC) and its expression in the developing mouse embryo.";
ncogene 11:2243-2254(1995).
                                                                                                                                                                                                                                                                                         STRAIN-BALB/C; TISSUE-Brain;
MEDLINE-96112625; PubMed-8570174;
                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090
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                                                            CARBOHYD
                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00041; fn3; 6.
Pfam; PF00047; ig; 4.
PRINTS; PR00014; FNTYPEIII.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Repeat; Anti-oncogene;
SIGNAL 1 25
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SMART; SM00408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X85788; CAA59786.1; -. HSSP; P56276; ITLK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEVELOPING BRAIN AND NEURAL TUBE. IN ADULT, HIGHLY EXPRESSED BRAIN WITH VERY LOW LEVELS FOUND IN TESTIS, HEART AND THYMUS
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SM00410;
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iPR003962; FnIII_repeat.
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ipR003598; ig_c2.
ipR003600; ig_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          email to license@isb-sib.ch).
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161
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                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).

IG-LIKE C2-TYPE DOMAIN 1.

IG-LIKE C2-TYPE DOMAIN 2.

IG-LIKE C2-TYPE DOMAIN 3.

IG-LIKE C2-TYPE DOMAIN 3.

IG-LIKE C2-TYPE DOMAIN 4.

FIBRONECTIN TYPE-III 1.

FIBRONECTIN TYPE-III 3.

FIBRONECTIN TYPE-III 4.

FIBRONECTIN TYPE-III 5.

FIBRONECTIN TYPE-III 5.
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N-LINKED CHCNAC...)

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            N-LINKED
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native initiation; Alternative
MISSING
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EXTRACELLULAR (POTENTIAL).
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Similarity

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Score 98.5; Pred. No. 9

DB

Length 1447;

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CRC64;

Conservative

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Mismatches

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Indels

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Gaps

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                        use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-93123384; PubMed-1478958; Dahlstrand J., McKay R.D.G., Zimmerman L.B., Lendahl "Characterization of the human nestin gene reveals a evolutionary relationship to neurofilaments."; J. Cell Sci. 103:589-597(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P48681; 000552;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
entities requires a license agreement (S or send an email to license@isb-sib.ch).
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"Heterogeneity of neural progenitor cells revealed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Placenta;
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                                                                                                                                                    nestin gene.";
Biol. 205:309-321(1999).
TISSUE SPECIFICITY: CNS STEM CELLS.
TISSUE SPECIFICITY: CNS STEM CELLS.
DEVELOPMENTAL STAGE: UPON TERMINAL NEURAL DIFFERENTIATION,
IS DOWN-REGULATED AND REPLACED BY NEUROFILAMENTS.
SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
                                                                                   ween the Swiss Institute of Bioinformatics European Bioinformatics Institute. There a
                                                                                                                      SWISS-PROT entry is copyright. It is produced through a collaboration
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                   (See http://www.isb-sib.ch/announce/
                                                                              There are no restrictions
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Best Local Similarity
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                                                                                                                         UBP4_HUMAN STANDARD; PRT; 963 ÅA.
Q13107; 043452; 043453;
Q1-NOV-1997 (Rel. 35, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ubiquitin carboxyl-terminal hydrolase 4 (EC 3.1.2.15) (Ubiquitin thiolesterase 4) (Ubiquitin-specific processing protease 4)
(Deubiquitinating enzyme 4) (Ubiquitous nuclear protein homolog).
USP4 OR UNP OR UNPH.
                        TISSUE=Brain cortex;
MEDLINE=95303480; PubMed=7784062;
                                                                                     Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                               Homo sapiens (Human).
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DOMAIN
                                                   SEQUENCE FROM N.A.
                                                                            NCBI_TaxID=9606;
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   'Elevated
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MIM; 600915; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                   525
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                                                                                                                                                                                                                                                                                          P---IPPTPQAPSPAVDAEIRAQDAP
                                                                                                                                                                                                                                                                                                                 PADRVERVTQALRSALDSCTSSSEAP
                                                                                                                                                                                                                                                                                                                                        TPEGRRLGSLLPV----LSPTSLPSPLPA---
                                                                                                                                                                                                                                                                                                                                                             FLQGRATGRYYGYYFDGLLHPDSVPSPFRVAPLFSLPTQLPAFL---DALQGGCSTSAGR 633
                                                                                                                                                                                                                                                                                                                                                                                           HLKMSLSLE
                                                                                                                                                                                                                                                                                                                                                                                                              HQRRRILQEGGVVILLFSPAAVAQCQQWLQ-----LQTVEPGPHDALA---AWLSCVLPD
                                                                                                                                                                                                                                                                                                                                                                                                                                       RAALEQRIEGRWQERLRATEKFQLAVEALEQEKQGLQSQIAQVLEGRQQLA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NDDNMGSLWACPMDKYIHRRWVL----VWLACLLLAAALFFFLLLKKDRRKAARG---SR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LRVAHEEERVGLNAQAACAPRLPAPPRPPAPAPEVEEL-ARRLGEAWRGAVRGYQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NLAEELEGVAGR----CEQURLARERTTEEVARNRRAVEAEKCARAWLSSQGAELERELEA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NEPQDFQLVAGHPNLCVQV----STWEK-----VQLQAC--SWADSLGPFKD---DM 367
, Inazawa J., Gupta K., Wong A., Ueda R., Takaha:
expression of Unph, a proto-oncogene at 3p21:3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              te filament;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMKTGLNNTSVCA----LEPSGCTPLPSMASTRAARLGEELLQDFRSHQCMQLW 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 97.5;
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COIL 1A.
LINKER 1.
COIL 1B.
LINKER 12.
COIL 2A.
LINKER 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COIL
                                                                                      Catarrhini; Hominidae;
                                                                                                  Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -VGALASALSQMPLRVAVDLWSRRELSAHGALAWFH 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HEAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            coil; Neurone.
                                                                                                                                                                                                                                                                                          410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C9E9AA48C66534D0 CRC64;
                                                                                                                                                                                                                                                                                                                                        -TLETPVPAFLKNQEFLQARTPTLAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
            Takahashi
                                                                                      Homo
 in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                       336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         237
                                                                                                                                                                                                                                                                                                                                                                                                               576
                                                                                                                                                                                                                                                                                                                                                                                                                                         288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21;
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Glery Match
Best Local Similarity
Matches 107; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proto-oncogene;
ACT_SITE 311
ACT_SITE 873
ACT_SITE 881
VARSPLIC 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Q20657; AAB72237.1; --
EMBL; AF017305; AAC27355.1; --
EMBL; AF017306; AAC27356.1; --
MEROPS; C19.010; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The human UNP Locus at 3p21.31 encodes two tissue-selective, "The human UNP Locus at 3p21.31 encodes two tissue-selective, cytoplasmic isoforms with deubiquitinating activity that have reduced expression in small cell lung carcinoma cell lines."; Oncogene 16:153-165(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oncogene
         291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nterPro; IPR001394; UCH-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fam; PF00442; UCH-1; 1. fam; PF00443; UCH-2; 1.
                                                                                                                                                                                                                     62 VPTRLQTELVLRCPQKT------DCAL---RVRVVVHLAVHGHWAEPEEAGKSD 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                        ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Cytoplasmic.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; UNDEL (SHOWN HERE) AND UNPES;
ARE PRODUCED BY ALTERNATIVE SPLICING.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY C19; ALSO KNOWN AS
FAMILY 2. OF UBIQUITIN CARBOXYL-TERMINAL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: Ubiquitin C-terminal thiolester + H(2)O = ubiquitin + a thiol.
                                                                                                                                                                                                                                                                                                               VSWFLLSLALGRNPVVVSLERIMEPQDTARCSLGLSCHLWDGDVLCLPGSLQSAPGPVL- 61
                                                                                                                                        SELQESRN---
                                                                                                                                                                           IPAERETRLWNKYMSNTYEQLSKLDNTVQDAGLYQGQVLVIEPQNEDGTW--PRQTLQSK 232
                                                                                                                                                                                                                                                                    VEVYLLELKLCEN-----SDPTNV-----LSCHFSKADTI---ATIEKEMRKLEN 174
EPPSSHIQPGLCGLGNLGNTCF---MNSALQCLSNTAPLTDYFLKDEYEAEIN---
                                          --PADLVQPGQ-SVGSAVFDCFEASLGAEVQIWSYTKP-----RYQKELNLTQQLPD 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tumors.";
yene 10:2179-2183(1995)
                                                                                      SSTAPSRNFTTSPKSSASPYSSVSASLIANGDS--TSTCGMHSSGVSRGGSGFSASYNCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS00972; UCH_2_1; 1.
PS00973; UCH_2_2; 1.
PS50235; UCH_2_3; 1.
PS50235; UCH_2_3; 1.
n conjugation; Hidrolase; Thiol protease; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (OCT-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 311
373
744
                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         311
373
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873
881
279
                                                                                                                                                                                                                                                                                                                                                                                     2.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108564
                                                                                                                                 --ASLQAQVVLSFQAYPIARCALLEVQV----
                                                                                                                                                                                                                                                                                                                                                                66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ₹
:
                                                                                                                                                                                                                                                                                                                                                           Score 97; DB 1
Pred. No. 7.1;
66; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSGVSRG -> N (IN ISOFORM UNPES).
C->A: LOSS OF ACTIVITY.
S -> R (IN REF. 3).
R -> S (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KSSTAPSRNFTTSPKSSASPYSSVSASLIANGDSTSTCGMH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1B62B752F9410CD7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Usage
                                                                                                                                                                                                                                                                                                                                                              Indels 170;
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RYR3_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                      Martin C., Chapman K.E., Seckl J.R., Askiev R.H.;

"Partial cloning and differential expression of ryanodir
receptor/calcium-release channel genes in human tissues
hippocampus and cerebellum.;
Neuroscience 85:205-216(1998).
                                                              proliferation."
                                                                                                                                           SEQUENCE OF 3943-4870 FROM N.A.
                                                                                                                                                                                                                                                                                         SEQUENCE OF 520-660 FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RYR3 OR HBRR.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RYR3_HUMAN STANDARD; PRT; 4870 AA.

Q15413; Q15412; O15175;

16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)

Ryanodine receptor 3 (Brain-type ryanodine receptor) (RyR3) (RYR-3)

(Brain ryanodine receptor-calcium release channel).
                                                                       Hakamata Y., Nishimura S., Nakai J., Nakashima Y., Kita T., Imoto "Involvement of the brain type of ryanodine receptor in T-cell
                                                                                                            MEDLINE-95010709; PubMed-7523185;
                                                                                                                                                                                                                                                         MEDLINE=98268728; PubMed=9607712;
                                                                                                                                                                                                                                                                            TISSUE-Skeletal muscle,
                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98055474; PubMed=9395096;
                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 2), AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leeb T., Brenig B.;
"CDNA cloning and sequencing of the human ryanodine (RYR3) reveals a novel alternative splice site in th FEBS Lett. |423:367-370(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Fetal brain;
MEDLINE-98175492; F
                                                                                                                                                                                                                                                                                                                         FEBS Lett. 417:157-162(1997).
                                                                                                                                                                                                                                                                                                                                                                         Nakai J., Allen P.D.,
                                                                                                                                                                                                                                                                                                                                                          Molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., ALTERNATIVE SPLICING,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IFVYEVCSTSVDGSECVTLPVYFRERKSRPSSTSSASALYGQPLLLSVPKHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TFHGLFKSTLVCPECAKVSVTF----DPFCYLTLPLPLKKDRVMEVFLVPADPHCRPTQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QQQDSQELLAFLLDGLHEDLNRVKKKPYLELKDANGRPDAVVAKEAWENHRLRNDSVIVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NHTDLYPCLCIQVWSLEPDSERVEFCPF----REDPGAHRNLWHIARLRVLS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --PGVWQLDAPCCLPGKVTLCWQAPDQSPCQPLVPPVPQKNATVNE----PQD-----
                                                                                                                                                                                                                                                                                                                                                                       Y., Nishimura S., Maeda A., Allen P.D., Imoto K., Kita T
                                                                                                                                                                                                                                                                                                                                                        cloning and characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=9515741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --AYAELIKQMWSGRDAHVAPSMFKTQVGRFAPQFSGY
                                                                                                                                                                                                                                                                                      AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -PSMASTRAARLGEELLQDFRSHQ 415
                                                                                                                                                                                                                                                                                                                                                                                      Barsoumian E.L., Hakamata Y.
                                                                                                                                                                                                                                                                                                                                                          얁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AND VARIANTS
                                                                                                                                                                                                                                                                                                                                                      a human brain ryanodine
                                                                                                                                                                                                                         ryanodine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the RYR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor type he RYR3 gene.";
                                                                                                                                                                                                         including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene.
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TISSUE=Cervical carcinoma, and Hepatoma;

4644-4842 FROM N.

FEBS Lett.

352:206-210(1994)

EQUENCE OF

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PRINTS; PR00795;
SMART; SM00472;
SMART; SM00449;
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use by non-profit institutions as low
modified and this statement is not remove
entitles requires a license agreement (so
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lynn S., Morgan J.M., Lamb H.K., Meissner G., Gillespie J.I.; "Isolation and partial cloning of ryanodine-sensitive Ca2+ release Channel protein isoforms from human myometrial smooth muscle.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-94102751; PubMed-8276408; Sorrentino V., Giannini G., Malzac P., Mattei M.G.; "Localization of a novel ryanodine receptor gene (RYR3) chromosome 15q14-q15 by in situ hybridization."; Genomics 18:163-165(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AJ001515;
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MISCELLANEOUS: Ryanodine is an alkaloid that binds to the Carelease channel in junctional SR and modulates its activity.

SIMILARITY: BELONGS TO THE RYANODINE RECEPTOR FAMILY.

SIMILARITY: CONTAINS 3 SPRY DOMAINS.

CAUTION: Ref. 2 sequence differs from that shown due to probab frameshift errors at position 742-766.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: Homotetramer (Potential).

SUBCELLULAR LOCATION: Integral membrane protein (Probable).

ALTERNATIVE PRODUCTS: 3 isoforms; 1 (shown here), 2 and 3; are produced by alternative splicing.

TISSUE SPECIFICITY: Brain, skeletal muscle, placenta and possibly liver and kidney. In brain, highest levels are found in the correbellum, hippocampus, caudate nucleus and amygdala, with lower levels in the corpus callosum, substantia nigra and thalamus.

MISCELLANEOUS: The calcium release channel is modulated by calcium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ions, magnesium ions, ATP and calmodulin.

MISCELLANEOUS: The calcium release channel activity resides in C-terminal region while the remaining part of the protein constitutes the 'foot' structure spanning the junctional gap between the SR and the T-tubule. It is possible that the foot structure interacts with the cytoplasmic region of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: Communication between transverse-tubules and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              triggered by release of calcium ions from SR depolarization of T-tubules (By similarity).
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PF02815;
PF01365;
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X74270; CAA52327.1; -.
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AJ002512;
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IPR003878;
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IPR003608;
Transmembrane; Ionic channel; Calcium channel; Repeat;
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Channel_pore_Ca_Na.
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                                FLLSLALGRNPVVVSLERLMEPQDTARCSLGLSCH-LW-----
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CYTOPLASMIC (BY SIMILARITY).
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Pred. No. 61;
79; Mismatches
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                                                                                                      Overbergh L., Torrekens S., van Leuven F., van den Berghe H.;
Molecular characterization of the murinoglobulins.";
J. Biol. Chem. 266:16903-16910(1991)
-1- FUNCTION: A PROTEINASE ACTIVATES THE INHIBITOR BY SPECIFIC PROTEOLYSIS IN THE BAIT REGION, WHICH, BY AN UNKNOWN MECHANISM LEADS TO REACTION AT THE CYSTEINUL-GUJTAMYL INTERNAL THIOL ESTER SITE AND TO A CONFORMATIONAL CHANGE, WHERBEY THE PROTEINASE IS TRAPPED AND/OR COVALENTLY BOUND TO THE INHIBITION. WHILLE IN THE TETRAMERIC PROTEINASE INHIBITORS STERIC INHIBITION IS SUFFICIENTLY STRONG, MONOMERIC FORMS NEED A COVALENT LINKAGE BETWEEN THE ACTIVATED GLUTAMYL RESIDUE OF THE ORIGINAL THIOL ESTER AND A GENERALMAN AND A THE ORIGINAL THIOL ESTER AND A THE ORIGINAL THIOL ESTER AND A THE ORIGINAL THIOL ESTER AND A THE ORIGINAL THIOL ESTER AND A THE ORIGINAL THIOL ESTER AND A THE ORIGINAL THIOL ESTER AND A THE ORIGINAL THIOL ESTER AND A THE ORIGINAL THIOL ESTER AND A THE ORIGINAL THIOL ESTER AND A THE ORIGINAL THIOL ESTER AND A THE ORIGINAL THIOL ESTER AND A THE ORIGINAL THIOL ESTER AND A THE ORIGINAL THIOL ESTER AND A THE ORIGINAL THIOL ESTER AND A THE ORIGINAL THIOL ESTER AND A THE ORIGINAL THIOL ESTER AND A THE ORIGINAL THIOL ESTER AND A THE ORIGINAL THIOL ESTER AND A THE ORIGINAL THIOL ESTER AND A THE ORIGINAL THIOL ESTER AND A THE ORIGINAL THIOL ESTER AND A THE ORIGINAL THIOL ESTER AND A THE ORIGINAL THIOL ESTER AND A THE ORIGINAL THIOL ESTER AND A THE ORIGINAL THIOL ESTER AND A THE ORIGINAL THIOL ESTER AND A THE ORIGINAL THIOL ESTER AND A THE ORIGINAL THIOL ESTER AND A THE ORIGINAL THIOL ESTER AND A THE ORIGINAL THIOL ESTER AND A THE ORIGINAL THIOL ESTER AND A THE ORIGINAL THIOL ESTER AND A THE ORIGINAL THIOL ESTER AND A THE ORIGINAL THIOL ESTER AND A THE ORIGINAL THIOL ESTER AND A THE ORIGINAL THIOL ESTER AND A THE ORIGINAL THIOL ESTER AND A THE ORIGINAL THIOL ESTER AND A THE ORIGINAL THIOL ESTER AND A THE ORIGINAL THIOL ESTER AND A THE ORIGINAL THIOL ESTER AND A THE ORIGINAL THIOL ESTER AND A THE ORIGINAL THIOL ESTER AND A THE ORIGINAL THIOL ESTER AND A THE OR
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
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MUG1 OR MUG-1.
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Mammalia; Eutheria;
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                                                                          TERMINAL AMINO GROUP OF A LYSINE OR LETTER PROTEINASE, FOR INHIBITION TO BE
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InterPro; iPR001899; A2M_N.
InterPro; iPR001599; Alpha_2_macroglobln

ERIOSITE; ESUG4//; ALPHA_Z_MACKOGLOBULIN; 1. Serine protease inhibitor; Glycoprotein; Plasma; Bait region; Signal; ALPHA_2_MACROGLOBULIN;

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telomerase-associa
conserved hypothet
ubiquitin thiolest
ATP-dependent heli
                                                                                                                                                                                      genome polyprotein
probable transcrip
ATP-dependent heli
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complement C4 - ch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mouse
probable helz protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: B70841
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.;
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Hc
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
                                                                                                                                                                RESULT
B70841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: \bar{1}^-267 <NIG> A; Cross references: GB:M63696; GB:M63700; GB:M63702; GB:M63718; GB:M63698 C; Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Nigro, J.M.; Cho, K.R.; Fearon, E.R.; K
Cell 64, 607-613, 1991
A;Title: Scrambled exons.
A;Reference number: A38442; MUID:91121517
A;Accession: A38442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable tumor suppressor · human (fragment)
C;Species: Homo sapiens (man)
C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 16-Feb-1997
C;Accession: A38442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-267 <NIG
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A38442
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93.5	93.5	93.5	93.5	93.5	94	94	94.5	94.5	94.5	95	95	96	96.5	96.5	96.5	
2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.7	2.7	2.7	2.7	
7160	6839	6831	1513	927	513	509	6260	837	445	10223	1573	564	2535	1691	1187	
ν	Ν	N	N	ν	N	N	N	2	ې	N	N	Ŋ	N	_	ν	
T27935	S57242	A88852	T23681	A48085	JC5289	JC5288	T30228	A34898	E70854	T30225	S01845	D96017	T04824	D54689	JE0347	
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hypothetical prote	twitchin [similari	protein unc-22 fim	hypothetical prote	transcription fact	SHP substrate-1 pr	SHP substrate-1 pr	polyketide synthas	granulocyte colony	probable membrane	polyketide synthas	DNA (cytosine-5-)-	probable peptidase	hypothetical prote	protein-tyrosine-p	hypothetical prote	,

ALIGNMENTS

Query Match Best Local Similarity 25.6%; Pred. No. 0.13; Matches 72; Conservative 31; Mismatches 100; Indels 78; Gaps 155 VFDCFEASLGAEVQIWSYTKPRYQKELNITQQLPDGDNVLLTLDVSEEQDFSFLL 209 :	Qy Db	Оy	Qy	Qy Db	Оу	¥ 8 0
78; Gaps DFSFLL 209 59 CPFRED 265 : CSAR-N 109QK 320QK 320 TVNWMK 162 TVNWMK 162 EMKTGL 376 : : EMKTGL 376 : : : : : : : : : : : : : : : : : : :	377 NNTSVCA	321 NATVNEF 163 NGDVVIE	266 PGAHRNI : 110 PASSRT	210 YLRPVPI : 60pmpj	155 VFDCFE2 :: 8 LYQC-E2	ery Match st Local Simi tches 72;
	ALEPSGCTPLPSMASTRAARL 403 : : : : LIVPKPIPSSSVLPSAPRDVVPVLVSSRFVRL 242	PODFQLVAGHPNLCVQVSTWEKVQLQACSWADSLGPFKDDMLLVEMKTGL 376	LWHIARLRYLSPGYWOLDAPCCLPGKYTLCWOAPD-OSPCOPLYPPYPOK 320	DALKSLWYKNLTGPQNITLNHTDLVPCLCIQVWSLEPDSERVEFCPFRED 265	ASIGAEVQIWSYTKPRYQKELNLTQQLPDGDNVLLTLDVSEEQDFSFLL 209	3.2%; Score 116; DB 2; Length 267; ilarity 25.6%; Pred. No. 0.13; Conservative 31; Mismatches 100; Indels 78; Gaps 16;

Holroyd,

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Materiate names: mucin-like extracellular matrix protein Sepecies: Mus musculus (house mouse)
Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_c
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ross-references: GB:AL021924; GB:AL123456; NID:g3261519; PIDN:CAA17284.1; PID:e12523;
xperimental source: strain H37Rv
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                                                                                             elin - mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                            412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     551 QWLQLQTVE------PGPHDALAAWLSCVLP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               370 TAAVLDEAGFGVLLPSW--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                320 -- RRWLDRPQELLLTELGRASRIFPELV-----PALRTACPSGLELDADGA--YRFLSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90 LAVHGHWAEP--EEAGKSDSELQESRNASLQAQVVLSFQAYPIARCALLEVQVPADL--- 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IHRRWV----LVWLACLLLAAALFFFLLLKKDRRKAARGSRTALLLHSADGAGYERLVGA 492
                                                                                                                                                                                                                       DGFTATLRPYQQRGLAWLAFLSSLGLGSCLADDMGLGKTVQ 567
                                                                                                                                                                                                                                                                      ERVTQALRSALDSCTS----SSEAPGCCEEWDLGPCTTLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VCALEPSGCTPLPSMASTRAARLGEELLQDFRSHQCM----QLWNDDNMGSLWACPMDKY 436
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                                                                                                                                                                                                                                                                                                                          KPTGRKTTAEILALAASHPDDVDTPLEVTAV-----RADGWLGDLLAGAAAASLQPLDPP 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LASALSQMPLRVAVDLWSRRELSAHGALAWFHHQRRRILQEGGVVILLFSP--AAVAQCQ 550
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20.4%; Pred. No. 0.91;
ative 75; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --W---DRRRKL---GLVLSAYTPVDGVVGKAS
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        #text_change 17-Mar-2000
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A; Map
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R;Lyne, M:, Rajandream, M.A.; Barrell, B.G.; Badcock, submitted to the EMBL Data Library, March 1998
A;Reference number: Z21879
A;Accession: T39784
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A; Residues: 1-2910 <COH>
A; Residues: 1-2910 <COH>
A; Cross references: EMBL.U96411; NID:g2760883; PID:g2760884; PIDN:AAB96561.1
A; Experimental source: strain BALB/c
A; Experimental source: strain BALB/c
A; Note: component of all the acellular membranes of the inner ear
                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:AL022304; PIDN:CAA18417.1; A;Experimental source: strain 972h-; cosmid cIBH10
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R;Cohen-Salmon | M.; El-Amraoui, A.; Leibovici, M.; Petit, C.
R;Cohen-Salmon | M.; El-Amraoui, A.; Leibovici, M.; Petit, C.
Proc. Natl. Acad. Sci. U.S.A. 94, 14450-14455, 1997

A;Title: Otogelin: A glycoprotein specific to the acellular
A;Reference number: Z22079; MUID:98070772
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 1-361 <LYN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local :
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local 54;
                                                59
                                                                                                                                                                         16 PVVVSLERLMEPQDTARCSLGLSCHLWDGDVLCLPGSLQSAPG------PVL 61
                                                                                                                                                                                                                                                Local Similarity
VLSFQAYPIARCALLEVQVPADLVQPGQSVGSAVFDCFEASLGAEVQIWSYTKPRYQKEL 181
                                            KVHTLKLQLIKRI--
                                                                                     VPTRLQTELVLRCPQKTDCALRVRVVVHLAVHGHWAEPEEAGKSDSELQESRNASLQAQV 121
                                                                                                                               PLKLALPRSTTPKDPARCTLDIR---MESPPLVFLGSPETSSGALASGILKLTILHQPFI 58
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                                                                                                                                                                                                                            84;
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                                            -TVLHPAI-SHCS----ACAGSKEVLQTWDLAANTTY 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 110; DB Pred. No. 7.9;
                                                                                                                                                                                                                                                Pred.
                                                                                                                                                                                                                                            Score 108.5; DB-2;
Pred. No. 0.74;
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                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                       Indels 143;
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Query Match
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Matches 118
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Jence 286, 1571-1577, 1999

Active: Genome sequence of the radioresistant bacterium Deinococcus radiodurans number: A75250; MUID:20036896
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secies: Deinococcus radiodurans
secies: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
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                                                516 AHGALAWFH-----HQRRRILQEGGVVILLFSPAAVAQCQQWLQLQTVEFGPHDALAAW 569
                                                                                                                                                                                                                                                                                                                                                                                405
                                                                                                                                    251 ADAAQTRHLARLAALGRACALLLLPAEQHGRLRLARTLARRLRGDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134 LARAPGQLPGTVPAHSVLYAQEEASALSAPAAGDGLTLH------LGGPD---RLAHW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        213 PVP---DALKSLWYKNLTGPQNITLNHTDLVPCLCIQVWSLEPDSERVEFCPFREDPGAH 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74 ALFAQLAAIRQRGGSPHERAQLEEVLRAGAGPQSALRADPRERPLLREAAQRIRRWLARR 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QLDAPCCLPGKVTLCWQAPDQSPCQPLVPPVPQKNATVNEPQDFQLVAGHPNLCVQVSTW
                                                                                                                                                                                                                                                                                                                                                                    EELLQDFRSHQCMQLWNDDNMGSLWACPMDKYIHRRWVLVWLACLLLAAALFFFLLLKKD 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PVPGAGDVLVSLGNSEVVRQLARTLGDLLLLPGGAAQVWQA---LDRVEDDPFPPQPGDD 73
                                                                                                                                                                                                                                                                                                                                                                                                                                            QGLRL---SWR-SLGP--NWQLLVQDETSQPVSGGQLALLRPD----LP--ASER-----
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23.2%; Pred. No. 1.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca; S.C.; Franco, M.C.; Fr J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajina, J.P.; Krieger, J.E.; Kuramae, E.E.; La chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.Y.; Martins, A.Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menok, C.F.M.; Miracca, E.C.; Miyaki, C., F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sava-A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, A.R.; Startelli, R.V.; Sava-A; M.S.; Van Silva, A.S.; Verjovski-Almeida, S.; Vettore, A.L., A.Reference number: A59328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-698 <SIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: A82593
R;anonymous, The Xylella fastidiosa Consortium of the Organi Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fa;Reference number: A82515; MUID:20365717
A;Note: for a complete list of authors see reference number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein XF2169 [imported] - Xylella fastidiosa (strain 9a5c) C:Species: Xylella fastidiosa C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113
                                                                                        285
                                                                                                                                                                        354
                                                                                                                                                                                                                                                                                                                                                                                        173 TKPRYQKELNLTQQLPDGDNVLLTLDV----SEEQDFSFLLYLRPVPDALKSLWYKNLTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    150 TIALRRGOVDQALTMLSQAVELLPEEPAVLFSLGFA-YLQKGHIAFAERAFQRVIELNPH 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                209 VIPVRALIAQLAQRQGRLDDALRILEEALSLPEGDTPALHRUTGEFELLAGHPDRALTHL 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        621 DALQGGCSTSAGRPADRVERVTQALRSAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 LVPTRLQTELVLRCPQKTDCALRV-RVVVHL-----AVHGHWAEPE-EAGKSDSELQES 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 SLAIGRNPVVVSLERLME-----PQDTA-RCSLGLSCHLWDGDVLCLPGSLQSA--PGPV
                                                                            VWQLDAPCCLPGKVTLCWQAPDQSPCQPLVPPVPQKNATVNEP----QD----FQLVAG 335
                                                                                                                                                            LHDIQ-NNPEAAETVARQIVAIEPGRLSGEQRIVEALLQRDPPT-
                                                                                                                                                                                                                                    PQNITLNHTDLVPCLCIQVWSLEP----DSERVEFCPFREDPGAHRNLWHIARLRVLSPG 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNASIQAQVVLSFQAYPIARCALLEVQVPADLVQPGQSVGSAVFDCFEASIGAEVQIWSY 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VFPLGPDPLEVRLPGDRLLTLRPDYRAEL 428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALLHLPP-----HYAAQVQQAAEHAASAAEPLREAATDPLVGREAGPPVLPATGHFI 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ASGQVAFAQTPAECLAAARRSLQRLEPLLGRFSPAQVA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QVLATWPEDPRTLEALLTAWKQLDMDDDARTTDAALD-----
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                                                                                                                                                                                                                                                                                                                    -NHDLWLARLAVAPVGSDEARIVIERWLSAMPEHLPAL -- ETLMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 105.5;
Pred. No. 3;
QQLIESVPEHERTILRPWLGLVQDRAGQFE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        257;
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Best Local S
Matches 76
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esidues: 1-1451 <OVE>
ross-references: GB:M65238; NID:g199888; PIDN:AAA73041.1; PID:g199889
uperfamily: alpha-2-macroglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              piol. Chem. 266, 16903-16910, 1991 Gen Bellitle: Molecular characterization of the murinoglobulins eference number: A41185; MUID:91358495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ha-2 macroglobulin homolog MUG2 - mouse
pecies: Mus musculus (house mouse)
ate: 28-May-1992 #sequence_revision 28-May-1992 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            verbergh, L.; To
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                                                                                                                                                                                                                                                                                     560
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                                                                                321
                                                                                                                        662
                                                                                                                                                                                            610 IYNLPGMQ-----HNKFIPSSSLSEDREDCILYSSWVAE---KHTDWVPHGREKDVYRYV
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                                                                                                                                                                                                                                                                                                                                                                   514
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374 TGLNNTSVCALE 385
                                                                                                                                                                                                                                        223 YKNLTGPQNITLNHTDLVP----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  616 LPAFLDALQGGCSTSAGRPADRVERVTQALRSALDS 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                564 DAL---AAWLSCVLPDFLQGRATGRYVGVYFDGLLHPDSV-PSPFRVA----PLFSLPTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        544 ARGIEDGNVIDWLLWWDNSLLTALRPHLPEGRLIIVLRDPRDM--LLDWIAYGSPIPLAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              516 AHGA-----LAWFHHQ----RRRILQEGGVVILLFSPAAVAQCQQWLQLQTVEPGPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 503 ----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 QTELVLRCPQ-----KTDCALRVRVVVHLAV------HGHWAEPEEA--- 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                        DPPPKDPLAETIRKYFPETWV----
                                                                          NATVNEPODFOLVAGHPNLCVQVSTWEKVQLQACSWA--
                                                                                                                                                                                                                                                                                                                  LGAEVQIWSYTKPRYQKELNLTQQLPDGDNVLLTLDVSEEQDFSFLLYLRPVPDALKSLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FFFLLLKKDRRKAARGSRTALLLHSADGAGYERLVGALASALSQMPLRVAVDLWSRRELS
                                                                                                                EDMDLKAFTNLKIKLPKICFDSAPMSGPRGKFDLAFSSEVSGTLQKGSSKRPQPEEPPRE
                                                                                                                                                                                                                                                                                                                                                                   GNFDLE----
                                                                                                                                                                                                                                                                              VDLSFSS-SQSLPASQTRLQVTAS-PQSLCGLRAVDQS-----VLLLKP-EDELSPSW
                                                                                                                                                                                                                                                                                                                                                                                                                                         ETSSILPCNQIHTVQAHFILKGDLGVLKELVFYYLVMAQGSIIQTGNHTHQVEPGEAPVK 513
                                                                                                                                                      ---NLWHIARLRVLSPGVWQLDAPCCLP-GKVTLCWQAPDQSPCQ-----PLVPPVPQK 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPPSLEAPR----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAIPAEILARPLL-----IWGPPGSHVERVTMMMAWASSMLC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASTRAARLGEELLQDFRSHQCMQLWNDDNMGSLWACPMDKYIHRRWVLVWLACLLLAAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----AALATWLQFQAEQAKYRLPLPP---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Torrekens, S.; Van Leuven,
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                                                                                                                                                                                                                                                                                                                                                          ----IPVEFSMAPMAKMLIYTILPDGEVI--ADSVNFEIEKCLRNK 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 105.5; E
Pred. No. 7.5;
48; Mismatches
                                 -WDIVTVNSTGVAEVEMTVPDTITEWKAGALCLSND
                                                                                                                                                                                                                                      -CLCIQVWSLEPDSERVEFCPFREDPGAHR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F.; Van den Berghe,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         159;
                                                                          ----DSLGPFKDDMLLVEMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1451;
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RESULT
A49502
  protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type 4E, splice form A precursor
C;Species: Drosophila melanogaster
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 24-Apr-1998
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F;1525/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1531/Binding site: substrate phosphate (Arg) #status predicted
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F;1271-1615/Domain: intracellular #status predicted <INT>
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C;Species: Drosophila melanogaster
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_char
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J. Biol. Chem. 268, 23964-23971, 1993
A;Title: Alternative splitcing in a novel tyrosine phosphatase gene
A;Reference number: A49502; MUID:94043220
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A; Residues: 1-1615 <00N>
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49; Mismatches 136;
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Pred. No. 9.4;
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Matches 98
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Biol. Chem. 268, 23964-23971, 1993
Fitle: Alternative splicing in a novel tyrosine phosphatase Reference number: A49502; MUID:94043220
Accession: A49502
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ross-references: FlyBase:FBgn0004368
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ternate names: perlecan
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Dnan, D.M.; Fulle, A.; Valente, P.; Cai,
Lol. Chem. 266, 22939-22947, 1991
                                                                                            onan, D.M.; Fulle,
                        erence number: S18252;
                                           ion molecule.
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                                                          The complete sequence
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                          MUID: 92078153
                                                        of perlecan,
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Pred. No. 11;
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F:199-234/Domain: LDL receptor ligand-binding repeat homology F:285-319/Domain: LDL receptor ligand-binding repeat homology F:325-359/Domain: LDL receptor ligand-binding repeat homology F:368-403/Domain: LDL receptor ligand-binding repeat homology F:764-811/Domain: LDL receptor ligand-binding repeat homology F:764-811/Domain: laminin-type EGF-1ike homology <LEGS
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A;Residues: 1272-1274,'X',1276,'X',1278-1279 <SCH>
C:Superfamily: LDL receptor ligand-binding repeat
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R;Schulze, B.; Mann, K.; Battistutta, R.; Wiedemann, H.; Timpl, R.
Eur. J. Biochem: 231, 551-556, 1995
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J. Biol. Chem. 263, 16379-16387, 1988
A;Title: Identification of cDNA clones encoding
A;Reference number: A92680; MUID:89034110
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A;Cross-references: EMBL:M77174; NID:g200295; PIDN:AAA39911.1; PID:g200296
A;Cross-references: EMBL:M77174; NID:g200295; PIDN:AAA39911.1; PID:g200296
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A; Residues: 1870-2600 < NO3>
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A;Accession: B31917
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3464-3492/Domain:
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RLGEE
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                                                                                                                                                                                                                                                                                                                                                                                  DNVLLTLDVSEEQDFSFLL-----YLRPVPDALKSLWYKNLTGPQN--ITLNHTDLVP 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---CPQKTDCALRVRVVVHLAVHGHWAEPEEAGKSDSELQESRNASLQAQVVLSFQAYPI 130
                                                YGGFLRYKVRYELARGM--
                                                                                          LGPFKDDMLLVEMKTGLNNTSVCALEP---
                                                                                                                                                                                         CWQAPDQSPCQPLVPPVPQKNATVNEP-QDFQLVAGHPNLCVQVSTWEKVQLQACSWADS
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406
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laminin-type EGF-like homology <EG7>
laminin-type EGF-like homology <LEG8>
EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                          ----SRGOTV----TFTCVATGVPTPIINWRLNWGHIPAHPRVTMTSEGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.9%; Score 103.5; 20.5%; Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NID:g200252; PIDN:AAA39899.1; PID:g200253
                                           -LEPVQKPDVILVGAGYRLHSRGHTPTHPGTLNQRQV
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          Conable transcription regulator PA3921 [imported] - Pseudomonas aeruginosa 15 [imported] - Pseudomonas aeruginosa 15 [imported] - Pseudomonas aeruginosa 15 [imported] - Pseudomonas aeruginosa 15 [imported] - Pseudomonas aeruginosa 15 [imported] - Pseudomonas aeruginosa 15 [imported] - Pseudomonas aeruginosa 15 [imported] - Pseudomonas aeruginosa 15 [imported] - Pseudomonas aeruginosa 15 [imported] - Pseudomonas aeruginosa 15 [imported] - Pseudomonas aeruginosa 15 [imported] - Pseudomonas aeruginosa 15 [imported] - Pseudomonas aeruginosa 15 [imported] - Pseudomonas aeruginosa 15 [imported] - Pseudomonas aeruginosa 15 [imported] - Pseudomonas aeruginosa 15 [imported] - Pseudomonas aeruginosa 15 [imported] - Pseudomonas aeruginosa 15 [imported] - Pseudomonas aeruginosa 15 [imported] - Pseudomonas aeruginosa 15 [imported] - Pseudomonas aeruginosa 15 [imported] - Pseudomonas aeruginosa 15 [imported] - Pseudomonas aeruginosa 15 [imported] - Pseudomonas aeruginosa 15 [imported] - Pseudomonas aeruginosa 15 [imported] - Pseudomonas aeruginosa 15 [imported] - Pseudomonas aeruginosa 15 [imported] - Pseudomonas aeruginosa 15 [imported] - Pseudomonas aeruginosa 15 [imported] - Pseudomonas aeruginosa 15 [imported] - Pseudomonas aeruginosa 15 [imported] - Pseudomonas aeruginosa 15 [imported] - Pseudomonas aeruginosa 15 [imported] - Pseudomonas aeruginosa 15 [imported] - Pseudomonas aeruginosa 15 [imported] - Pseudomonas aeruginosa 15 [imported] - Pseudomonas aeruginosa 15 [imported] - Pseudomonas aeruginosa 15 [imported] - Pseudomonas aeruginosa 15 [imported] - Pseudomonas aeruginosa 15 [imported] - Pseudomonas aeruginosa 15 [imported] - Pseudomonas aeruginosa 15 [imported] - Pseudomonas aeruginosa 15 [imported] - Pseudomonas aeruginosa 15 [imported] - Pseudomonas aeruginosa 15 [imported] - Pseudomonas aeruginosa 15 [imported] - Pseudomonas aeruginosa 15 [imported] - Pseudomonas aeruginosa 15 [imported] - Pseudomonas aeruginosa 15 [imported] - Pseudomonas aeruginosa 15 [imported] - Pseudomonas aeruginosa 15 [imported] - Pseud
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esidues: 1-851 <WIL>
ross-references: EMBL:AL117204; PIDN:CAB55154.1;
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eference number: Z21041
ccession: T31520
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ns: 99/3; 124/2;
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Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey,
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Pred. No. 6;
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   M.J.;
                                                                                                                                  PAO1
   В
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C;Comment: The sequence contains ten fibronectin type III repeats and two protein-tyre;Superfamily: protein-tyrosine-phosphatase, receptor type OST; fibronectin type III C;Keywords: phosphoprotein; phosphoric monoester hydrolase; receptor; transmembrane p F;1-18/Domain: signal sequence #status predicted <SIG:
F;19-1711/Product: protein-tyrosine-phosphatase, receptor type OST #status predicted
                                                                                                                                                                                              A; Reference number: A; Accession: A55148
                                                                                                                                                                                                              R;Mauro, L.J.; Olmsted, E.A.; Skrobacz, B.M.; Mourey, R.J.; Davis, A.R.; Dixon, J. Ball. Chem. 269, 30659-30667, 1994
A;Title: Identification of a hormonally regulated protein tyrosine phosphatase A;Reference number: A55148; MUID:95074080
                                                                                                                                                                                                                                                                                                                A; Molecule type: |mRNA
A; Residues: 1-1711 < MAU>
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                                                                                                          A; Cross-references: GB:L36884
                                                                                                                                                                       A; Status: not compared with conceptual translation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-906 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: A82950; A; Accession: G83156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an A; Reference number: A82950; MUID: 20437337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000
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                                                                                                                                                                                                                                                                                                           ; Accession:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          313 LVPPVPQKNATVNEPQDFQLVAGHPNLCVQVSTWEKVQLQACSWADSLGPFKDDMLLVEM 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GRYVGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPAAVAQCQQWLQLQTVEPGPHDALAAWLS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FAQRYGNPLFEALVHYDRARVLQARGEVARAEEEVRQGLERLQHLPAQRRYAVRGRLLLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MDKYIHRRWVLVWLACLL-----LAAALEFFL------LL------KKD 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRLILLYGWALA-LACQIDAAEELAGQLARFIPAPDESAQRDILAQWQALSGVIARGRGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -- AWFHHORRRILQEGGVV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 103; DB 2; Pred. No. 6.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136;
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                                                                                                                                                                                                                                                                              J.E.
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protein-tyrosine-phosphatase,

receptor type OST #status predicted

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Matches 149;
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Best Local Similarity
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350/Active site: Cys (phosphocysteine intermediate) #status p
356/Binding site: substrate phosphate (Arg) #status predicted
ol. Chem. 266, 16903-16910, 1991
le: Molecular characterization of the murinoglobulins
number: A41185; MUID:91358495
                                                     ccies: Mus musculus (house mouse)
e: 28-May-1992 #sequence_revision 28-May-1992 #text_change 12-Apr-1995
ession: A41185
ersetion: A41185
erbergh, L.; Torrekens, S.; Van Leuven, F.; Van den Berghe, H.
erbergh, L.; Torrekens, S.; Van Leuven, F.; Van den Berghe, H.
erbergh, L.; Torrekens, S.; Van Leuven, F.; Van den Berghe, H.
                                                                                                                                                                               1-2 macroglobulin MUG1 - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             537
                                                                                                                                                                                                                                                                                                  921
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 237 TDLVP--CLCIQVW----SLEPDSERVEFCP-----FREDPGAHRNLWH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43 DGDVLCLPGSLQSA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VILLESPAAVAQCQQWLQLQTVEPGP-HDAL----AAWLS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSGPLGOGACHAQLSDAGHLSWEQPLKLGQELFMLRDLTPGHTISMSVRCRAGPLQASTH 825
                                                                                                                                                                                                                                                                                                                                             STSA 631
                                                                                                                                                                                                                                                                                                                                                                                --VVERLYPGGGTHEVFQVNTSGDALLLPNLMPTTSYRLS--LTVLGRNSRWSRAVSLVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LWL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GRSRYQVTLYQESTRTATSIMGP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KSLVPGSSYTVSAWAWAGNLGSDSQKIHSCTRPAPPTNLSLGFAHQPAALKASWYHPPGG
                                                                                                                                                                                                                                                                                                  STSA 924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------GALASALS------QMPLRVAVDLWSRRELSAHGALAWFHHQRRRILQEGGV 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KY--KVEVISWAGPLYTAAANVSAWTYPLIPNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KYIHRRWYLVWLACLLLAAA---LFFFLLLKKDRRKAARGSRTALLLHSADGAGYERLV- 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLNNTSVCALEPSGCTPLPSMASTRAARLGEELLQDFRSHQCMQLWNDDNMGSLWACPMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----SANATGWTP------PSAPTL-VNVTSDAPTQLQV-SWAHVPG-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPVPQKNATVNEPQDFQLVAGHPNLCVQVSTWEKVQLQACSWADSLGPFKDDMLLVEMKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RDAFHLRLYRLRPLTLESEKVLPREAQNFSWAQLTAGCEFQVQLSTLWGSERSS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PADLVQ------PGQ----SVGSAVFDCFEASIGAEVQIWSYTKPRYQKELNLTQQLPD 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----IARLRVL---SPGV------W-QLDAPCCLPGKVTLCWQAPDQSPCQPLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----ISRSSPSDLTIAWGPAPGQLEGYKVTWHQDGSQRSPGDLVDLGPDTLSLTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PSGATHVIFCGLVPGAHYRVDIASSTGDISQSISG-----YTSPLPPQSLEV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AALPREVPGARL---WLDGLEASK-----QPGRRALLYSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DGYVLKLSGPMESTSTLGPEECNAVFPGP-LPPGHYTLQLKVLAGPYDAWVEGSTWLAES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -SVEPGPVEDVLCHPEATYLALNWTMPAGDVDVCLV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 102.5;
; Pred. No. 16;
79; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---PGPVLVPTRLQTEL-VLRCPQK-----TDC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     229;
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A;Cross-references: GDB:119838; OMIM:120470
A;Map position: 18q21.1-18q21.1
C;Keywords: transmembrane protein; tumor suppressor
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-1447/Product: tumor suppressor protein DCC #status predicted
                                                                                                                                                                                                                                                                                                                   R;Cross-references: EMBL:X76132; NID:g453209; PIDN:CAA53735.1; PID:g453210 R;Fearon; E.R.; Cho, K.R.; Nigro, J.M.; Kern, S.E.; Simons, J.W.; Ruppert, Science 247, 49-56, 1990 A;Title: Identification of a chromosome 18q gape that is altered in colored A;Reference number: A40098; MUID:90100559
                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: | mRNA
A; Residues: 1-1447 < HED>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: The DCC gene product in cellular differentiation and A;Reference number: A54100; MUID:95011532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; Hedrick, L.; Cho, K.R.; Fearon, E.R.; Wu, T.C.; Kinzler, Genes Dev. 8, 1174-1183, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C:Species: Homo saplens (man)
C:Date: 02-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 05-Nov-1999
C:Accession: A54100; A40098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1476 <OVE>
A;Cross-references: GB:M65736
C;Superfamily: alpha-2-macroglobulin
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                                                                                                                                                                                                                      C; Genetics:
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A; Residues: 1-750
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Maximum Match 100%
Listing first 45 summaries
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112pp;	peptide encoding inflammation e.	'n	Burkhead S	CS INC	IS-034885	2000WO-US18383				2cyt gene	receptor	st entry)		Protein;			997 1433	2969	1728	1447	1013	1042	866	866	866	866	966	330	86 4	864 864	864	864	864	617	204 617
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ish.	human cytokine r rheumatoid arthr	•	Pownder SL;							human; inflammation; py; vaccine.	or14.			692 AA.		ALIGNMENTS	ABG08088 ABG08373	ABG28379 AAW56442	AAR13144	AAY33498	AAG81163 AAR68553	ABG26706	AAB62066	AAY97181	AAY99941 AAY97131	AAW92409	AAW04185	AAY75947	AAB62060 AAY72748	AAY97180 AAB03806	AAY97130	AAW92408	AAW04184	5598	AAE10920 AAY76048
•	receptor ritis			•												•	•																		
	Zcytor14,									rheumatoid							Novel Novel	Novel Fragm	Human Delet	Human	Mycobact	Human Novel	Human	Human	. Human	Human	Human	Murine	Murine	Murine Murine	Murine Murine	Murine	Murine	Skin	Human
	for									d arthritis;							human diagn human diagn	humai ent Ho		DCC pro	Mycobacterium tube	- 5						ne skin cell s	ne IL-17R poly	ne interleukin ne interleukin	ne IL-17R prot ne interleukin	interleu IL-17R	ro -	0.0	gene 12 enc

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Query Match
Best Local Similarity 67.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention provides a new human cytokine receptor desinated Zcytor14. Czytor14 can be expressed by standard recombinant methodology. The encoding nucleic acid is useful for detecting the expression of a Zcytor14 gene in a biological sample. Anti-Zcytor14 antibodies can be used to screen biological samples in vitro for the presence of Zcytor14. Proteins, polypeptides and peptides having Zcytor14 activity can be administered to a subject who lacks an adequate amount of this polypeptide, for treating inflammation and conditions such as rheumatoid arthritis. In contrast, Zcytor14 antagonists (e.g. anti-Zcytor14 antibodies) can be used to treat a subject who produces an excess of Zcytor14. Zcytor14 nucleotide Edguences can also be used to provide zcytor14 to a subject. The present sequence represents the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                            SAGRPADRVERVTQALRSALDSC--TSSSEAPG
                                                                                                                                                                                                                                                                                              | | |||:|: | ||||| ||: |||:|| ||||||: :| ||:: :| |
| wqaarlriltiqswildapcsipaeaalcwrapgdpcqplvpplswenvtvdkvlefpl
                                                                                                                                                                                                                                                                                                                 WHIARLRYLSPGVWQLDAPCCLPGKVTLCWQAPDQSPCQPLVPPVPQKNATVNEPQDFQL
                                                                                                                                                                                                                                                                                                                                                 rsgrlqeraeqvsralqpaldsyfhppgtpapg
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Pred. No. 5.4e-218;
66; Mismatches 138; I
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ESULT NU29322

Novel nucleic acids encoding PRO polypeptides, used to diagnose the presence of tumours, such as prostate and breast tumours, in mammals to screen for modulators of the compounds -

mammals

and

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08-NOV-2000;
01-DEC-2000;
20-DEC-2000;
                                                                                                                 25-APR-2000;
25-APR-2000;
03-MAY-2000;
17-MAY-2000;
22-MAY-2000;
30-MAY-2000;
02-JUN-2000;
05-JUN-2000;
28-JUL-2000;
28-JUL-2000;
24-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRO polypeptide; mammal; dog; cat; pig; goat; rab
                                                                              (GETH
                                                                                                                                                                                                  25-APR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     adrenal;
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                                   2001-602746/68.
DB; AAS46223.
                                                                              J
                                                                ξP
                                                                                                                                                                                                                                                                                                                                                                                                                                                        at; pig; goat; rabbit; tumour; cancer; human; cattle; horse; she at; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alp chondrocyte cell; cell proliferation; cell differentiation;
                                                       Smith V, Watanabe CK,
                                                                              GENENTECH
                                                                                                                                                                                                                                                                                                                                                                                                                                                     lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                           2000WO-US30952
                                                                                                                   2000WO-US23328
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2000WO-US13705
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2000US-199397P
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198121P.
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                                                       Wood WI, Zhang
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                                                              Godowski
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PJ,
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                                                              Gurney AL;
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Claim 11; Fig
  598;
774pp; English
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Sequences ANU29024-ANU29328 represent PRO polypeptides of the invention.

The PRO polypeptides and their associated nucleic acids can be used to detect the presence of a tumour in a mammal by comparing the level of expression of a PRO polypeptide in a test sample of cells from the animal and a control sample of normal cells, whereby a higher level of expression in the test sample indicates the presence of a tumour in the mammals include dogs, cats, cattle, horses, sheep, pigs, goats and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor, (TNP) alpha release from human blood, when contacted with it. Asspectfic polypeptide can be used to stimulate tumour necrosis factor, or lypeptide can be used to grotelns can be used to determine the presence of tumours and also susceptibility to tumour development, particularly adrenal, lung, colon, breast, prostate, rectal, cervical, or liver tumours, in mammalian subjects. The oligonucleotide probes specific for the PRO nucleic acids can be used for genetic analysis of individuals with genetic disorders. of cells from the animal

Query Match 63.9 Best Local Similarity 65.9 Matches 466; Conservative 63.5%; 65.9%; Score 2376; DI Pred. No. 1.1e 66; Mismatches ; DB 22; 1.1e-216; hes 135; Length 705;

66;

Indels

40;

Gaps

7;

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296

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465 477 $a als lill k k d hak gwlr llk q dvrs gaaarg\cdot raal lly saddsg fer lv galasalc$ AALFFELLLKKDRRK-------AARGSRTALLLHSADGAGYERLVGALASALS 522 523

464

406

583 EP---GPHDALAAMLSCVLPDFLQGRATGRYVGVYFDGLLHPDSVPSSPFRVAPLFSLPTQ lscvlpdflqgrapgsyvgacfdrllhpdavpalfrtvpvftlpsq 643

644 640 ${\tt lpdflgalqqpraprsgrlqeraeqvsralqpaldsyfhppqtpapg}$ LPAFLDALQGGCSTSAGRPADRVERVTQALRSALDSC--TSSSEAPG 684

> RESULT AAU04956 Human Interleukin 17 receptor, IL-17RH2. 24-OCT-2001 AAU04956; AAU04956 w standard; Protein; 705

PRO20040; Interleukin-17 receptor; IL-17RH2; agonist; antagonist; PRO20040; DNA 164625-2890; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; diabetes mellitus; degenerative cartilaginous allergic Interleukin-17 receptor; asthma; demyelinating disease; ilaginous disorder; transplanta IL-17RH2; disease

Homo sapiens

WO200146420-A2 Region Domain Region Region Region Region Modified Modified-site Modified Modified Modified-site Modified Modified-site Region Modified-site Region Protein Peptide Key -site -site -site -site -site /note= "As.. 391..394 /note= "1 453..473 /note- "A 357..360 /note= "/ 319..324 /note- " 248..251 /note= " 238..241 /note- 198..201 /note= 700..7(696..701 /note= "cAMP/GMP-dependent protein kinase 552..555 438..443 334..337 /note-118..121 'note= /note-/note-/note-186..189 152..157 Location/Qualifiers 'note-/note-/note-/label Signal_peptide note-/note-/label= Mature_IL_17RH2 ..705 Asn "Asn "Asn "N-myristoylation "Glycosaminoglycan attachment site" "N-myristoylation site" "Transmembrane domain" "N-myristoylation site" "Asn is "Asn "N-myristoylation site" "N-myristoylation site" "N-myristoylation site" "Asn is N-glycosylated" "N-myristoylation "Asn is N-glycosylated" is N-glycosylated* is N-glycosylated" is is N-glycosylated* is is N-glycosylated N-glycosylated" N-glycosylated" N-glycosylated* site" site"

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The sequence is PRO20040 which is the human Interleukin 17 receptor, II-17RH2, encoded by DNA 164625-2890. A composition containing ant/agonists to the PRO polypeptides or individual components are useful for treating a manmal with an immune related disease, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an idiopathic inflammatory myopathy. Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, a demyelinating disease, an autoimmune or immune-mediated skin disease, contact dermatitis, an altergic disease e.g. food hypersensitivity, asthma, a transplantation associated disease, or a degenerative cartilaginous disorder comprises administering a PRO1031 or PRO1122 polypeptide agonist, or antagonist to the mammal. Numerous examples of the diseases and disorders are given in the specification.
                                                                                                                                                                                                                                   Matches
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Best Local 9
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diagnosis
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28-NOV-2000;
01-DEC-2000;
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11-JAN-2000;
18-FEB-2000;
02-MAR-2000;
21-MAR-2000;
21-MAR-2000;
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22-JUN-2000;
22-AUG-2000;
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Gurney AL, Li H, Hillan KJ, Tumas D, Van Lookeren
Watanabe CK, Williams PM, Wood WI, Yansura DG;
                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arthritis
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24 - OCT - 2000;
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       181
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           YQKELNLTQQLPDCRGLEVRDSIQSCWVLPWLNVSTDGDNVLLTLDVSEEQDFSFLLYLR
                                                                  LQAQVVLSFQAYPIARCALLEVQVPADLVQPGQSVGSAVFDCFEASLGAEVQIWSYTKPR 176
                                                    lqaqvvlsfqayptarcvllevqvpaalvqfgqsvgsvvydcfeaalgsevriwsytqpr
                                                                                                                                                                                                                                   466;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polypeptides homologous to interleukin-17, useful for the and treatment of immune related disease e.g. rheumatoid and diabetes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fig 14;
                                                                                                                                                                                                                                                                                                     705 AA;
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2000WO-US05841

2000WO-US05841

2000US-0191007

2000WO-US07532

2000WO-US07532

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2000US-0644848

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2000US-0242837

2000US-0253646

2000WO-US30873

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2000WO-US30873
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99WO-US31274.
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Pred. No. 1.16
66; Mismatches
-alpwlnvsadgdnvhlvlnvseeqhfglslywn
                                                                                                                                                                                                                            ; DB 22;
1.1e-216;
hes 135;
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n Lookeren.M,
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Vandlen RL;
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             Eaton DL,
Grimaldi
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22-FEB-2000;
01-MAR-2000;
03-MAR-2000;
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15-SEP-1999;
07-DEC-1999;
09-DEC-1999;
11-JAN-2000;
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                                                                                                                                                                                                              Homo sapilens
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                                                                                                                                                                                                                                                                                             AAB87606
                                                                                                           18-FEB-2000;
                                                                                                                                                                                                                              Human; PRO protein;
                                                                                                                                                                                                                                               Human PRO20040
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PVPDALKSLWYKNLTGPQNITLNHTDLVPCLCIQVWSLEPDSERVEFCPFREDPGAHRNL
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                                    GENENTECH INC
            Ć,
                                                                                                                                                                                                                                                                                             standard;
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                      Filvaroff
                                                                          2000US-0175481.

2000WO-US04341.

2000WO-US04342.

2000WO-US04414.

2000WO-US04414.

2000WO-US05601.

2000US-0187202.
                                                           2000US-0199397
2000WO-US14042
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             Gurney
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                                                                                                                                                                                                                                                                                            Protein;
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             Ε,
AL,
             Gerritsen
Watanabe
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             CK,
             Goddard A, Wood WI;
                    Godowski PJ
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WPI; 2001;183260/18.

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AAF92138
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Eighty four nucleic acids encoding PRO polypeptides, useful in molecular biology, including use as hybridization probes, and chromosome and gene mapping. chromosome and gene mapping. in

Claim 12; Fig 162; 278pp; English.

SXCCCCCCCXXXX PT XX

The present sequence is Thuman PRO polypeptide (secreted and transmembrane). The PRO protein, and PRO agonists, PRO antagonists or anti-PRO antagonies are usefulger preparation of a medicament useful in the treatment of a condition which is responsive to the PRO protein, agonists, antagonists of anti-PRO antibodies. The PRO protein may also be employed as molecular weight markers for protein electrophoresis. The PRO coding sequence has applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping.

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                                                                      AALFFFLLLKKDRRK------AARGSRTALLLHSADGAGYERLVGALASALS 522
                                                                                                                                               lkghpnlcvqvnsseklqlqeclwadslgplkddvllletrgpqdnrslcalepsgctsl 405
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                   LPAFLDALQGGCSTSAGRPADRVERVTQALRSALDSC--TSSSEAPG
                                                                                                                                                                 PSMASTRAARLGEELLQDFRSHQCMQLWNDDNMGSLWACPMDKYIHRRWVLVWLACLLLA 476
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                                                    -GPHDALAAWLSCVLPDFLQGRATGRYYGYYFDGLLHPDSVPSPFRVAPLFSLPTQ 639
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Pred. No. 1.1e-216;
""smatches 135;
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                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polypeptide encoding a human cytokine receptor Zcytor14, treating inflammation e.g. rheumatoid arthritis -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytokine receptor; Zcytor14; human; inflammation; rheumatoid arthritis; antiinflammatory; gene therapy; vaccine.
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                                                                                                                                                                                                                                                                                                                                          protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zcytor14 protein
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The invention provides a new human cytokine receptor desinated Zcytor14. Zcytor14 can be expressed by standard recombinant methodology. The encoding nucleic acid is useful for detecting the expression of a Zcytor14 gene in a biological sample. Anti-Zcytor14 antibodies can be used to screen biological samples in vitro for the presence of Zcytor14. Proteins, polypeptides and peptides having Zcytor14 activity can be administered to a subject who lacks an adequate amount of this polypeptide, for treating inflammation and conditions such as rheumatoid
                                                                                                                                                                                                                                                WPI;
                                                                                                                                                           Claim 2; Page 107-109;
                                                                                                                                                                                       New polypeptide encoding a human cytokine receptor Zcytor14, treating inflammation e.g. rheumatoid arthritis -
                                                                                                                                                                                                                                                                                                                                               07-JUL-1999;
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65.5%;
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Pred. No. 7.9e
63; Mismatches
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.9e-211;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
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417 PSMASTRAARLGEELLQDFRSHQCMQLWNDDNMGSLWACPMDKYIHRRWVLVWLACLLLA 476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptide encoding a human cytokine receptor Zcytor14, for sting inflammation e.g. rheumatoid arthritis -
                                                                                                                                              WHIARLRYLSPGYWQLDAPCCLPGKVTLCWQAPDQSPCQPLVPPVPQKNATVNEPQDFQL 356
                                                                                                                                                                                                                        YQKELNLTQQLPDCRGLEVRDSIQSCWVLPWLNVSTDGDNVLLTLDVSEBQDFSFLLYLR 236
                                                                                                                                                                                                                                                                  lgaqvvlsfqayptarcvllevqvpaalvqfgqsvgsvvydcfeaalgsevriwsytqpr
                                                                                                                                                                                                                                                                               LQAQVVLSEQAYPIARCALLEVQVPADLVQPGQSVGSAVFDCFEASLGAEVQIWSYTKPR 176
                                                                                                                                                                                                                                                                                                                                      LVPTRLQTELVLRCPQKTDCALRVRVVVHLAVHGHWAEPEE----AGKSDSELQESRNAS 116
                                                        VAGHPNLCVQVSTWEKVQLQACSWADSLGPFKDDMLLVEMKTGLNNTSVCALEPSGCTPL 416
                                                                                    wqaarlrlltlqswlldapcslpaeaalcwrapggdpcqplvpplswenvtvd-----
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be expressed by standard recombinant methodology. The
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                                             Ecytor14 can be expressed by standard recombinant methodology. The encoding nucleic acid is useful for detecting the expression of a Zcytor14 gene in a biological sample. Anti-Zcytor14 antibodies can be used to screen biological samples in vitro for the presence of Zcytor14. Proteins, polypeptides and peptides having Zcytor14 activity can be administered to a subject who lacks an adequate amount of this polypeptide, for treating inflammation and conditions such as rheumatoid arthritis. In contrast, Zcytor14 antagonists (e.g. anti-Zcytor14 antibodies) can be used to treat a subject who produces an excess of Zcytor14. The present sequence represents a variant of the human cytokine receptor Zcytor14, designated Zcytor14. This
                      the human cytokine receptor zcytor14, designated zcytor1 variant is a truncated form of the receptor polypeptide amino acid residues 1-113 of zcytor14.
                                                                                                                                                                                                                               The invention provides a new human cytokine receptor desinated Zcytor14
                                                                                                                                                                                                                                                              Disclosure; Page 2-3; 112pp; English.
                                                                                                                                                                                                                                                                                           New polypeptide encoding a human cytokine receptor Zcytor14, treating inflammation e.g. rheumatoid arthritis -
                                                                                                                                                                                                                                                                                                                                         N-PSDB; | AAC85029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human variant
                                                                                                                                                                                                                                                                                                                                                                                     Presnell
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Best Local
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                                                          99WO-US09847.
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                                                                                                                                                                                                                                                       endocrine disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----alpwinvsadgdnvhlvlnvseeqhf 105
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                                                                                                                                                                                                                                                                            infection; AIDS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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PVPDALKSLWYKNLTGPQNITLNHTDLVPCLCIQVWSLEPDSERVEFCPFREDPGAH

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Best Local S
Matches 211
                                                                                                                                                                                                                                                                                                                                                                                                     The genes and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 97 genes, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, developmental abnormalities, and foetall deficiencies, blood disorders, diseases of the immune system, autoimmune diseases, inflammation, allergies, Alzheimer's and cognitive disorders, schizophrenia, arthritis, asthma, psoriasis, sepsis, skin disorders, diseases, diabetes, cardiovascular disorders, kidney disorders, diseases, infections and AIDS. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-MAY-1998;
12-MAY-1998;
12-MAY-1998;
18-MAY-1998;
18-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAZ65250 to AAZ65350 represent 97 isolated human secreted protein genes AAY76124 to AAY76223 are the secreted proteins encoded by the 97 human genes. The gene encoding this protein was found to be on chromosome 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated human genes and the secreted polypeptides they encode, useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Olsen
                                                                                                                                                                                                                                                                                                                                                                             polypeptides are also useful for identifying their binding partners. The sequences shown in AAY76224 to AAY76424 represent fragments of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB;
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18-MAY-1998;
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18-MAY-1998;
    181
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                                                                                                                         MPVSWFLLSLALGRNPVVVSLERLMEPQDTARCSLGLSCHLWDGDVLCLPGSLQSAPGPV 60
              YQKELNLTQQLPDCRGLEVRDSIQSCWVLPWLNVSTDGDNVLLTLDVSEEQDFSFLLYLR
                                                                             LQAQVVLSFQAYPIARCALLEVQVPADLVQPGQSVGSAVFDCFEASLGAEVQIWSYTKPR
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yekexnhtqqlpdcrglevwnsipscwalpwlnvsadgdnvhlvlnvseeghfglslywn
                                                             lqaqvvlsfqayptarcvllevqvpaalvqfgqsvgsvvydcfeaalgsevriwsytqpr
                                                                                                                                                        LVPTRLQTELVLRCPQKTDCALRVRVVVHLAVHGHWAEPEE----AGKSDSELQESRNAS 116
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                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                  proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 372-373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Florence K, Ni J
                                                                                                                                                                                                                                                     Conservative
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98US-0085928.
98US-0085925.
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98US-0085923.
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                                                                                                                                                                                                                                                  29.1%; Score 1088.5;
71.0%; Pred. No. 9.36
tive 21; Mismatches
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                                                                                                                                                                                                                                                                      .3e-95;
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pet DR;
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RESULT 10
AAM25864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neurological disorder.
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AAM25963 The proteins can have activities based on the tissues and CC cells they are expressed in, such as: antinflammatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; central nervous system; virucide; anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; antiaggregant; haemostatic; vulnerary; antidabetic; cytostatic; neuroprotective; antidalergic; antisathmatic; entiparkinsonian; and immunostimulant. The proteins and polynucleotides encoding them can be used in gene therapy, antisense therapy and vaccine production. The proteins and polynucleotides are useful for screening for disorders associated with the activity of a protein e.g. inflammation, neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, haematopoietic disorders, thrombocytopaenia, wounds, burns, ulcers, rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression, alzenier's disease, parkinson's disease, neurodegenerative and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-DEC-1999;
21-JAN-2000;
25-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20; Page 283; 1217pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated human polynucleotides encoding polypeptides, utreatment and diagnosis of e.g. cancer, ulcers and HIV
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2000US-0552317.
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Homo sapiens

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Best Local
This invention relates to nucleic acid sequences AAF93744 - AAF93916 which encode human secretory or membrane proteins represented by AAB88317 - AAB88419. Included in the invention are primers AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the invention. The invention also includes methods for the production of antibodies directed against the proteins, and cDNA
                                                                                                                                                                                                                                                    08-JUL-1999; 99JP-0194179
11-JAN-2000; 2000JP-0118775
02-MAY-2000; 2000JP-0183766
                                                                                            Claim 1; SEQ ID 264; 609pp + CD ROM;
                                                                                                                    Nucleic acids encoding secretory proteins/membrane proteins, useful gene therapy or as candidate target molecules in drug development -
                                                                                                                                                             N-PSDB;
                                                                                                                                                                          WPI; 2001-093989/11.
                                                                                                                                                                                                      Ota T,
                                                                                                                                                                                                                             (HELI-) HELIX RES INST.
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                                                                                                                                                                                                                                                                                                                                     10-JAN-2001.
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                                                                                                                                                                                                                                                                                                                                                                                       Homo
                                                                                                                                                                                                                                                                                                                                                                                                                               Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human membrane or secretory protein clone PSEC0233.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 LVPTRLQTELVLRCPQKTDCALRVRVVVHLAVHGHWAEPEE----AGKSDSELQESRNAS
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                                                                                                                                                                                                                                                                                                                                                                                                                       secretory protein; membrane protein; vaccine; gene therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                           English.
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 179;
Human; immune system-related protein; allergy; rheumatoid arthritis; cancer; Gaucher's disease; viral hepatitis; gene therapy; cytostatic; diabetes mellitus; arrhythmia; wound healing; ischaemic lesion; AIDS; Acquired Immune Deficiency Syndrome; virucide; hepatotropic; vasotropi autoimmune disorder; inflammation; cardiovascular disorder; hair loss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnosis of diseases associated with inappropriate secretory protein/membrane protein expression. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples. They may also be used to study the expression and function of secretory proteins/membrane polypeptides and their role in metabolism. The polypeptides may be used as antigens in the production of antibodies against them and in assays to identify modulators (agonists and antagonists) of expression and activity. The antibodies and antagonists may also be used as therapeutic agents to down regulate expression and activity. The antibodies may also
                                                                                                                                                                                                                                                                               AAE10920 standard; Protein; 204
                                                                                                                                         Human gene 12 encoded immune system-related protein HADEX14.
                                                                                                                                                                                               18-DEC-2001
                                                                                                                                                                                                                                            AAE10920;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            arthritis and diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       be used as diagnostic agents for detecting the presence of the polypeptides in samples (e.g. by enzyme linked immunosorbant assay (ELISA). Examples of diseases which may be treated include rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            can be used in gene therapy. The proteins they encode may be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequences, which can
can be used in gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                  237
                                                                                                                                                                                                                                                                                                                                                                                            226 qvqgppkprwhknlvrpppsqvhshcrpmpv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117
                                                                                                                                                                                                                                                                                                                                12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MPVSWFLLSLALGRNPVVVSLERLMEPQDTARCSLGLSCHLWDGDVLCLPGSLQSAPGPV
                                                                                                                                                                                                                                                                                                                                                                                                                                      PVPDALKSLWYKNLTGPQNITL-NHTDLVPCLCIQVWSLEPDSERVEFCPFREDP 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YQKELNLTQQLPDCRGLEVRDSIQSCWVLPWLNVSTDGDNVLLTLDVSEEQDFSFLLYLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lapthlqtelvlrcqketdcdlclrvavhlavhghweepedeekfggaadsgveeprnas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          yekelnhtqqlp-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LQAQVVLSFQAYPIARCALLEVQVPADLVQPGQSVGSAVFDCFEASLGAEVQIWSYTKPR 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LVPTRLQTELVLRCPQKTDCALRVRVVVHLAVHGHWAEPEE----AGKSDSELQESRNAS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    {\tt mpvpwfilslalgrspvvlslerlvgpqdathcspglscrlwdsdilclpgdivpapgpv}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----alpwlnvsadgdnvhlvlnvseeqhfglslywn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 875.5; DB 2
Pred. No. 1.4e-74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in vaccines. The polynucleotide sequences
                                                                                                                                                                                                                                                                                   Ã
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polynucleotide sequences and the in the prevention, treatment and with inappropriate secretory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           267;
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100d

preservative.

cell

proliferation;

inflammation; cardiovascular proliferation; skin aging; end

endocrine disorder;

vasotropic;

2

autoimmune disc wound healing;

Key Domain

Homo sapiens

Domain

/label= Immunogenic_epitope 151..168

Immunogenic_epitope

RESULT 13
AAY76048
ID AAY760

AAY76048

standard;

Protein;

Location/Qualifiers

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                                                                                                                                                                 Qγ
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Best Local (
                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                               or DNA is useful for preventing hair loss, skin aging due to sunburn, maintain organs before transplantation, to treat weight disorders, to modulate mammalian characteristics, to change a mammal's mental or physical state, or as a food additive or preservative. Immune-system related DNA is useful in gene therapy, for chromosome identification, radiation hybrid mapping, long range restriction mapping and in foren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to human immune system-related protein and their DNA. Human immune-system related protein and DNA are useful for preventing, treating or ameliorating a medical condition in a mammalian subject. For diagnosing, preventing or treating immune system-associated disorders, autoimmune disorders (rheumatoid arthritis), inflammatory disorders (allergies), immunedeficiencies (AIDS), inflammatory disorders (allergies), infectious diseases (e.g., viral hepatitis), complement activation disorders, immune complex diseases, neoplastic disorders (cancer) hyperproliferative disorders (Gaucher's disease), disorders associated with neovascularisation, diseases at the cellular level,
                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cardiovascular disorders (arrhythmias), wound healing and epithelial cell proliferation, endocrine disorders (diabetes mellitus) and neurological disorders (ischaemic lesions). Immune-system related protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated immune system-related polypeptide useful for treating rheumatoid arthritis, AIDS, allergy, cancer, Gaucher's disease, diabetes mellitus, arrhythmia, wound healing, ischemic lesions and
                                                                                                                                                                                                                                                                                                                                                                                         protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11;
                                                                                                                                                                                           biolog. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             viral hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gruber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ( HUMA - )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-MAR-2000;
11-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-MAR-2001;
                                                                                                   819
                                                                                                                                            561 VILLESPAAVAQCQQWIQLQTVEP---GPHDALAAWLSCVLEDELQGRATGRYVGVYEDG 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-SEP-2001.
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181
                                 677
                                                                  121
                                                                                                                           61 vvllfspgavalcsewlqdgvsgpgahgphdafraslscvlpdflqgrapgsyvgacfdr
hppgtpapg
                               -TSSSEAPG
                                                         LLHPDSVPSPFRVAPLFSLPTQLPAFLDALQGGCSTSAGRPADRVERVTQALRSALDSC- 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001-589939/66
                                                                                                                                                                                                                                                                      122;
                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hilbert D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAD18278.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 312-313; 315pp; English.
                                                                                                                                                                                                                                                                                                                                                        204 AA
                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Endress
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-187873P
2000US-224367P
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                                 684
189
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s GA, Ruben
                                                                                                                                                                                                                                                                                                                                                                                                     sequence represents a human immune-system
                                                                                                                                                                                                                                                                                  15.8%;
                                                                                                                                                                                                                                                                    21;
                                                                                                                                                                                                                                                                 Score 591.5; DB 22;
Pred. No. 9.5e-48;
11; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Moore PA,
1 SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Choi GH,
                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                  Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Soppet DR,
                                                                                                                                                                                                                                                                 <u>ن</u>
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                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      forensic
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                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to novel nucleic acid sequences derived from rat dermal papilla, human keratinocytes and neonatal foreskin fibroblasts, and mouse embryonic skin, keratinocyte stem cells and transit amplifying cells. Polypeptides of the invention may be used to treat inflammation, cancer and neurological diseases. The proteins may be used to stimulate cancer cells, to modulate angiogenesis and tumour vascularisation, to modulate skin inflammation, to modulate epithelial cell growth and to inhibit binding of HIV-1 to leukocytes. The invention may also be used to treat growth and developmental defects, skin wounds and hair follicle disorders. Sequences AAY75942-Y7613 represent polypeptides encoded by cDNA sequences AAY75942-Y75947, AAY76020, AAY76094-Y76104 and types. Sequences AAY75942-Y7547, AAY76000-Y76021, AAY76094-Y76104 and the polypeptides are received from several mouse, rat or human skin cell types. Sequences AAY75942-Y75947, AAY76000-Y76021, AAY76094-Y76104 and the polypeptides are received from several mouse, rat or human skin cell types.
                                                                                                                                                                                                                                                                                                                                  AAY76119 are proteins with an N-terminal signal sequence, indicating that they are secreted. Sequences AAY75986-Y75989, AAY76661-Y76071, AAY76106-Y76109 and AAY76121-Y76122 are proteins with one or more putative transmembrane domains.
                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Page 179-180; 235pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strachan L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-APR-1998;
09-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Skin; dermal papilla; keratinocyte; neonatal foreskin fibroblast; embryonic skin cell; keratinocyte stem cell; transit amplifying c secreted; transmembrane; inflammation; cancer; neurological disea
                                                                              182
                                                                                                                                                                     175 PRYQKELNLTQQLPDCRGLEV-----RDSIQSC--WVLPWLNVSTDGDNVLLTLDVSEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                anti-inflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           anglogenesis; tumour vascularigation; growth disorder; developmental disorder; skin wound; hair follicle disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murine skin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY76048
                                287 REDPGAH-RNIWHIARLRVLSPG---VWQLDAPCCLPGKVTLCWQAPDQSPCQPLVPPVP 342
                                                                                                                                                 137
                                                                                                                                                                                                                   Local Similarity
nes 134; Conserv
gswpeaygsdfwqsirftdysqhnqmvmaltlrcplkleaslcwrqdpltpcetl----
                                                                                                    QDFSFLLYLRPVPDALKSLWYKNLTGPQNITLNHTDLVPCLCIQVWSLEPDSERVEFCPF
                                                                                                                                      pefsfdl-----lpevqavrvtipagpkasvrlcyqwalecedlsspfdt-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polynucleotides useful for the treatment of various ding wounds and cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAZ61753
                                                                                                                                                                                                                                                                                                        617
                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cell protein, SEQ ID NO:303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sleeman M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytostatic; neuroprotective;
                                                                                                                                                                                                                               8.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                & DEV CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Watson JD,
                                                                                                                                                                                                               66;
                                                                                                                                                                                                             Score 312; DB 21;
Pred. No. 2.1e-20;
6; Mismatches 224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kumble A,
                                                                                                                                                                                                                                            Length 617;
                                                                                                                                                                                                           Indels 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Murison JG;
                                                                                                                                                                                                           Gaps
                                                                                                                                                                       226
                                                                     221
                                                                                                                                        181
 276
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RESULT 14
AAB55987
The present sequence is a polypeptide which is expressed in mammalian skin cells. The polypeptide is useful for stimulating keratingcyte growth and motility, inhibiting the growth of cancer cells, modulating angiogenesis, inhibiting angiogenesis and vascularisation of tumours, modulating skin inflammation, stimulating the growth of
                                                                                                                                                            New isolated polynucleotide used in the identification disorders and encoding polypeptides used for treating i disease, cancer and neurological diseases
                                                                                                                             Claim 4;
                                                                                                                                                                                                                                                                                                            Watson
                                                                                                                                                                                                                                                                                                                                                                                          14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                             15-MAY-2000; 2000WO-NZ00075
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Skin cell protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-MAR-2001
                                                                                                                                                                                                                                                                                                                                                  (GENE-) GENESIS RES & DEV CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               keratinocyte growth stimulation; cancer; angiogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nootropic; neuroprotective; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB55987
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                                                                                                                                                                                                                                                                                                            ď,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      skin cell;
                                                                                                                                                                                                                                                  AAC99686
                                                                                                                         Page 244-245; 352pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --LRSALDSCTSSSEAP 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neurological disease.
                                                                                                                                                                                                                                                                                                                                                                                          9905-0312283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO:
                                                                                                                                                                                                                                                                                                        Onrust R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antiinflammatory; anti-HIV;
                                                                                                                                                                                                                                                                                                                                                  LTD
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                                                                                                                                                                                                                                                                                                        Sleeman
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                                                                                                                                                                                                                                                                                                        Kumble KD,
                                                                                                                                                                               of genetic inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----rslgsgrt
                                                                                                                                                                                                                                                                                                        Murison
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                              Human; Interleukin-17 receptor; IL-17RH3; agonist; antagonist; pRO9877; DNA 119502-2789; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; diabetes mellitus; allergic disease; asthma; demyelinating disease;
                                                                                                                                            Human Interleukin 17 receptor,
                                                                                                                                                                                   24-OCT-2001
                                                                                                                                                                                                                        AAU04957;
                                                                                                                                                                                                                                                            AAU04957 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 epithelial cells, inhibiting the binding of human immunodeficiency virus (HIV)-1 to leukocytes, and treating inflammmatory disease, cancer and neurological diseases. The polynucleotide can be used as a marker, in the identification of genetic disorders, and for the design of
 HOMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
sapiens.
                                                                                                                                                                                                                                                                                                                                                 | :| | |: :|
| chlleleaakddyggstnsp
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                                                                                                                                                                                                                                                                                                                                                                                        A----LRSALDSCTSSSEAP 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                            YFDGLLHPDSVPSPFRVAPLFSLPTQLPAFLDALQGGCSTSA-----GRPADRVERVTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ILQEGGVVILLESPAAVAQCQQWLQLQTVEPGPHDALAAWLSCVLPDFLQGRATGRYVGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WISG ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLVEMKTGLNNTSVCALEPSGC---TPLPSMASTRAARLGEELLQD-----FRSHQCMQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REDPGAH-RNLWHIARLRVLSPG----VWQLDAPCCLPGKVTLCWQAPDQSPCQPLVPPVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QDFSFLLYLRPVPDALKSLWYKNLTGPQNITLNHTDLVPCLCIQVWSLEPDSERVEFCPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pefsfdl----lpevqavrvtipägpkasvrlcyqwalecedlsspfdt----
                                                                                                                                                                                                                                                                                                                                                                                                                         {f y}fsrlcak{f g}dipr{f p}lral{f p}rrllralda{f q}patlass{f w}shl{f g}ak{f r}clk{f n}rle{f q}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        {\tt rpvlllhaadsea} qrrlvgalaellrtalgggrdvivdlwegthvarigplpwlwaarer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -pnataqesegwyilenvdlhpqlcfkfs-fensshvecphqsgslpswtvsmdt-qaqq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.3%; Score 312; DB 22; ilarity 23.9%; Drad. No. 2.1e-20; Conservative, 66; Mismatches 224
                                                                                                                                                                                 (first entry)
                                cartilaginous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        =
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                                                                                                                                                                                                                                                            Protein; 667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -vhfawkhvlcpddapyptqlll-----
                                                                                                                                                                                                                                                                                                                                                     611
                                disorder;
                                                                                                                                              IL-17RH3.
                                                                                                                                                                                                                                                           B
                              transplantation associated disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      224;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----rslgsgrt
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T

777777

Peptide

, Key

Location/Qualifiers

lupus erythematosus

e.g.

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Chen ...
Gurney AL, ...
Chan c. ...
                                                                                                                       diagnosis
arthritis
               The sequence is PRO9877 which is the human Interleukin IL-17RH3, encoded by DNA 119502-2789. Composition containing ant/agonists to the PRO polypeptides or indiare useful for treating a mammal with an immune related
                                                                                            Claim 10;
                                                                                                                                                       Novel PRO
                                                                                                                                                                                                                                                                                                                                                                        24-AUG-2000;
24-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                       22-JUN-2000;
22-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                     02-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-MAR-2000;
21-MAR-2000;
                                                                                                                                                                                                                                                                                               (GETH )
                                                                                                                                                                                                                                                                                                                                            28-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-JUN-2001.
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                                                                                                                                                                                                                                                                                                                                                           10-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein
                                                                                                                                                                                     2001-451708/48.
)B; AAS09516.
                                                                                                                                                                                                                                                                                             GENERTECH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -site
                                                                                                                                                                                                                               Filvaroff E, Fong S, Goddard A, Godowski I, Li H, Hillan KJ, Tumas D, Van Lookeren CK, Williams PM, Wood WI, Yansura DG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -site
                                                                                                                       polypeptides homologous to interleukin-17, useful for the and treatment of immune related disease e.g. rheumatoid and diabetes -
                                                                                         Fig 16; 188pp; English.
                                                                                                                                                                                                                                                                                                                            2000WO-US30873.
2000US-0253646.
2000WO-US32678.
                                                                                                                                                                                                                                                                                                                                                                                   2000WO-US07532.
2000WO-US15264.
2000US-0213087.
2000US-0644848.
2000WO-US23328.
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2000WO-US05841
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US31274
00US-0175481
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482..486
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455..47
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453..462
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318..322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                545..649
/note= "CAMP/GMP-dependent protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       358..364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "camp/GMP-dependent protein
phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104..108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Mature_IL_17RH3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label=
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                                                                                                                                                                                                                  Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ
EMBL; BC006411; AAH06411.1; -
Hypothetical protein.
SEQUENCE 538 AA; 59127 MW; 65E6344DA6A5AFF
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUE-ENDOMETRIAL ADENOCARCINOMA;
                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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"Herpesvirus Sainiri encodes a new cyto
novel cytokine receptor.";
Immunity 3:811-821(1995).
EMBL; U31993; AAC52357.1;
MGD; MGI:107399; I117r.
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MEDLINE-96111968; PubMed-8777726;
Yao Z., Fanslow W.C., Seldin M.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-DEC-2001 (TrEMBLrel. 19, INTERLEUKIN 17 RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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        314
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                                                                                                                                                                                                                                                                                                                                                                                     240
                                                                                                                                                                                                                                                                                                                                                                                                                                                  198 SIQSCW-----VLPWLNVSTDGDNVLLTLDVSEEQDFSFLLYLRPVP------
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                                                                      WCCHHHVQVQPFFSSCLNDCLRHAVTVPCPVISNTTVPK-
                                                                                                                                                                                                                                      PGKYTLCWQAPDQSPCQP----LVPPVPQKNATVNEPQDFQLVAGHPNLCVQVSTWEKVQ
                                                                                                                                                                                                                                                                                                                                                                       ---DALKSLWY--KNLT--GPQNITLN------HTDLVPCLCIQVWSLEPD----
                                                                                                                                                                                                                                                                                                                                                                                                                 AIRRCWPRVVPGPALGWL------LLLLNVLAPGRASPRLLDFPAPVCAQEGLSCRV
                                                                                                  *CA-| **** LEP--SGC-----TPLPSMASTRAARLGEELLQDFRSHQCMQLWNDD
                                                                                                                                     VDFTLWNEST-PYQ----VLLESFSDSENHSCFDVVKQIFAPRQEEFHQRANVTFTLSKFH
                                                                                                                                                                          LQACSWADSLGPFKDDMLLVEMKTGLNNTSV-----
                                                                                                                                                                                                                                                                             AELSVLQLNTNERLCVKF-QFLSMLQHHRKRWRFSFSHFVVDPGQEYEVTVHHLPKP---
                                                                                                                                                                                                                                                                                                                                                KNSTCLDDSWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVE-WTLQTDASILYLEG
                                      NMGSLWACPMDKYIHRRWV--LVWLACLLLAAALFFFL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AALSLILLLKKDH----AKGWLRLLKQDVRSGGEWEQALGGGPPPGSQACASSPLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AALFFFLLLKKDRRKAARGSRTALLLHSADGAGYERLV-----GALASALSQMP 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PSWASTRAARLGEELLQDFRSHQCMQLWNDDNMGSLWACPMDKYIHRRWVLVWLACLLLA 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                        ----IPDGDPNHKSKIIFVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        864 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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PVADYI-PLWVYGLITLIAILLVGSVIVLIICMTWRLSGADQEKHGDDSKIN
                                                                                                                                                                                                                                                                                                             SER--VEFCPFREDPGAHRNLWHIARLR-VLSPG-----VWQLDAPCCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.7%;
20.5%;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 177; DB 11;
Pred. No. 4e-07;
5; Mismatches 189;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        343FD51AA687DA31 CRC64;
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                                    -LLKKDRRKAARGS---
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Best Local Similarity
Matches 140; Conserv
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043844; PRT; 866 AA.
01-JUN-1998 (TREMBLrel. 06, Created)
01-JUN-1998 (TREMBLrel. 06, Last sequence update)
01-DEC-2001 (TREMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-98035683; PubMed-9367539;
Yao Z., Spriggs M.K., Derry J.M.J., Strockbine L., Park L.S.,
YandenBos T., Zappone J., Painter S.L., Armitage R.J.;
"Molecular characterization of the human interleukin (I1)-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytokine 9:794-800(1997).
EMBL; U58917; AAB99730.1; -..
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                             421 STRAARLGEELLQDFRSHQCMQLWNDDNMGSLWACPMDKYIHRRWVLVWLACLLLAAALF 480
                                                                                                    361 PNLCVQVSTWEKVQLQACSWADSLGPFKDDMLLVEMKTGLNNTSVCALEPSGCTPLPSMA 420
                                                                                                                                                                                    307
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                                                                        273 LKGCCR----HQVQIQ-
                                                                                                                                                                                                                                                                                           149
                                                                                                                                                                                                                                                                                                                    210 VSTDGDNVLLTLDVSEEQDFSFLLYLRPVPDALKSLWYKNLTGPQNITLNHTDLVPCLC- 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 EAGKSDSELQESRNASLQAQVVLSF----QAYPIARCALLEVQVPADLVQPGQSVGSAVF 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55 SAPGP-----VLVP----TRIQTELVLRCPQKTDCALRVRVVVHLAVHGHWAEPE 100
                                                                                                                                                                                                              GSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHMENHSCFEHMHHI------ 252
                                                                                                                                                                                                                                                                                                                                                                                        DCFEASL----GAEVQIWSYTKPRYQKELNLTQQLPDCRGLEVRDSIQ---SCWVLPWLN 209
   DT----PEPIPDY----MPLW----
                                                                                                                                                                          PGVWQLDAPCCLPGKVTLCWQAPDQSPCQPLVPPVPQKNATVNEPQDFQ-----LVAGH 360
                                                                                                                                                                                                                                                                                  FVVDPD-----QEYEVTVHHLPKPIPDGDPNHQSKNFLVPDCEHARMKVTTPCMSS 199
                                                                                                                                                                                                                                                                                                                                                                                                                            -----NLTPSSPKDLQIQLHFAHTQQGDLFPVAH---IEWTLQTD------- 103
                                                                                                                                                                                                                                                                                                                                                                ---- ASILYLEGAELSV----
                                                                                                                                                                                                                                               -----IQVWSLEPDSERVEFC------PFREDPGAHRNLWHIARLRVLS 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -GDLFTAAMMILPDFKRPACFCTWWCYFSGICSERDVPDLFNITSRYPL 528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.9%; Score 147.5; DB 4; Length 866;
ilarity 19.3%; Pred. No. 0.00019;
Conservative 78; Mismatches 239; Indels 269
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                                                                                                                                         272
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-----VYWFITGISILLVGSVI-
                                                                    -- CLRHSATVSCPEMP 307
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	420	QY 361 PNLCVQVSTWEKVQLQACSWADSLGPFKDDMLLVEMKTGLNNTSVCALEPSGCTPLPSMA
	272	Db 253
	360	QY 307 PGVWQLDAPCCLPGKVTLCWQAPDQSPCQPLVPPVPQKNATVNEPQDFQLVAGH
	252	Db 200 GSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHMENHSCFEHWHHI
•	306	QY 269IQVWSLEPDSERVEFCPFREDPGAHRNLWHIARLRVLS
	199	149 FYDDD
	268	Qy 210 VSTDGDNVLLTLDVSEEQDFSFLLYLRPVPDALKSLWYKNLTGPQNITLNHTDLVPCLC-
	148	HH
	209	QIWSYTKPRY
	103	67NLTPSSPKDLQIQLHFAHTQQG
	156	Qy 101 EAGKSDSELQESRNASLQAQVVLSFQAYPIARCALLEVOVPADLVOPGOSVGSAVF
	100	Qy 55 SAPGPVLVPTRLQTELVLRCPQKTDCALRVRVVVHLAVHGHWAEPE
32;	Gaps	Query Match 3.9%; Score 147.5; DB 4; Length 866; Best Local Similarity 19.3%; Pred. No. 0.00019; Matches 140; Conservative 78; Mismatches 239; Indels 269; G:
		TISSUE=U Strausbe
		NCBI_TaxID=9606; [1]
		Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E Mammalia; Eutheria: Primates: Catarrhini Hominidae.
		(Tremblrel. 19, Last (Tremblrel. 19, Last NTERLEUKIN 17 RECEPTC
		Q96F46; 01-DEC 2001 (TrEMBLrel.
		GF GSU
		Qy 669 LRSALD 674 :
	566	Db 517 FGAAPRYPLMDRFEEVYFRIQDLEMFQPGRMHRVGELSGDNYLRSPGGRQ
	668	Qy 628 FRVAPLFSLPTQLPAPLDALQGGCSTSAGRPADRVERVTQA
	٠.	Db 457 ALLGRGAPVRLRCDHGKPVGDLFTAANNMILPDFKRPACFGTYVVCYFSEVSCDGDVPDL
	. 627	QY 575 QWLQLQTVEPGP-HDALAAWLSCVLPDFLQGRATGRYVGVYFDGLLHPDSVPSP
	-	397 KFAQF
		Qy 516 ALAS-ALSOMPLRVAVDLWSRRELSAHGALAWFHHORRRILOEGGVVILLFSPAAVAOCO
		338 -LLIVCMTWRLAGPGSEKYSDDTKYTDGLPAADLIPPPLKP
	515	Qy 481 FFLLLKKDRRKAARGS

264 167 107

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Query Match 3.2%;
Best Local Similarity 20.8%;
Matches 150; Conservative 8
                                                                                                                           InterPro; IPR001410; DEAD.
InterPro; IPR00150; Helicase_C.
InterPro; IPR000330; SNF2_N.
Pfam; PF00271; helicase_C; 1.
Pfam; PF00176; SNF2_N; 1.
SMARR; SM00487; DEXDC; 1.
SMARR; SM00487; DEXDC; 1.
ATP-binding; Complete proteome; H.
SEQUENCE 1013 AA; 111629 MW; (
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053499;
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                                                                                                                                                                                                                                                                                                                                                                                       "Deciphering the biology of Mycobacterium complete genome sequence."; Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-98295987; PubMed-9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HELZ OR ATTACK
Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Bacteria; Corvnebacterineae; Mycobacteriaceae; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                               TubercuList; Rv2101;
                                                                                                                                                                                                                                                                                                                                              -i- SIMILARITY: TO HELICASE C-TERMINAL DOMAIN. EMBL; AL021924; CAA17284.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HELZ OR RV2101 OR MTV020.01.
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                 Score 119.5; DB Pred. No. 0.085; 0; Mismatches 2
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Seelig R., Weber P., Seeling H.P., Ledger N., Bottner C., Renz Seelig R., Weber P., Seeling H.P., Ledger N., Bottner C., Renz Seelig R., Weber P., Seeling H.P., Ledger N., Bottner C., Renz Seelig R., Weber P., Seeling H.P., Ledger N., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R., Bottner C., Renz Seelig R.,
                                                                                                                                    Hepatitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
NCBI_TakID-11103;
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                                                                                                                                                                                                                                                    POLYPROTEIN
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                                                                                                                                                                                                                                         (TremBLrel. 01, Created)
(TremBLrel. 01, Last sequence update)
(TremBLrel. 19, Last annotation update)
PROTEIN (CONTAINS: ENVELOPE GLYCOPROTEIN
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Matches 147; Conserv
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SEQUENCE
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ATP-binding; Coat protein;
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MEROPS; U39.001;
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302 LRVLSPGVWQLDAPCCLPGKVTLCWQAPDQSPCQPLVPPVPQKNATVNEPQDFQLVAGHP
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                                                                                                                                                GGSAAHGVSTLTSLFSSGP------QQKLQLVKTNGSWHINSTALNCNESINTGFIA 439
                                                                                                                                                                   RNASLQAQVVLS--FQAYPIARCALLEVQVPADLVQPGQS--VGSAVFDCFEA-SLGAEV 167
                                                                                                                                                                                                             PTRLQTELVLRCPQKTDCALR-----VRVVVHLAVHGHWAEPEEA----GKSDSELQES 112
                                                                                                                                                                                                                                                    FLLSLALGRNPVVVSLERLMEPQDTARCSL---GLSCHLWDGDVLCLPGSLQSAPGPVLV 62
                       CAWMNSTG----FLKTCGAPPC-NIYGGGGNPNNESHLFCPTDCFRKHPDATYSR----
                                           LWYKNLTGPQNITLNHTDLVPCLCIQVWSLEPDSERVEFCP---FREDPGAHRNLWHIAR
                                                                                      ---VLPWLNV----
                                                                                                       GLFYYHK-----FNSTGCPQRLSSCKPITFFRQGWGSLTDANVTGASADKPYCWHYAPR
                                                                                                                             QIWSYTKPRYQKELNLT---QQLPDCRGL-----EVRDSIQS-----
                                                                                                                                                                                         VSH-----VLRLPQTLFDIIAGAHWGILAGLAYYSMQGNWAKVAVIMVMFSGVDAETYIT 388
                                                                                                                                                                                                                                  FLVGQAFTFRP-----RRHQTVQTCNCSLYPGHLSGHRMAWDMM-----MNWSPAVGMV
                                                               PCDVVPALNVCGPVYCFTPSPVVVGTTDRKGV-PTYNWGENESDVFLLESLRPPSGRWFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF00998;
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                                                                                                                                                                                                                                                                                                                                192
384
736
1013
1664
1718
1718
1979
2431
                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0002518; HCV_NS2...
000410; HCV_NS3...
0000745; HCV_NS4a...
0001490; HCV_NS4b...
0002868; HCV_NS5a...
0002166; HCV_RdRM...
0001650; Helicase_C...
HCV_capsid; 1...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HCV_env; 1.
HCV_NS1; 1.
HCV_NS2; 1.
HCV_NS3; 1.
HCV_NS4a; 1.
HCV_NS4b; 1.
HCV_NS5b; 1.
HCV_NS5b; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             helicase_C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HCV_core;
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735
1012
1663
1717
1978
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HCV_capsid.
HCV_core.
                                                                                                                                                                                                                                                                                                                                                                                                                                        e_C; 1.
NS1; 1.
ein; Envelope protein; Glycoprotein; Helicase;
ein; Envelope protein; Glycoprotein; Helicase;
                                                                                                                                                                                                                                                                              88;
                                                                                                                                                                                                                                                                                                                           NS3 PROTEIN.
NS4A PROTEIN.
NS4B PROTEIN.
NS5A PROTEIN.
NS5A PROTEIN.
NS5B PROTEIN.
NS5B PROTEIN.
                                                                                   ---STDGDNVLLTLDVSEEQDFSFLL-YLRPVPDALKS
                                                                                                                                                                                                                                                                          Score 114; DB
Pred. No. 1.2;
88; Mismatches
                                                                                                                                                                                                                                                                                                                              MW;
                                                                                                                                                                                                                                                                                                                                                                                                   ENVELOPE PROTEIN.
NS1 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                         CORE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN.
                                                                                                                                                                                                                                                                                                DB 12;
                                                                                                                                                                                                                                                                            258;
                                                                                                                                                                                                                                                                                                Length 3021;
                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                           218;
                                                                                                                             -CW----
                                                                                                                                                                                                                                                                          Gaps
                                                               552
                                                                                                        493
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                                                                                    244
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RESULT
Q63155
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  Query Match
Best Local S
Matches | 88
                                         SMART; SM0040,
SMART; SM00410; IG_like; SMART; SM00410; IG_like; Immunoglobulin domain; Repeat.
                                                                                                                                                                                                                                                                                                              SEQUENCE OF 387-420 FROM N.A.
MEDLINE-90100559; PubMed-2294591;
Fearon E.R., Cho K.R., Nigro J.M., Kern
Ruppert J.M., Hamilton S.R., Preisinger
                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-97015074; PubMed-8861902;
Keino-Masu K., Masu M., Hinck L., Leonardo E.D., Chan S.S.Y.,
Culotti J.G., Tessier-Lavigne M.;
"Deleted in Colorectal Cancer (DCC) encodes a netrin receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TremBLrel. 01, 01-JAN-1998 (TremBLrel. 05, 01-DEC-2001 (TremBLrel. 19,
                                                                                                                        Pfam; PF00041; fn3; 6.
Pfam; PF00047; ig; 4.
PRINTS; PR00014; FNTYPEIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                SMART;
                                                                                                                                                                 InterPro;
                                                                                                                                                                          InterPro; IPR003600;
                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                   InterPro; IPR003962; FnIII_repeat.
InterPro; IPR003961; FN_III.
                                                                                                                                                                                                                               HSSP;
                                                                                                                                                                                                                                           EMBL;
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                                                                                                                                                                                                                                                                  Science
                                                                                                                                                                                                                                                                              cancers
                                                                                                                                                                                                                                                                                        "Identification of a chromosome 18q gene that is altered in colorectal
                                                                                                                                                                                                                                                                                                     Vogelstein B.;
                                                                                                                                                                                                                                                                                                                                                                               Cell 87:175-185(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q63155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAGYERLVGALASALSQMPLRVAVDLWSRRELSAHGA------LAWFHHQRRRIL 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CVALWLMISQAEAALENLVTLKAVAAAGTHGIGWYLVAFCAAWHVRGKLVPLVTYSLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KVRMFVGGFEHRFTAACNWTRGERCNIEDRDRSEQHPLLHSTTELAILPCSFTPMPAL-S
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                                                                                                                                                                                                                         M32291; AAA41086.1; -. P56276; ITLK.
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                                                                                  SM00060; FN3; 6.
SM00408; IGC2; 3.
SM00410; IG_like; 2.
  88; Conserv
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                                                                                                                                                                                                                                                                 247:49-56(1990).
                                                                                                                                                                IPR003006;
                                                                                                                                                                                          IPR003598;
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   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                          Ig_c2.
Ig_like.
            3.0%; Score 112;
21.5%; Pred. No. 0.
                                                                                                                                                               Ig_MHC
47;
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 Mismatches
                                                            084F625954481988 CRC64;
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A.C.,
            DB 11;
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 155;
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Thomas
                        Length 1445;
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Murinae; Rattus
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 120;
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 Gaps
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                                                          Matches
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Best Local Similarity
                                                                                                                         Kinase.
SEQUENCE
      1268
                                                                                                                                                       MOI. Biol. 0:0-0(2001).

MOI. Biol. 0:0-0(2001).

EMBL; AF350881; AAK31202.1; -

InterPro; IPR000536; Cation_chan_non_lig.

InterPro; IPR002111; Cat_channel_TrpL.
                                                                                                                                                                                                           systanova L.V., Pavur K.S., Petrov A.N., Dorovkov M.V.,
"Novel type of signaling molecules: protein kinases cove
to ion channels.";
Mol Biol A.
                                                                                                                                                                                                                                                                                                                   MEDLINE-99147092; PubMed-10021370;
Ryazanov A.G., Pavur K.S., Dorovkov M.V.;
"Alpha-kinases: a new class of protein kinases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9BX84;
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-OCT-2001 (TrEMBLrel. 18,
                                                                                                                                                                                                                                                                                            Curr. Biol. 9:R43-R45(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                          TISSUE-KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                   Pfam; PF00520;
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                   1 MPVSWFLLSLALGRNPVVVSLERLMEPQDTAR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51
MPSS-LLRSLAGGRHPPRVQRGALLEITNSKREATNVRNDQERQETQSSIVVSGVSPNRQ 1326
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                                                          142;
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                                                                                                                         2012
                                                        Conservative
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                                                                                                                                              ion_trans;
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                                                                  3.0%;
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                                                                                                                        230493 MW;
                                                         87;
                                                     Score 111.5; I
Pred. No. 1.2;
87; Mismatches
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Last annotation update)
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                                                                                                                      8AD583235D8080AF CRC64;
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                                                                             DB 4;
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                            -- CSLGLS
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RESULT
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055225;
01-JUN-1998
01-JUN-1998
01-DEC-2001
                   InterPro;
InterPro;
                                                  Proc. Natl. Acad. Sci. U.:
EMBL; U96411; AAB96561.1;
HSSP; P56682; 1CCV.
MGD; MGI:1202064; Otog.
                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1812
                                                                                                                                     MEDLINE-98070772; PubMed-9405633;
Cohen-Salmon M., El-Amraoui A., Leibovici
Cotgelin: A glycoprotein specific to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1755
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                                                                                                                                                                                              STRAIN-BALB/C
                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WLNVSTDGDNVLLTLDVSEEQDFSFLLYLRPVPDALKSLWYKNLTGPQNITLNHTDLVPC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --VHGHWA---EPEEAGKSDSELQESRNASLQAQVVLSFQAYPIARCALLEVQVPADLVQ 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHLWDGDVLCLPGSLQSAPGPVLVPTRLQTELVLRCPQ-----KTDCALRVRVVVHLA--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -SSLSDNSTRSAQSSECSEVG--PWLQP----NTSFWINPLRRYRPFARSHS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----ERNNLMRLSQTIPFTPVQLFAGEEITVYRLEES-SPLNLDKSMSSWSQRGRA
                 IPR002086;
IPR000359;
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                                                                                                                                                                                                                                                           Chordata;
Rodentia;
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Aldehyde_dehydr
Cys_knot.
TIL.
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                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                      94:14450-14455(1997).
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01-NOV-1998 (Tremblrel. 0:
01-NOV-1998 (Tremblrel. 0:
01-DEC-2001 (Tremblrel. 1:
GENOME POLYPROTEIN.
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Best Local Similarity
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InterPro; IPR001007; VwFC.
Pfam; PP001826; TIL; 3.
Pfam; PP001826; TIL; 3.
Pfam; PP00094; Vwd; 4.
SMART; SM00041; CT; 1.
SMART; SM00214; VWC; 1.
SMART; SM00216; VWD; 4.
PROSITE; PS00125; CTCK 2>=17.
PROSITE; PS01255; CTCK 2>=17.
SEQUENCE 2910 AA; 313410 MW; 7270FC61A23264CD CF
                                                       "Full-length GBV-C/Hgy genomes from nine Japanese isolates:characterization by comparative analyses."; Arch. Virol. 143:1-13(1998). EMBL; D87709; BAA25374.1; -. HSSP; P27958; THEI.
                                                                                                                                                                                                                      Hepatitis GB virus C.
Viruses; ssRNA positive-strand viruses,
GBV-C/HGV group.
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 InterPro; IPR002518;
                                         MEROPS; S29.002; -. MEROPS; U39.001; -.
                                                                                                                                        Katayama K., Fukushi S., Kurihara C., Ishiyama
                                                                                                                                                      MEDLINE-98166861; PubMed-9505962;
                                                                                                                                                                         STRAIN-K1737;
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           InterPro; IPR000923; Copper_blue1.
InterPro; IPR001410; DEAD.
                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LCVQVSTWEKVQLQACSWADSLGPFKDDMLLVEMKTGLNNTSVCALEPSGC----TPLPS 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----TEDPCCL-GSVCVC----NQTLCEGLAPTCRPGHSLITHFQEDSCCPSYSCECDPG 2530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GVWQLDAPCCLPGKVTLCWQAPDQSPCQPLVPPVVPQKNATVNEPQDFQLVAGH-----PN 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEQCQVLGEGCVCTEGTILHRRHSALCIPEDKCACTDSTGVPRALGETWNSSLSG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QPCVALTVYVAMCHKFHVCIEWRGSDYCPFLCSSDSTYQACVAACEPPDTCQDGVLGPLD 2386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83;
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19.8%; Pred. No. 1.9;
HCV_NS2
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                                                                                                                                        Okamura
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Best Local
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                         2543 LYA-LASDHPEWV--RALGKY---YASGTMVTPQGVPVGERYC-----RSSGVLTTSA 2589
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Pfam; PF01001; |
Pfam; PF01506; |
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                                                                                                                                                                               489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; pF00998; HCV_RdRP; 1.
Pfam; pF00271; helicase_C; 1.
PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                        325
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InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 VVISFQAYPIARCALLEVQVPADLVQPGQSVGSAVFDCFEASL---GAEVQIWSYTKPRY 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 LYPTRLQTELVLRCPQKTDCALRVRVVVHLAVHGHWAEPEEAGKSDSELQESRNASLQAQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MPVSWFLLSLALGRNPVVVSLERLMEPQDTARCSLGLSCHLWDGDVLCLPGSLQSAPGPV 60
GGCST---SAGRPADRVERVTQALRSALDSCTSSSEAPGC---
                                                     LAAWLSCYLPDFLQGRATGRYYGYYFDG-LLHPDSVPSPFRVAPLFSLPTQLPAFLDALQ
                                                                                   AYAFQYTPNQRVKE----MLRLWESKKTPCAICVDATCFDSSITEEDVALET
                                                                                                           ALAWEHHORRRILGEGGVVILLE----SPAAV---AQC-----QOWLQLQTVEPGPHDA 589
                                                                                                                                         FKDRKEERGPR-LIVFPPLDFRIAEKLILGDPGRVAKAV---
                                                                                                                                                                                                                           LQDFRSHQCMQLWNDDNMGSLWACPMDKY-IHRRWVLVWLACLLLAAALFFFLLLKKD-- 488
                                                                                                                                                                                                                                                                  APRVH--
                                                                                                                                                                                                                                                                                                                 SY IWSGVPLTRATPAKPPVVR-----PVGSLLVADTTKVYVTNPDNVGRRVDKVTFWR
                                                                                                                                                                                                  IRTVRPHAAMG-WGSKVSVKDLATPAGKMAVHDR-----LQEILEGTPVPFTLTVKKEVF
                                                                                                                                                                                                                                                                                    KVÓLQACSWADSLGPFKDDMLLVEMKTGLNNTSVCALEPSGCTPLPSMASTRAARLGEEL
                                                                                                                                                                                                                                                                                                                                                                                   HTAYCD --
                                                                                                                                                                                                                                                                                                                                                                                                      RVEFCPFREDPGAHRNLWHIARLRVLSPGVWQLDAPCCLPGKVTL--------
                                                                                                                                                                                                                                                                                                                                                                                                                                 SVLKALFPQSDATRKLTVRMSCCVEKSVTRFFSLGLTVAD-VASLCEMEIQ-----N 2271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QKE---LNLTQQLPDCRGLEVRDSIQSCWVLPWLNVSTDGDNVLLTLDVSEEQD-----F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rPro; IPR001650; Helicass; PF01538; HCV_NS2; 1. PF01538; HCV_NS3; 1. PF01907; HCV_NS4a; 1. PF01001; HCV_NS4b; 1. PF01506; HCV_NS5a; 1. PF01506; HCV_RdRP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VAPSEVSSEVSIEIGTETE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  161;
                                                                                                                                                                    RRKAARGSRTALLLHSADGAGYERLV----GALASALSQMPLRVAVDLWSRRELSAHG 542
                                                                                                                                                                                                                                                                                                                                             CWQAPDQSPCQPLVPPVPQKNATVNEPQDFQLVAGHPNLCV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 20.3
61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---DLPPAAAALQAIENAARILEP--HIDVIMEDCSTPSLCGSSREMPVWGEDIPRT 2167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR002166;
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HCV_NS4a.
HCV_NS4b.
HCV_NS5a.
                                                                                                                                                                                                                                                        -DKFLVDSIERARKSAQACL-----SMGYTY-----EEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Helicase_C.
                                                                                                                                                                                                                                                                                                                                                                        ----KVRTP--LELQVGCLVGNELTLECDKCEARQETLASF 2312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----YGPGQSVTI-DGGRYTLPHQLRMRD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 111; DB 1
Pred. No. 2.1;
92; Mismatches ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----DSELTEA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2873;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 278;
                                                                                  3----E
                                                                                                                                                                                                                                                                                                                                               -QVSTWE
                                                                                                                                           ---LGG
-CE-- 687
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ESULT
 Query Match
Best Local Similarity
Matches 144; Conserv
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Q81495;
01-NOV-1996 (TrEMBLrel. Q1, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
GENOME POLYPROTEIN (CONTAINS: ENVELOPE GLYCOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2650
                                                                                                                                                                                                                                                                                                                        Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-95053917; PubMed-7964640;
Yamada N., Manihara K., Mizokami M.,
Date T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D28917; BAA06044.1; HSSP; P27958; 1HEI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2590 SNCLTCYIKVKAACDRVGLKNVSLLIAGDDCLIICERPICDPSEALGRALAIYGYACEPS 2649
                                                                                  SEQUENCE
                                                                                                            ATP-binding; Coat protein; Envelope protein; Glycoprotein; Helicase; Nonstructural protein; Polyprotein; RNA-directed RNA polymerase;
                                                                                                                                                ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEROPS; S29.001;
MEROPS; U39.001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              comparative study with different genotypes.";
J. Gen. Virol. 75:3279-3284(1994).
-i- SIMILARITY: TO HEPATITIS C VIRUS ENVELOPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Full-length sequence of the genome of hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-K3A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-K3A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=11103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viruses; ssRNA positive-strand viruses, Hepacivirus.
                                                                                                                                                                                                                                                                                                                                                                                        interPro;
                                                                                                                                                                                                                                                                                                                                                                                                       [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (nterPro; IPR001410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lepatitis C virus
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                                                                                                                                                                                                                                                                                                                                                                        interPro;
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                                                                                                                                                                                                                                                                                                                                                         nterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EQUENCE FROM N.A
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                                                                                  3021
    Conservative
                                                                                                                                                                            HCV_NS4a; 1.
HCV_NS4b; 1.
HCV_NS5a; 1.
HCV_RdRP; 1.
                                                                                                                                                                                                                                           HCV_NS2; 1.
HCV_NS3; 1.
                                                                                                                                           helicase_C; 1.
52; HCV_NS1; 1.
                                                                                                                                                                                                                                                                        HCV_NS1;
                                                                                                                                                                                                                                                                                      HCV_env;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          696
                                                                                                                                                                                                                                                                                                                        _capsid; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEAD.

HCV_capsid.

HCV_core.

HCV_env.
                                                                                                                                                                                                                                                                                                                                                                                   HCV_NS4a.
HCV_NS4a.
                2.9%;
                                                                                328386 MW;
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                                                                                                                                                                                                                                                                                                                                                                     HCV_NS5a
                                                                                                                                                                                                                                                                                                                                                         HCV_RdRP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the EMBL/GenBank/DDBJ databases.
Score 108; DB 12;
Pred. No. 4.3;
7; Mismatches 247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VIRUS ENVELOPE
                                                                              A97418FF36C062A4 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLYCOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Takada A.,
                                Length 3021;
   Indels
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 248;
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Gaps
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RESULT 13
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Q96Q25;
Q96Q25;
Q1-DEC-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
                                                           SEQUENCE PROM N.A.

Nakatsura T., Senju S., Shichijo Ogawa M., Itoh K., Nishimura Y.;

"Cellular Identification of Human Originally Defined by SEREX Meth Submitted (APR-2001) to the EMBL
SEQUENCE FROM N.A.
MEDLINE=21134339; PubMed=11237751;
Nakatsura T., Senju S., Yamada K.,
                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                           NCBI_TaxID=9606;
[1]
                                                                                                                                                                                                                       Homo sapiens (Human).
                                                                                                                                                                                                                                        KM-PA-2
                                                                                                                                                                                                                                                       KM-PA-2 PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           452 CPQRLSSCKPITFFKQGWGPLTDANITGPSDDKPYCWHYAPRPCGIVPALNVCGPVYCFT 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185 -- QQLPDCRGLEV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 PIARCALLEVQVPADLVQPGQS--VGSAVFDCFEA-SLGAEVQIWSYTKPRYQKELNLT- 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PSPVVVGTTDAKGAPTYTWGANKTDVFLLESLRPPSGRWFGCTWMNSTGFVKTCGAPPCN 571
                                                                                                                                                                                                                                                                                                                                                                                                                                         AVAQCQQWLQLQTVEPGPHDALAAWLSCVLPDFLQGRATGRYVGVYFDGLLHPDSV 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALSOMPLRVAVDLWSRRELSAHGA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TARCSLGLSCHL-----WDGDVLCLPGSLQSAPGPVLVPTRLQTELVLRCPQKTDCALR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --VRVVVHLAVHGHWAEPE------EAGKSDSELQESRNASLQAQVVLSFQAY 128
                                                                                                                                                                                          Chordata;
Primates;
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19,
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                                                                                                                          Shichijo S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human Pancreatic (
Method.";
EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                        Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                  PRT;
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                                                                                                                           Χ.,
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                                                                                              Cancer Antigen
                                                                                                                             Ohkouchi S.,
                                                                 databases
                                                                                                                                                                                                        Euteleostomi;
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                                                                                                                             Yamada K.,
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                                                                                              KM-PA-2,
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Jotsuka T.,

Ogawa M.,

Nishimura Y.;

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SPRRR
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Matches 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
SIMILAR TO BLOCK OF PROLIFERATION 1 (FRAGMENT).
    Strausberg R.;
Submitted (DEC-2000)
                                                                                                                                                                                                                                 OMAB60
                                    SEQUENCE FROM N.A.
FISSUE=MUSCLE, RHP
                                                                                                                                                                                                                ; OMVBED
                                                                                    CBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                            573
                                                                                                                                                                                                                                                                                                          617 T----QPWV 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochem. Biophys. Res. Commun. EMBL; AB060694; BAB70666.1; -. SEQUENCE 634 AA; 71930 MW;
                                                                                                                                                                                                                                                                                                                                        568 AAVAQCQQWL 577
                                                                                                                                                                                                                                                                                                                                                                                                          508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   260 HTDLVPCLCIQVWSLEPDSERVEFCPFREDPGAHRNLWHIARLR-----VLSPGVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                203 WVLP---WLNVSTDGDNVLLTLDVSEEQDFSFLLYLRPVPDALKSLWYKNLTGPQNITLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                    GSVIVCHGMVYNDLLQNPLLVPV----KVLKGH--
                                                                                                                                                                                                                                                                                                                                                                                             AGYERLVGALASALSOMPLRVAVDLWSRRELSAHGALAWFHHORRRILQEGGVVILLFSP
                                                                                                                                                                                                                                                                                                                                                                                                                            SLAVHPAGDNVICGSYDSKLVWFDLDLSTKPYRMLRHHKKALRAVAFHPRYPLFASGSDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLWACPM-DKYIHRRW--VLVWLACLLLAAALFFFLLLKKDRRKAARGSRTALLLHSADG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VQR-----VAFHPA--RPFLLVASQRSVRLYHLLRQELTKKLMPNCK--W----VS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VEMKTGLNNTSVCALEPSGCTPLPSMASTRAARLGEELLQDFRSH---QCMQLWNDDNMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RQVGLRLRICHGKPVTQV-TWHGRGDYLAVVLATQGHTQVLIHQLSRRRSQSPFRRSHGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PQ-DFQLVAGHPNLCVQVSTWE-------KVQLQACSWADSLGPFKDDMLL 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSDLVRCL----SVSPGG---QWLVSGSDDGSLR-LWEVATARCVRTVPVGGVVKSVAW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FDCF----EASIGAEVQI-WSYTKPRYQKELNLTQQLPDCR-----GLEVRDSIQSC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGKS-----DSELQESRNASLQAQTVLSFQAYPIARCALLEVQVPA-DLVQPGQSVGSAV 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FSGDVMIHPVTNRPADKRSFIPSLVEKEKVSR------MVH-AIKMGWIQPRR 160
                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.9%; Score 107.5; D
llarity 21.1%; Pred. No. 0.55;
Conservative 72; Mismatches
                                  RHABDOMYOSARCOMA;
to the EMBL/GenBank/DDBJ databases
                                                                                           Craniata; Ve
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E7A5608B28D65C36 CRC64;
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                                                                                                                                                                                                                       680 AA
                                                                                                        Vertebrata; Euteleostomi;
                                                                                              Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---KMHVPAPKLALPGHA----
                                                                                                                                                          update)
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                                                                                                                                                                                                                                                                                                                                                                  -VLTRDLGVLDVIFHP
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Best Local Similarity

Matches 129; Conserv
                                            O9BSA7;
01-UUN-2001 (TIEMBLIEL 17, Created)
01-UUN-2001 (TIEMBLIEL 17, Last seq
01-DEC-2001 (TIEMBLIEL 19, Last ann
SIMILAR TO BLOCK OF PROLIFERATION 1
     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                       Q9BSA7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Repeat; WD repeat.
NON_TER 1
SEQUENCE 680 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001680; WD40.

Pfam; PF00400; WD40; 7.

SMART; SM00320; WD40; 7.

PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.

PROSITE; PS50082; WD_REPEATS_2; 2.

PROSITE; PS50294; WD_REPEATS_REGION; 2.
                                                                                                                                                                                                                       568
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EMBL; BC001086; AAH01086.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       161 FSGDVMIHPVTNRPADKRSFIPSLVEKEKVSR------MVH-AIKMGWIQPRR 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        207 PRDPTPSFYDLWAQEDPNAVLGRH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42 WDGDVLCLPGSLQSAPGPVLVPTRLQTELVLRCPQKTDCALRVRVVVHLAVHGHWAEPEE 101
                                                                                                                                                                                                                    AAVAQCQQWL
                                                                                                                                                                                                                                           GSVIVCHGMVYNDLLQNPLLVPV----KVLKGH---
                                                                                                                                                                                                                                                                 AGYERLVGALASALSOMPLRVAVDLWSRRELSAHGALAWFHHORRRILQEGGVVILLFSP 567
                                                                                                                                                                                                                                                                                               SLAVHPAGDNVICGSYDSKLVWFDLDLSTKPYRMLRHHKKALRAVAFHPRYPLFASGSDD
                                                                                                                                                                                                                                                                                                                         SLWACPM-DKYIHRRW--VLVWLACLLLAAALFFFLLLKKDRRKAARGSRTALLLHSADG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YLCPRORKMRVNVDPEDLIPKLPRPRD-----LQPFP-TCQALVYR---
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                                                                                                                                                                                           VW40-
                                                                                                                                                                                                                                                                                                                                                     -----VAFHPA--RPFLLVASQRSVRLYHLLRQELTKKLMPNCK--W----VS
                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             680 AA; 76791 MW;
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                                                                                                                                                                                         667
                                                                                                                                                                                                                    577
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                                          Last sequence update)
Last annotation updat
RATION 1 (FRAGMENT).
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Pred. No. 0.6;
Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A26BA8F6F0CB1F2F CRC64;
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                                                                                                                                                                                                                                          -VLTRDLGVLDVIFHP
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-!- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
EMBL; BC005160; AAH05160.1:
InterPro; IPR001680; WD40.

Pfam; PF00400; WD40; 7.

R SMART; SM00320; WD40; 7.

R PROSITE; PS00078; WD_REPEATS_1; UNKNOWN_1.

R PROSITE; PS00082; WD_REPEATS_2; 2.

PROSITE; PS50082; WD_REPEATS_2; 2.

R PROSITE; PS50082; WD_REPEATS_2; 2.

R PROSITE; PS50082; WD_REPEATS_2; 2.

R PROSITE; PS50082; WD_REPEATS_2; 2.

R PROSITE; PS50082; WD_REPEATS_REGION; 2.

R PROSITE; PS50082; WD_REPEATS_REGION; 2.

R PROSITE; WD repeat.
1

NON_TER 1

SEQUENCE 689 AA; 77638 MW; 80F6FFDFEE623B7B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 129; Conserv
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TISSUE-BRAIN, NEUROBLASTOMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606; [1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102 AGKS-----DSELQESRNASLQAQVVLSEQAYPIARCALLEVQVPA-DLVQPGQSVGSAV 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             203 WVLP---WLNVSTDGDNVLLTLDVSEEQDESFLLYLRPVPDALKSLWYKNLTGPQNITLN 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           156 FDCF----EASLGAEVQI-WSYTKPRYQKELNLTQQLPDCR-----GLEVRDSIQSC--- 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   170 FSGDVMIHPVTNRPADKRSFIPSLVEKEKVSR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           314 YLCPRORKMRVNVDPEDLIPKLPRPRD-----LOPFP-TCQALVYR------G 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       255 -ESYNPPPEYLLSEEERLAWEQQEPGERKLSFLPRKFPSLRAVPAYGRFIQERFERCLDL 313
                                                                                                                                           508 AGYERLVGALASALSQMPLRVAVDLWSRRELSAHGALAWFHHORRRILQEGGVVILLESP 567
                                                                                                                                                                                                                         568
                                                                                                                                                                                                                                                                           451 SLWACPM-DKYIHRRW--VLVWLACLLLAAALFFFLLLKKDRRKAARGSRTALLLHSADG 507
                                                                                                                                                                                                                                                                                                                                        525
                                                                                                                                                                                                                                                                                                                                                                                      394 VEMKTGLNNTSVCALEPSGCTPLPSMASTRAARLGEELLQDFRSH----QCMQLWNDDNMG 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                      466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    406 NPSPAYCLVAAAVEDSVLLLNPALGDRLVAGSTDQLLSAFVPPEEPPLQPARWLEASEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      311 QLDAPCCLPGKVT----
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                                                                                                           628 GSVIVCHGMVYNDLLQNPLLVPV----KVLKGH---
  672 T----QPWV 676
                                              568 AAVAQCQQWL 577
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Run

on:

OM protein -

Q9d2v7 Q9wu16 Q9wu16 Q43593 P03203 Q94761

homo sapien epstein-bar

homo sapien

mus musculu

P40223 Q14202 P09848 P98157

DOMO rattus

homo

sapien sapien lus gall

gallus

P55146

rattus mus musculu

norv

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993 - 2000 Compugen Ltd
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PGBM_MOUSE
GSPL_KLEPN
FL3L_HUMAN
A2M1_MOUSE
CKRA_HUMAN
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BISC_ECOLI
TS13_MOUSE
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TYO3_MOUSE
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AEX3_CAEEL
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1102.662 Million cell updates/sec
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 DCC_MOUSE
P70211;
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"Cloning of the mouse homologue of the deleted in colorectal cancer gene (mDCC) and its expression in the developing mouse embryo.";
oncogene 11:2243-2254(1995).
                     EMBL; X85788; CAA59786.1; -. HSSP; P56276; lTLK. MGD; MGI:94869; Dcc.
                                                                                                   use
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                                                                                                                                   This
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STRAIN-BALB/C; TISSUE=Brain;
MEDLINE=96112625; PubMed-8570174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Mus musculus (Mouse).
Aboria; Rodentia;
                                                                or send
                                                                             entities
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01-NOV-1997 (Rel. 35, Last seg
01-MAR-2002 (Rel. 41, Last ann
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                                                               European Bioinformatics Institute. There are no rest by non-profit institutions as long as its content ified and this statement is not removed. Usage by an itles requires a license agreement (See http://www.isbsend an email to license@isb-sib.ch).
                                                                                                                                                                                              TISSUE SPECIFICITY: IN THE EMBRYO, EXPRESSED AT HIGH LEVELS IN THE DEVELOPING BRAIN AND NEURAL TUBE. IN ADULT, HIGHLY EXPRESSED IN BRAIN WITH VERY LOW LEVELS FOUND IN TESTIS, HEART AND THYMUS. DEVELOPMENTAL STAGE: LOW LEVELS IN EARLY GESTATION. HIGHEST LEVELS EXPRESSED DURING MID GESTATION. LEVELS DECREASE IN LATE GESTATION AND REMAIN AT THIS LEVEL IN THE ADULT.
                                                                                                                                                      SIMILARITY: CONTAINS SIMILARITY: CONTAINS
                                                                                                                                                                                      SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. DCC
                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                              SUBFAMILY
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IPR003962; FnIII_repeat.
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41, Last annotation updat
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LTH RAT
GCSR_MOUSE
Z 261_HUMAN
LPH_HUMAN
LRP1_CHICK
W701_MOUSE
HAKE_MOUSE
HAKE_HUMAN
EBN4_EBV
RCQ4_HUMAN
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Result

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Query Match
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Matches 99
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Pfam; PF00047; 1g; 4.
PRINTS; PR00014; FNTYPEIII.
SMART; SM00060; FN3; 6.
SMART; SM00410; IG_11ke; 2.
SMART; SM00408; IGC2; 3.
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SMART; SM00408; IGC2; 3. **
Glycoprotein; Immunoglobulin domain; Transmembrane; Signal;
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                 ITLNHTDLVPCLCIQVWSLEPDSERVEFCPFREDPGAH----RNLWHIARLRVLSP
                                                         WV-----LPWLNVSTDGDNVLLTLDVSEEQDFSFLLYLRPVPDALKSLWYKNLTGPQN
                                                                                                  GQSVGSAVFDCF---EASL--GAEVQIWSYTKPRYQKELNLTQQLPDCRGLEVRDSIQSC
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                                                                                                                                            QAQVVLSFQAYPI-ARCALLEVQVPA-----DL-----
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                                         CVSGYPPPSFTWLR----GEEVI-
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IPR003598;
IPR003600;
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IG-LIKE C2-TYPE DOMAIN 2.
IG-LIKE C2-TYPE DOMAIN 3.
IG-LIKE C2-TYPE DOMAIN 4.
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 4.
FIBRONECTIN TYPE-III 5.
FIBRONECTIN TYPE-III 5.
FIBRONECTIN TYPE-III 6.
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MISSING (IN EMBRYONIC
WW; OD1F1097C22D5B9F (
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DCC_HUMAN STANDARD,

P43146;

01-NOV-1995 (Rel. 32, Created)

01-NOV-1995 (Rel. 32, Last sequence update)

01-MAR-2002 (Rel. 41, Last annotation update)

01-MAR-2002 (Rel. 41, DCC precursor (Colorectal cancer suppressor).
                                                                                                                    human esophageal squamous cell carcinomas and their metastasis.".
Cancer Res. 54:3007-3010(1994).
-!- FUNCTION: IMPLICATED AS A TUMOR SUPPRESSOR GENE.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
                                                                                                                                                                                                            VARIANT CARCINOMA THR-168, AND VARIANT GLY-201.
MEDLINE-94243823; PubMed-8187090;
Miyake Si, Nagai K., Yoshino K., Oto M., Endo M., Yuasa Y.;
"Point mutations and allelic deletion of tumor suppressor gen
human esophageal squamous cell carcinomas and their relation
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-!- TISSUE SPECIFICITY: FOUND IN AXONS OF THE CENTRAL AND INERVOUS SYSTEM AND IN DIFFERENTIATED CELL TYPES OF THE -!- DISEASE: COLORECTAL TUMORS THAT LOST THEIR CAPACITY TO DIFFERENTIATE INTO MUCUS PRODUCING CELLS UNIFORMLY LACK EXPRESSION. INACTIVATION OF DOT DOT TO THE CONTRACT OF THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO THE CAPACITY TO TH
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Genomics | 19:525-531(1994).
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MEDLINE-94245241; Pubmed-8188295;
Cho K.R., Oliner J.D., Simons J.W., Hedrick L.,
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SEQUENCE OF 1-750 FROM N.A.

MEDLINE-90100559; PubMed-2294591;

Fearon E.R., Cho K.R., Nigro J.M., Kern

Fearon F.R., Hamilton S.R., Preisinger
                                                                                                                                                                                                                                                                                                                                                                                                          Cho K.R. Oliner J.D., Simons J.W., Hedrick L., Preisinger A.C., Hedge P., Silverman G.A., Vogel The DCC gene: structural analysis and mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oliner J.D., Kinzler K.W., "Scrambled exons.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-91121517; pubMed=1991322;
Nigro J M., Cho K.R., Fearon E.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           colorectal cancers.";
Science 247:49-56(1990).
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Vogelstein B.;
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Identification of a chromosome 18q gene that is colorectal cancers.";
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"The DCC gene
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-->zoa; Chordata;
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InterPro: IPR003600; Ig_like.
Pfam; PF00041; fn3; 6.
Pfam; PF00047; 19; 4.
PRINTS; PR00014; FNTYPEIII.
SMART; SM00400; FN3; 6.
SMART; SM00410; IG_11ke; 2.
SMART; SM00408; IGC2; 3.
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L; M32288; AAA52175.1; ALT_SEQ.
L; M3290; AAA52176.1; -.
L; M63696; AAA52177.1; -.
L; M63700; AAA52179.1; -.
L; M63718; AAA52179.1; -.
L; M63718; AAA52180.1; -.
L; M63698; AAA52181.1; -.
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IPR003600; Ig_like.
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IG-LIKE C2-TYPE DOMAIN 1.

IG-LIKE C2-TYPE DOMAIN 2.

IG-LIKE C2-TYPE DOMAIN 3.

IG-LIKE C2-TYPE DOMAIN 4.

FIBRONECTIN TYPE-III 1.

FIBRONECTIN TYPE-III 2.

FIBRONECTIN TYPE-III 3.

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                                                                                                                                                                                                                                                                                                                                    -----LPSMASTRAARLGEELLQDFRSHQCMQLWNDDNMGSLWACPMDKYIHRRWVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----LPWLNVSTDGDNVLLTLDVSEEQDFSFLLYLRPVPDALKSLWYKNLTGPQNI
   (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 38, Last annotation update)
(Ral. 38, Last annotation update)
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233
421
1447
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                                                                 STANDARD;
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                                                                                                                                                                                                                                       -VAVDLWSRRELSAHGALAWFHHQRRRILQEGGVVILLFSPAAVAQCQ
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329
421
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                                                                                                                                                                                                                                                                -----AKGNIQTFTVFFSREGDNRERALNTTQPGSLQLTV
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MISSING (IN REF. 3
MISSING (IN REF. 3
MISSING (IN REF. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------DDSGMYTCVVTYKNENISASAELTVLVP-
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                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 112; DB 1; Length 1447; Pred. No. 0.71;
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SSING (IN REF. 3).
SSING (IN REF. 3).
4A8612766EDO471F CRC64;
                                                                1711 · AA
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Pfam; PF00041; fn3; 7.

Pfam; PF00102; Y_phosphatase; 1.

PRINTS; PR00014; FNTYPEIII.

PRINTS; PR000700; PRTYPHPHTASE.

SMART; SM00060; FN3; 6.

SMART; SM00014; PTPC; 1.

SMART; SM00012; PTPC_DSPC; 1.

PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.

PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
                                       DOMAIN
TRANSMEM
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASSOCIATED WITH DIFFERENTIATION IN BONE AND TESTIS.

-I- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein tyrosine + phosphate.

-I- SUBCELULIAR LOCATION: Type I membrane protein.

-I- ALTERNATIVE PRODUCTS: A PRESUMED ALTERNATE TRANSCRIPT OF 4.8-5.0 KILOBASES, WHICH MAY LACK PTP DOMAINS, IS PRESENT IN PROLIFERATING OSTROBLASTS, BUT NOT DETECTABLE AT OTHER STAGES.

-I- TISSUE SPECIFICITY: BONE AND TESTIS. IN THE LATTER, RESTRICTED TO THE BASAL PORTION OF THE SEMINITEROUS TUBULE.

-I- DEVELOPMENTAL STAGE: UP-REGULATED IN LIFE STAGE MINERALIZING CULTURES. IN TESTIS, EXPRESSION IS HIGHEST BETWEEN STAGES I AND VOIL WHEN MATURING SPERMATIDS REMAIN BURIED WITHIN THE SERTOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
   DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000340; DS_phosphatase.
InterPro; IPR003961; FN_III.
InterPro; IPR003962; FIIII_repeat.
InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR000242; Tyr_prot_phphtase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Identification of a hormonally regulated protein tyrosine phosphatase associated with bode and testicular differentiation.";
J. Biol. Chem. 269:30659-30667(1994).

-I- FUNCTION: MAY FUNCTION IS SIGNALING PATHWAYS DURING BONE REMODELING, AS WELL AS SERVE A BROADER ROLE IN CELL INTERACTIONS ASSOCIATED WITH DIFFERENTIATION IN BONE AND TESTIS. OPTIMAL PH FOR PHOSPHATASE ACTIVITY IS 5.6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; L36884; AAA63911.1; -. HSSP; P18052; 1YFO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Osteosarcoma;
MEDLINE-95074080; Pu
                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SITES.
-!- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.
-!- SIMILARITY: CONTAINS 10 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EPITHELIUM.
INDUCTION: |
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THE CYTOPLASMIC DOMAIN CONTAINS POTENTIAL PHOSPHORYI
     18
1075
1096
32
125
216
304
     1074
1095
1711
124
215
303
392
                                                                                                                                                 1711
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ed E.A., Skřobacz B.M., Mourey R.J., Davis A.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN CONTAINS POTENTIAL PHOSPHORYLATION
CYTOPLASMIC (POTENTIAL).
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 4.
                                                                                                      OSTEOTESTICULAR PROTEIN TYROSINE PHOSPHATASE. EXTRACELLULAR (POTENTIAL).
                                                                                            POTENTIAL.
                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                Signal; Glycoprotein.
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Ωy	Qу рь	Оу	Qy Db	Qу	Db Qy	Оу	Оу	Оу	Qy Db	Que Bes Mat	
502 LHSA : 752 VSMQ	5 NDD	385 GPF 681 G	325 CWQ 1 639 LWG	290 PGAH 579 PAAL	252 519 DLVD	200 QSC	142 ADL 0 LAV	43 DGD 333 DGY	ry Match t Local ches 15	DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN CARBOHYD	
ADGAGYERLV : QAGSAVVNLAWPSGPLG	SLWAC FLGLT	KDDMLLVEMKTGLNNTSVCALEPSGCTP	APDQSPCQP	RNLWH : : KASWYHPPGG	-GPQNITLNHTDLV :: LGPDTLSLTLKSLV	WVLPWLNVSTDGDNVI	-VQPGQSVGSAVFDCF:::	HGHWAEPEEAGK	VLCLPGSLQSA	2 Similarity 20 2; Conservativ	393 470 471 562 563 652 563 741 742 830 831 921 1150 1350 1429 1711 1350 1350 42 42 42 42 74 42 74 72 117 117 117 117 117 117 174 150 620 620 620 620 620 620 620 620 620 62
GALASALS † : 	PMDKYIHRRWVLVWLACLLLAAA : : : :	NTSVCALEPSGCTPLP : RYQVTLYQESTRTATS	LVPPVPQKNATVNEPQDFQLV	TARLRVLSPG : RDAFHLRLYRLRPLTLESEK	PCLCIQVWS	LPWLNVSTDGDNVLLTLDVSBEQDFSFLLYLRPVPDAL ISRSSPSDLTIAWGPAPGQL	-VQPGQSVGSAVFDCFEASLGAEVQIWSYTKPRYQK : : NISVPSGATHVIFCGLVPGAHYRVDIASSTGDISQS	SDSELQESRNASLQAQVV : : : GSTWLAESAALPREVP	PGPV EECNAVFPGP-	.9%; Score 109 .6%; Pred. No. e 74; Mismat	FIBRONECTIN T FIBRONECTIN T FI
QMPLRVAVD : :: SWEQPLKLGQE	ALFFFLLLKKDR : : : : ANVSAWTYPLIPNE-	SMAS IMGP	QLVAGHPNLCVQVSTWEKVQLQAC 	VW- VLPREAQNFSWA	-CLCIQVWSLEPDSERVEFCP : : ::: : : ::: SCYTVSAWAWAGNLDSDSQKIHSCTRPAP	EGY	ELNLTC ISGYTS	GARLWLDGLEAS	VLVPTRLQTEL-VLRCPC 	.5; DB 1; 1.4; ches 241;	YPE-III 5 YPE-III 7 YPE-III 7 YPE-III 7 YPE-III 1 YPE-III 1 YPE-III 1 YPE-III 1 YPE-III 1 YPE-III 1 YPE-III 1 NAC
LWSRRELSAHGALAW : : : EMLRDLTPGHTISM	RRKAARGSRTALL	TRAARLGEELLQDFRSHQCMQLW	WEKVQLQACSWADSL DAPTQLQV-SWAHVP	QLDAPCCLPGKVTL 	PAPPTNLSLGFAHQ	KSLWYKNLT :::: KVTWHQDGSQRSPG	QLPDCRGLEVRDSI : ;PLPP-QSLEV	AYPIARCALLEVQVP	POKTDCALRVRVVVH 	Length 1711; Indels 271; Ga	HHATASE 1. HHATASE 2. (POTENTIAL)
546 811	501 751	444 704	384 680	32 4 638	289 578	251 518	199 481	141 426	89 377	aps	

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Y124_HUMAN
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Matches 129
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SEQUENCE
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REPEAT
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DNA Res. 2:167-174(1995).

DNA Res. 2:167-174(1995).

DNA Res. 2:167-174(1995).
                                                                                                                                                                                                                                                         SMART; SM00320; WD40; 5.

PROSITE; PS00678; WD_REPEATS_1; 1.

PROSITE; PS50082; WD_REPEATS_2; 2.

PROSITE; PS50294; WD_REPEATS_REGION;
                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                 modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                REPEAT
                                                                                                                                                                                                                  REPEAT
                                                                                                                                                                                                                                                                                                             InterPro; IPR001680; WD40. Pfam; PF00400; WD40; 7.
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                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-96127530; PubMed-8590280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOY-1997 (Rel. 35, Created)
01-NOY-1997 (Rel. 35, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation updat
Hypothetical protein KIAA0124 (Fragment).
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Q14137;
       102
                               163
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                                                                                                                                                                                                                                                    lypothetical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         547 FHHORRRILQEGGVVILLFSPAAVAQCQQWLQLQTVEPGP-HDAL----AAWLS-----
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                                                                                                                                                                                                                                                                                                                                                          send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: STRONG, TO YEAST YMR049C.
AGKS-----DSELQESRNASLQAQVVLSFQAYPIARCALLEVQVPA-DLVQPGQSVGSAV 155
                          FSGDVMIHPVTNRPADKRSFIPSLVEKEKVSR-
                                              WDGDVLCLPGSLQSAPGPVLVPTRLQTELVLRCPQKTDCALRVRVVVHLAVHGHWAEPEE 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TQLPAFLDALQGGCSTSA 635
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                                                                             129;
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                                                                                       Similarity
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388
468
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554
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                                                                           Conservative
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428
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                                                                                                                                      MW;
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                                                                         Score 108.5; |
Pred. No. 0.5;
72; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AEX3_CAEEL STANDARD; PRT; 1409 AA. 002626; 027467; 16-0CT-2001 (Rel. 40, Created) 16-0CT-2001 (Rel. 40, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update) Regulator of presynaptic activity aex-3. AEX-3 OR CO2H7.3.
                                                                                                                                                                              Leimbac D., Minx M.;
Submitted (FEB-1996)
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-97282461; PubMed-9136770;
Iwasaki K., Staunton J., Saifee O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAEEL
in synaptic transmission.";
EMBO J. 19:4806-4816(2000).
                                        Iwasaki K., Toyonaga R.;
"The rab3 GDP/GTP exchange factor homolog
                                                                                              INTERACTION WITH CAB-1.
MEDLINE=20428446; PubMed=10970871;
                                                                                                                                                                                                                                 STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                             elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                  Neuron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans.
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RESULT 6
OM6_CHLPS
ID OM6_CHLPS
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Matches 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics. Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is got removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: GUANINE NUCLEOTIDE EXCHANGE FACTOR (GEF) FOR REGULATE TWO DIFFERENT PATHWAYS FOR NEURAL ACTIVITIES. SUBUNIT: BINDS TO CAB-1.
                                                                              MPLRVAVDLWSRRELSAHGALAWFHHQRRRILQE 557
                                                                                                                                                    ---QKVRRLLGKAHIGLVCSKEINKLLDE---
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                                                            SPKTKILCLWRRHDDKVH--MHKFHTKKCRELYQ
                                                                                                       GSRLVQKQSFTVCPGQSSDGQMMFMEVCDDAVVLRSITGAATERWWYERLVN----
                                                                                                                                 GSR----
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                                                                                                                                                                                                                                                                                                                RVLSPGVWQLDAPCCLPGKVTLCWQAPDQSP----
                                                                                                                                                                       FRSHQCMQLWNDDNMGSLWACPMDKYIHRRWVLVWLACLLLAAALFFFLLLKKDRRKAAR 494
                                                                                                                                                                                                                   ---SLGPFKDDMLLVEMKTGLNNTSYCALEPSGCTPLPSMASTRAARL-----GEELLQD 434
                                                                                                                                                                                                                                                                                                                                    GQNVTPTSTNNHEIAQSTRSPALPPPV----PPREAPPI-PKRNPPPLGAPPKVPEGAR-
                                                                                                                                                                                                                                                                                                                                                           -QNITLNHTD------LVPCLCIQVWSLEPDSERVEFCPFREDP--GAHRNLWHIARL
                                                                                                                                                                                                                                                                                                                                                                                  LEIAHTHYWAMGGGEVITPSSSAPSTMTTPSEHSNDILKESRPKLPA-STIDLRTPTKPL
                                                                                                                                                                                                                                                                                                                                                                                                                              LNLGLEVKL---SEDEYVKEVQLTKGQFKAYVKILKACLEGIEVSFNTPGCCGFASVFHV
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1409 AA;
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     STANDARD;
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                                                                                                                                                                                                                                                                                       -APPPLPPRPKVKTTAVDETPQNLVPNNQPAQPSSPSFLADADEQTKPLL
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    PRT;
                                                                                                                            ----TALLLHSADGAG-----YERLVGALASALSQ
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OMCB OR OMP2 OR ENVB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 kDa outer membrane
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01-NOV-1991
                                                                                                                 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=83554;
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                       273
                                             IARNVVVD-
                                                                                                                                      Similarity
61; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FROM N.A.
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                                                                                                                                      Conservative
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VEFCPQKRGKVTNVATVSYCGGHKCSANVTTV
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41
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Watson M.W., Lambden P.R., Clarke I.N.;
"The nucleotide sequence of the 60 kDa cysteine protein of Chlamydia psittaci strain EAE/A22/M."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X53512; CAA37592.1; -. EMBL; M61116; AAB61619.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Sequence analysis and lipid modification of the cysteine-rich envelope proteins of Chlamydia psittaci 6BC."; J. Bacteriol. 173:3821-3830(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chlamydia psittaci (Chlamydophila psittaci).
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Everett K.D.E., Hatch T.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=91267949; PubMed=2050637;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
                                                                    VLLTLDVSEEQDFSFLLYLRPVPDALKSLWYKNLTGPQNITLNHTDLVP----CLCIQVW 272
                                                                                                            CFTAATYCACPELRSYTKCG-QPAICIKQEGPECACLR-----
                                                                                                                                                  CF-EASLGAEVQIWSYTKPRYQKELNLTQQLPDCRGLEVRDSIQSCWVLPWLNVSTDGDN 216
  SLEPDSERVEFCPFREDP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                requires a license agreement (See http://www.isb-sib
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Transmembrane; Signal; Virulence
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protein precursor (Cysteine-rich
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A -> S (IN STRAIN 6BC).
E -> G (IN STRAIN 6BC).
W; OD444F09EAAO73C6 CRC6
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--GAHRNLWHIARLRVLSPGVWQLDAPC----
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No. 1.1;
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                                                                                                                                                                                            Ishikawa K.-I., Nagase T., Nakajima D., Seki N., Ohira M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O., "Prediction of the coding sequences of unidentified human genes. 78 new cDNA clones from brain which code for large proteins in
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 1).
TISSUE-Kidney;
Benedict M.A., Nunez G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Cytochrome c and dATP-mediated oligomerization prerequisite for procaspase-9 activation."; J. Biol. Chem. 274:17941-17945(1999).
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Zou H., Henzel W.J., Liu X., Lutschg A., Wang X.;
"Apaf-1, a human protein homologous to C. elegans
in cytochrome c-dependent activation of caspase-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The mammalian CED4 homologue, human cells.";
Submitted (MAR-1999) to the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Peripheral blood, Heart, an MEDLINE-99373149; PubMed-10441496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1998 (Rel. 36, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Apoptotic protease activating factor 1 (Apaf-1).
                                                                                                                                                                                                                                                                                                      MEDLINE=98116655; PubMed=9455477;
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 385-1248 FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                           Benedict M.A., Nunez
Submitted (MAY-1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-T-cell;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hahn C., Hirsch B., Jahnke D., Duerkop I
Three new types of Apaf-1 in mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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Mammalia; Eutheria; Primates; Catarrhini;
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                                                                               Roberts D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A., Srinivasula S.M.,
                                                                                                                                                       4:307-313(1997).
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                                       810-864 AND 866-883 FROM N.A.
., Dalgleish R., Cohen G.M., MacFarlane
ian CED4 homologue, APAF1, exists as tw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EKVQLQACSWADSLGPFKDDMLL---
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EMBL/GenBank/DDBJ databases
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SEQUENCE OF 1-138 FROM N.A. (ISOFORM 1/4/5).
WON M., Lee J.-W., Ohr H.-H., Kim D.-U., Chung
YOO H.-S.;
"Cloning of variant Apafl.";
"Cloning of variant Apafl.";
                                                                                                                                                                                                  between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE 20047184; PubMed
Day C.L., Dupont C., Lad
"Solution structure and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (1.3 ANGSTROMS) OF 1-97.

MEDLINE-20013059; PubMed-10543941;

Vaughn D.E., Rodriguez J., Lazebnik Y., Joshua-Tor L.;

"Crystal structure of Apaf-1 caspase recruitment domain:

helical Greek key fold for apoptotic signaling.";

J. Mol. Biol. 293:439-447(1999).
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Moroni M.C., Hickman E.S., Denchi E.L., Caprara
Cecconi F., Mueller H., Helin K.;
"Apaf-1 is a transcriptional target for E2F and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-98315378; PubMed-9651578; Srinivasula S.M., Ahmad M., Fernandes-Alnemri T., A "Autoactivation of procaspase-9 by Apaf-1-mediated Mol. Cell 1:949-957(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRUCTURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CARD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INDUCTION BY E2F AND P53
                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Cytoplasmic.

ALTERNATIVE PRODUCTS: 5 isoforms; 1/Apaf-1XL (shown IL, 3/Apaf-1S, 4/Apaf-1M and 5/Apaf-1XS; are produce alternative splicing.

TISSUE SPECIFICITY: Ubiquitous. Highest levels of exadult spleen and peripheral blood leukocytes, and in
                                                                                                                                                                                ween the Swiss Institute of Bioinformatics European Bioinformatics Institute. There
                                                                                                                                                                                                                                              SIMILARITY: CONTAINS 1 CARD DOMAIN.
SIMILARITY: CONTAINS 13 WD REPEATS (TRP-ASP DOMAINS).
SIMILARITY: CONTAINS 1 NB-ARC DOMAIN.
CAUTION: Ref.7 sequence differs from that shown due to
                                                                                                                                                                                                                                                                                                                                                                                                                            dATP. Oligomeric Apaf-1 and pro-caspase-9 their respective NH2-terminal CARD domains mature caspase-9 is released from the comp
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATPI
SUBUNIT: Monomer. Oligomerizes upon binding of
Subunit: Monomer. Oligomerizes upon binding of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: Oligomeric Apaf-1 mediates the cytochrome c-cautocatalytic activation of pro-caspase 9 (Apaf-3), leactivation of caspase-3 and apoptosis. This activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: Oligomeric Apaf-1 media
                                                                                                                                                                                                                                    frameshift in position 109
                                                                                                                                                                                                                                                                                                      INDUCTION: By E2F and p53 in apoptotic neurons
                       AJ243004;
AJ243005;
AJ243006;
AJ243007;
AJ243008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell Biol. 3:552-558(2001).
                                                                                       AJ243003;
                                                                                                     AF013263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from Apaf-1.
                                                                                                                            an email to license@isb-sib.ch).
                                                                                                                                            requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY NMR OF 1-97.
                                  AAC51678.1;
CAB55579.1;
CAB55580.1;
CAB55581.1;
CAB55582.1;
CAB55583.1;
                    CAB55582.1;
CAB55583.1;
CAB55584.1;
                                                                                                                                                                                                                                                                                                                                lung. Isoform
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed-10578182;
                                                                                                                                       license agreement (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lackmann M., Va
and mutagenesis
                                                                                                                                                                                                                                                                                                                               1 is expressed
                                                                                                                                                                                                                                                                                                                                                                                                                          from the complex.
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is of
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the caspase
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                                                                                                                                                                                                                                                                                                                                                                                     produced
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             recruitment
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Query Match
Best Local Similarity
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SMART; SM00320; WD40; 10.
PROSITE; PS50209; CARD; 1.
PROSITE; PS00678; WD_REPEATS_1; 4.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00619; CARD; 1.
Pfam; PF00931; NB-ARC; 1
Pfam; PF00400; WD40; 11.
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InterPro;
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IPR001680;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          ATP-binding; Repeat; WD repeat; Alternative
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CAB55588.1;
CAB56462.1;
AAD38344.1;
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2.7%;
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Score
Pred.
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E -> ETLGFESK (IN ISOFORM 5).

MISSING (IN ISOFORM 3, ISOFORM 4 AND ISOFORM 5).

MISSING (IN ISOFORM 5).
                                                                                                                                                                                                                                                                                  NB-ARC
ATP (PW D 1.
WD 2.
WD 3.
WD 4.
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WD 6.
WD 9.
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WD 110.
WD 112.
WD 13.
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100.5;
No. 5;
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                                                               CAB55586).
CAB56462).
CAB55581).
CAB55587).
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CAB55584).
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        Length 1248;
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RESULT 8
A2M2_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                  A2M2_MOUSE STANDARD;
P28666; | Created)
01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last seq
01-NOV-1997 (Rel. 35, Last number)
                                                                                                                                                                            J. Biol.
                                                                                                                                                                                                                              TISSUE-Liver; MEDLINE-91358495; PubMed-1840592;
                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia: Eutheria;
                                                                             Overbergh L., Torrekens S., van Leuven F., van den Berghe H.;

"Molecular characterization of the murinoglobulins.";

"Molecular characterization of the murinoglobulins.";

J. Biol. (Chem. 266:16903-16910(1991).

-i- FUNCTION: A PROTEINASE ACTIVATES THE INHIBITOR BY SPECIFIC PROTECLYSIS IN THE BAIT REGION, WHICH, BY AN UNKNOWN MECHANISM LEADS TO REACTION AT THE CYSTEINYL-GLUTAMYL INTERNAL THIOL ESTER SITE AND TO A CONFORMATIONAL CHANGE, WHEREBY THE PROTEINASE IS TRAPPED AND/OR COVALENTLY BOUND TO THE INHIBITOR. WHILE IN THE THEREBY THE PROTEINASE IS TRAPPED AND/OR COVALENTLY BOUND TO THE INHIBITOR.
                                                                                                                                                                                                               Overbergh
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                           MUG2 OR MUG-2.
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                           TETRAMERIC PROTEINASE INHIBITORS STERIC INHIBITION IS SUFFICIENTLY STRONG, MONOMERIC FORMS NEED A COVALENT LINKAGE BETWEEN THE ACTIVATED GLUTAMYL RESIDUE OF THE ORIGINAL THIOL ESTER AND A
            TERMINAL AMINO GROUP OF A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NATVNEPQDFQLVAGHPNLCVQVSTWEKVQLQACSW-ADS-----LGPFKDDM
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                          (MuG2).
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              ANOTHER NUCLEOPHILIC
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InterPro; IPR001599; Alpha_2_macroglobin
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PIR; B41185; B41185.
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                                                                                                                                                                                                       454 ETSSILPCNQIHTVQAHFILKGDLGVLKELVFYYLVMAQGSIIQTGNHTHQVEPGEAPVK 513
                                                                                                                            163 LGAEVQIWSYTKPRYQKELNLTQQLPDCRGLEVRDSIQSCWVLPWLNVSTDGDNVLLTLD 222
                                                                                                                                                            514 GNFDLE---
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TISSUE SPECIFICITY: PLASMA.
SIMILARITY: TO OTHER PROTEINS OF THE ALPHA-MACROGLOBULIN FAMILY,
INCLUDING COMPLEMENT COMPONENTS C3, C4, AND C5.
                                                                        VSEEQDFSFLLYLRPVPDALKSLWYKNLTGPQNITLNHTDLVP-----
                                                                                                                                                                              GKSDSELQESRNASLQAQVVLSFQAYPIARCALLEVQVPADLVQPGQSVGSAVFDCFEAS 162
                                                                                                                                                                                                                                 QTELVLRCPQ-----KTDCALRVRVVVHLAV------HGHWAEPEEA--- 102
VAE---KHTDWVPHGREKDVYRYVEDMDLKAFTNLKIKLPKICFDSAPMSGPRGKFDLAF
                         SLEPDSERVEFCPFREDPGAHR-----NLWHIARLRVLSPGVWQLDAPCCLP-GKVTLCW
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    Plasma; Bait region; Signal;

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Pfam; PF00066; notch; 3.
PRINTS; PR00010; EGFBLOOD.
PRINTS; PR01452; NOTCH.
SMART; SM00248; ANK; 5.
SMART; SM00179; EGF_CA; 19.
SMART; SM00001; EGF_like; 16.
                                                                                             Pfam;
Pfam;
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HECH. DEV. 43:87-100(1993).

HECH. DEV. 43:87-100(1993).

HECH. DEV. 43:87-100(1993).

HE FUNCTION: IMPLICATED IN CELL FATE SPECIFICATIONS DURING EMBRYO DEVELOPMENT. MAY BE INVOLVED IN THE FORMATION OF THE NEURAL PLATE, NOTOCHORD AND BRAIN VESICLES.

HEURAL PLATE, NOTOCHORD AND BRAIN VESICLES.

SUBCELLULAR LOCATION: Type I membrane protein.

HE SUBCELLULAR LOCATION: Type I membrane protein.

HE SUBCELLULAR LOCATION IN THE MEMBRASH ALL CELLS IN PRESASTRULATION STAGES. DURING GASTRULATION IS DIFFERENTIALLY EXPRESSED, AND NOTOCHORD. AT THE END OF GASTRULATION, EXPRESSED ALONG THE ANTERIOR-POSTERIOR AXIS INCLUDING THE DEVELOPING NEURAL PLATE AND EXPRESSED ALONG THE ANTERIOR-POSTERIOR AXIS INCLUDING THE DEVELOPING NEURAL PLATE AND DIFFERENTIATING MESODERM. ALSO PRESENT IN THE DEVELOPING
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HSSP; P00740; 1EDM.
ZFIN; ZDB-GENE-990415-173;
                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                  Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                    use
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-!- SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS.

-!- SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.

-!- SIMILARITY: CONTAINS 6 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                     InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BRARE
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01-NOV-1995 (Rel. 32, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
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IPR000742;
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EGF-LIKE 6.

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CALCIUM-BIN

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CALCIUM-BIN

EGF-LIKE 34.

EGF-LIKE 35.

CALCIUM-BIN

EGF-LIKE 36.

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LIN/NOTCH 3.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirosawa M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. The complete sequences of 100 new cDNA clones from brain which complete in vitro.";
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                                                                                                                             mitochondrial glutaminase cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Brain;
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Mammalia; Eutheria;
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                      TISSUE=Colorectal carcinoma;
                                                    SEQUENCE OF 225-466 FROM N.A.
                                                                                                            Brain Res.
                                                                                                                                             "Isolation, characterization and
                                                                                                                                                                                                             MEDLINE=20185643; PubMed=10719215;
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                         Brain Res.
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                                                                                                      76:56-63(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entitiés requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified and this statement is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between Bioinformatics Institute. There are no restrictions on its
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-i- SIMILARITY: BELONGS TO THE GLUTAMINASE FAMILY.
-i- SIMILARITY: CONTAINS 1 ANK REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FOR THE RENAL CATABOLISM OF GLUTAMINE.

-i- CATALYTIC ACTIVITY: L-glutamine + H(2) o= L-g

-i- ALTERNATIVE PRODUCTS: 3 ISOFORMS; KGA (SHOWN
GAC; ARE PRODUCED BY ALTERNATIVE SPLICING.

-i- TISSUE SPECIFICITY: KGA IS EXPRESSED PREDOMIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         express different isoforms of glutaminase.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: CATALYZES THE FIRST REACTION IN THE PRIMARY PATHWAY
   201
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                       NSEGKELVASGENKIKQGLLPSLEDLLFYTIAEGQEKIPVHKFITALKSTGLRTSDPRLK
                                                                         LSSSPSEILQELGKGSTHPQPGVSPPAAPAA---
                                                                                               KSDSE----LQESRNASLQAQVVLSFQAYPIARCALLEVQVPADLVQPGQSVGSAVFDCFE
                                                                                                                      DLLLRSPAGVSATLRRAQPLVTLCRRPRGGGRPAAGPAAAARLHPWWGGGGWPAEPLARG
 SCWVLPWLNVSTDGDNVLLTLDVSEEQDFSFLLYLRP-
                                                   ASLGAEV --
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AF223943;
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ÀF097492; AAF00088.1;
AF097493; AAF00089.1;
AF097495; AAF00090.1;
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AAG17700.1;
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                                              -QIWSYTKPRYQKELNLTQQLPDCRGLEVRDS---IQ
                                                                                                                                                                                    Score 98.5;
Pred. No. 3.
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(IN REF. 1; AAF00090).
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P48681; O00552;
O1-FEB-1996 (Rel
O1-FEB-1996 (Rel
16-OCT-2001 (Rel
                                               the nestin gene.";
Dev. Biol. 205:309-321(1999).
-:- TISSUE SPECIFICITY: CNS STEM CELLS.
-:- DEVELOPMENTAL STACE: UPON TERMINAL NEURAL DIFFERENTIATION,
-:- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                             Dahlstrand J., McKay R.D.G., Zimmerman L.B., Lendah "Characterization of the human nestin gene reveals evolutionary relationship to neurofilaments."; J. Cell Sci. 103:589-597(1992).
                                                                                                                                                                                                                                                                                                                                                        HUMAN
                                                                                                         Yaworsky P.J., Kappen C.; "Heterogeneity of neural progenitor cells revealed by
                                                                                                                                                     [2]
                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                  MEDLINE-99117355;
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PROSITE: PS00226; IF: 1.
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MIM; 600915;
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                   FLQGRATGRYVGVYFDGLLHPDSVPSPFRVAPLFSLPTQLPAFL---DALQGGCSTSAGR
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                                                        HLKMSLSLE------VATYRTLLEAENSRLQTPGGGSKTSLSFQDPKLELQFPR
                                                                                     HQRRRILQEGGYVILLFSPAAVAQCQQWLQ-----LQTVEPGPHDALA----AWLSCVLPD
                                                                                                                      RAALEQRIEGRWQERIRATEKFQLAVEALEQEKQGLQSQIAQVIEGRQQLA
                                                                                                                                                 TALLHSADGAGYERL-----
                                                                                                                                                                                                          NDDNMGSLWACPMDKYIHRRWVL----VWLACLLLAAALFFFLLLKKDRRKAARG---SR
                                                                                                                                                                                                                                       LRVAHEEERVGLNAQAACAPRLPAPPRPPAPAPEVEEL-ARRLGEAWRGAVRGYQ-----
                                                                                                                                                                                                                                                                   LLV---EMKTGLNNTSVCA----LEPSGCTPLPSMASTRAARLGEELLQDFRSHQCMQLW 444
                                                                                                                                                                                                                                                                                                NLAEELEGVAGR----CEQLRLARERTTEEVARNRRAVEAEKCARAWLSSQGAELERELEA 139
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                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and this statement is not removed requires a license agreement (See
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LINKER 2.
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TAIL.
COIL 1A.
LINKER 1.
COIL 1B.
LINKER 12.
                                                                                                                                                                                                                                                                                                                                                                          Score 97.5;
Pred. No. 1
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TLETPVPAFLKNQEFLQARTPTLAST 387
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                                                                                                                                                                                                                                                                                                                                                          139;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Usage
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STRAIN=Sprague-Dawley; Itoh T., | Itoh A., Plea
                                                                                                                                                                            Q9EPV5;
01-MAR-2002 (Rel. 41,
01-MAR-2002 (Rel. 41,
01-MAR-2002 (Rel. 41,
                                                             NCBI_TaxID=10116;
                                                                                        Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                      SEQUENCE FROM N.A.
                                                                                                                         Rattus norvegicus (Rat).
Itoh A., Pleasure
                                                                                                                                                           protease activating
                                                                                                                                                                                                                                                  STANDARD;
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Last annotation update)
tivating factor 1 (Apaf-1).
   D.;
                                                                                     Craniata; Vertebrata; | Sciurognathi; Muridae;
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Euteleostomi;

Rattus.

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Matches 137;
                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Apoptosis;
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00114; CARD; 1. SMART; SM00320; WD40; 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001680; WD40. Pfam; PF00619; CARD; 1. Pfam; PF00931; NB-ARC; 1. Pfam; PF00400; WD40; 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF320222; AAG35067.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- INDUCTION: By brain injury.
-!- SIMILARITY: CONTAINS 1 CARD DOMAIN.
-!- SIMILARITY: CONTAINS 13 WD REPEATS (TRP-ASP DOMAINS).
-!- SIMILARITY: CONTAINS 1 NB-ARC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Differential expression of apoptotic protease-acaspase-3 genes and susceptibility to apoptosis development and after transfic brain injury.";
J. Neurosci. 21:7439-7446(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00320; GPROTEINBRPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yakovlev A.G., Ota K., Wang G., Movsesyan V., Bao W.-L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEVELOPMENTAL REGULATION, AND INDUCTION BY BRAIN INJURY MEDLINE-21450943; PubMed-11567033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases. [2]
79 DCALRVRVVVHLAVHGH-----WAEPEEAGKSDSELQE-SRNASLQA-QVVLSFQAY-- 128
                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: Regulates programed cell death; necessary for normal brain development. Participates with caspase-9 (Apaf-3) in the cytochrome c-dependent activation of caspase-3, leading to apoptosis. This activation requires Arp (By similarity). SUBUNIT: Monomer. Oligomedizes upon binding of cytochrome c and dATP. Oligometic Apaf-1 and pro-caspase-9 bind to each other via their respective NH2-terminal CARD domains (By similarity). SUBCELLULAR LOCATION: Cytoplasmic (By similarity). DEVELOPMENTAL STAGE: Highly expressed in brain cortex in embryos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (E17) and new-born rats up to
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                                                                                                                                                                                                                    106
613
655
697
741
796
838
880
959
1001
1004
11042
                                                      Conservative
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WD_REPEATS_1; 4.
WD_REPEATS_2; 9.
WD_REPEATS_REGION; 1.
                                                                                                                                                                                                                                         1040
1080
1122
                                                                          2.6%;
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                                                    78;
                                                                                                                                                               NB-ARC.
ATP (PC
WD 1
WD 2
WD 2
WD 3
WD 4
WD 5
WD 6
WD 7
WD 7
WD 9
WD 11
WD 11
WD 11
WD 11
WD 13
                                                                          Score 96.5;
Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARD
                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WD repeat.
                                                                                                                                                               7B4A8116FAD008E9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protease-activating factor-1
                                                                                             DB 1;
                                                  245;
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                                                                                             Length 1249;
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RESULT 13
C267_HUMAN
ID C267_HUMAN
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                                                     "From PREDs and open reading frames to cDNA human chromosome 21 transcription map."; Genomics 78:46-54(2001).
                                                                                                  SEQUENCE FROM N.A. (ISOFORMS A AND B).
MEDLLINE-2154202; PubMed-11707072;
Reymond A., Friedli M., Neergaard Henrichsen C., Ct
Deutsch S., Ucla C., Rossier C., Lyle R., Guipponi
Antonarakis S.E.;
                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
-i- ALTERNATIVE PRODUCTS: 2 isoforms, A (shown here) and B; produced by alternative splicing.
-i- TISSUE SPECIFICITY: Not detected in any tissue tested.
                                                                                                                                                                                                                                                                                 01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last seq
01-MAR-2002 (Rel. 41, Last ann
Protein C21orf67.
                                                                                                                                                                                                                                                                                                                                                                                                                                             1053 LRDSRLLSWSFDGTVKVWNVITGRIERDFTCHQGTVLSCAISSDA 1097
                                                                                                                                                                                                    NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PREDPGAHRNLWHIARLRVLSPGVWQLDAPCCLPGKVTLCWQAPDQSPCQPLVPPVPQKN 345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NRVFSSGIGHKKAVRHIQFTADGKTLISSSEDSVIQVWNWQTEEYVFLQAHQETVKDFRL 1052
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Matches
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Best Local :
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Poly(A) polymerase beta (EC 2.7.7.19) (PAP beta) (Polynucleotide adenylyltransferase beta) (Testis-specific poly(A) polymerase).
                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-slb.ch/announce/or send an email to license@isb-slb.ch).
                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases -i- CATALYTIC ACTIVITY: N ATP + (nucleotide)(M) - N dip)
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                 InterPro; IPR002934; NTP_transf.
InterPro; IPR001201; PAP_25A_core.
Pfam; PF01909; NTP_transf_2; 1.
mRNA processing; Transferase; Transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                  EMBL; AF218840; AAF81013.1; -.
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Nuclear protein
                                                                                                                                                                                                                                                                                                                                               - TISSUE SPECIFICITY: Testis-specific.
- SIMILARITY: BELONGS TO THE POLY(A) POLYMERASE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lee Y., Kim H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria;
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SUBCELLULAR LOCATION: NUCLEAR (Probable).
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Primates;
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36.6%;
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ACT_SITE
SEQUENCE
                                                                                                                                       SEQUENCE FROM N.A.
TISSUE-Breast cancer;
TISSUE-Breast cancer;
MEDLINE-98167917; PubMed-9499409;
Peng J.-M!, Zhu Y., Milton J.T., Price D.H.;
"Identification of multiple cyclin subunits
Genes Dev! 12:755-762(1998).
MEDLINE-99263518; PubMed-10329125; Ivanov D.) Kwak Y.T., Nee E., Guo Gaynor R.B.; "Cyclin Ti domains involved in com
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16-0CT-2001 (Rel. 40, Created
16-0CT-2001 (Rel. 40, Last se
16-0CT-2001 (Rel. 40, Last an
Cyclin Tl (Cyclin T) (CycTl).
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MEDLINE-98150851; PubMed-9491887;
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Bukaryota), Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Wei P., Garber M.E., Fang S.-M., Fischer W.H., Jor
"A novel (DN9-associated C-type cyclin interacts of the control of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts of the cyclin interacts 
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in complex formation with Tat and TAR RNA
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Pred. No. 7.7;
0; Mismatches 123
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COMPLEXES. ;

J. VIYOL. 73:5777-5786(1999).

-i- FUNCTION: REGULATORY SUBUNIT OF THE CYCLIN-DEPENDENT KINASE PAIR (CDK9/CYCLIN T) COMPLEX, ALSO CALLED POSITIVE TRANSCRIPTION ELONGATION EACTOR B (P-TEPB), WHICH IS PROPOSED TO FACILITATE THE TRANSITION FROM ABORTIVE TO PRODUCTION ELONGATION BY PHOSPHORYLATING THE CTD (CARBOXY-TERMINAL DOMAIN) OF THE LARGE
               CONFLICT
                                                                                                                                                                 DOMAIN
DOMAIN
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                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                        InterPro; ipr000553; Cyclin.
Pfam; PF00134; cyclin; 1.
SMART; SM00385; CYCLIN; 1.
PROSITE; PS00292; CYCLINS; FALSE_NEG.
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"The interaction between HIV Tat and human cyclin Tl requires zinc and a critical cysteine residue that is not conserved in the murine CycTl protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMMBL; AF045161; AAC39638.1; -.
EMMBL; AF048730; AAC39664.1; -.
TRANSFAC; T02727; -.
MIM: 602506; -.
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                                                                               MUTAGEN
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                                                                                                                                                                                                                                                                                                                     Cyclin;
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"Role of the human and murine cyclin T proteins in regulating HIV-1
Tat-activation.";
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Garber M.E., Wei P., KewalRamani V.N., Mayall T.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          are critical for tat-activation.";
J. Mol. Biol. 288:41-56(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT OF RNA POLYMERASE II (RNAP II). BINDS ALSO TO THE TRANSACTIVATION DOMAIN OF THE HIV-1 NUCLEAR TRANSCRIPTIONAL ACTIVATOR, TAT. IT IS PROBABLY THE CIS-ACTING TRANSACTIVATION RESPONSE ELEMENT (TAR) RNA-BINDING CORFACTOR FOR TAT. ALSO SERVES AS AN ESSENTIAL COFACTOR FOR HIV 2-TAT AND SIMIAN IMMUNODEFICIENCY VIRUS (APRICAN MANDRILL) TAT FUNCTION.
SUBUNIT: ASSOCIATES WITH CDK9 TO FORM p-TEFB. CYCLIN T1 IS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PREDOMINANT CYCLIN ASSOCIATED WITH CDK9.
SUBCELLULAR LOCATION: Nuclear.
TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED.
MISCELLANEOUS: INTERACTION BETWEEN TAT AND CYCLIN T1 REQUIRES
                                                                                                                                                                                                          Cell cycle; Cell division; Coiled coil;
iption regulation; Nuclear protein.
19253 270 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
254 272 TAT:TAR RECCONITION MOTIF (TRM).
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                                                                                                     253
254
384
317
517
717
               726 AA;
            80684 MW;
                                         C->Y: LOSS OF HIV-1 TAT TRANSACTIVATION.
Q -> R (IN REF. 2).
                                                                                                                              COILED COIL (POTENTIAL).
POLY-HIS.
POLY-SER.
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4637EFB2DDEDFE13 CRC64;
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214 VSTDGKHWWEYVDATVTLELLDELTHEFLQILEKTPNRLKRIW 256	210 VSTDGDNVLLTLDVSEEQDFSFLLYLRPVPDALKSLW 246	187 FSL	161 ASLGAEVQIWSYTKPRYQKELNLTQQLPDCRGLEVRDSIQSCWVLPWLN 209	128 QVQQLVILESIILQTLGFELTIDHPHTHVVKCTQL-VRASKDLAQTSYFMATNSLHLTT 186		79 PGN-SVAPAALFLAAKVEEQPKKLEHVIKVAHTCLHPQESLPDTRSEAYL 127	50 PGSLQSAPGPVLVPTRLQTELVLRCPQKTDCALRVRVVVHLAVHGHWAEPEEAGKSDSEL 109	Query Match 2.5%; Score 93.5; DB 1; Length 726; Best Local Similarity 19.3%; Pred. No. 9.1; Matches 43; Conservative 39; Mismatches 70; Indels 71; Gaps

Search completed: September 28, 2002, 19:43:38 Job time: 286 sec

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3.0%; Score 112; DB 2; Length 1447; 6; Conservative 74; Mismatches 210; Indels 302 RLMEPQDTARCSLGLSCHLMDGDVLCLPGSLQSAPG-PVLVPTRLQTELVL	ressor protein DCC precursor - human a names: colorectal cancer suppressor DCC HOmo sapiens (man) Aug-1994 #sequence_revision 02-Aug-1994 #text_change 0 1.; A54100; A40098 L.; Cho, K.R.; Fearon, E.R.; Wu, T.C.; Kinzler, K.W.; 8, 1174-1183, 1994 PDCC gene product in cellular differentiation and colonumber: A54100; MUID:95011532 1. A54100 type: mRNA 1-1447 <hed> 1-1447 <hed> 1-1447 <hed> 1-1447 <hed> 2.R.; Cho, K.R.; Nigro, J.M.; Kern, S.E.; Simons, J.W.; 49-56, 1990 Pentification of a chromosome 18q gene that is altered number: A40098; MUID:90100559 1-750 <fea> 1-750 <fea> Eerences: GB:M32292; NID:g181492; PIDN:AAA35751.1; PID: Cerences: GB:M32292; NID:g181492; PIDN:AAA35751.1; PID: 1-101: 18q21.1-18q21.1 transmembrane protein; tumor suppressor in: signal sequence #status predicted <sig> product: tumor suppressor protein DCC #status predicted</sig></fea></fea></hed></hed></hed></hed>	: :
Gaps 34; RC 74 RC e 05-Nov-1999 Colorectal tumorigenesis. PID:9453210 W.; Ruppert, J.M.; Hamilta ed in colorectal cancers. TD:9181493 TD:9181493	SLLVPA 309 SLLVPA 309 KRAARGS 496 : PALRTA 351 PRRKL- 356 PRRKL- 393 P 599 PLIRLR 451 PTQLPA 642 RADG 506 GPCTTL 697 : GLGKTV 566	

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139 QVPADLVQPGQS------

2267 QVESSLTSEGQTRFRPDSCATADCSPCLRMYSNRTFSACHSFVSPESFCELWIRDTKYVQ 2326

------VGSAVFDCFEASLGAE--VQIW-SYTKPRY 177

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C;Accession: T42214
R;Cohen-Salmon, M.; El-Amraoui, A.; Leibovici, M.; Petit, C.
Proc. Natl. Acad. Sci. U.S.A. 94, 14450-14455, 1997
A;Title: Otogelin: A glycoprotein specific to the acellular membranes of the inner (A;Reference number: Z22079; MUID:98070772
A;Reference number: Z22079; MUID:98070772
A;Accession: T42214
A;Accession: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-2910 <COH>
A;Residues: 1-2910 <COH>
A;Residues: 1-2910 <COH>
A;Ross-references: EMBL:U96411; NID:92760883; PID:92760884; PIDN:AAB96561.1
A;Experimental source: strain BALB/c
A;Note: component of all the acellular membranes of the inner ear
C;Superfamily: von Willebrand factor; von Willebrand factor type A repeat homology;
                                                                                                                                                                                                                                                                                                                                                                                                                              N;Alternate names: mucin-like extracellular matrix protein
C;Species: Mis musculus (house mouse)
C;Date: 03-Dec-1999 #text_change 17-Mar-2000
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    Query Match
Best Local
Matches 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      468 VWLACLLLAAALFFFLLLKKDRRKAARGS-RTALLLHSADGAGYERLVGALASALSOMPL 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       364 CVQVSTWEKVQLQACSWADSLGPFKDD----MLLVEMKTGLNNTSVCALEPSGCTP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      331 PWFLNHPSNL----YAYESMDIEFECTVSGKPVPTVNWMKNGDVVIPSDYFQIVGGSNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 309 VWQLDAPCCLPGKVTLCWQAPD-QSPCQPLVPPVP----QKNATVNEPQDFQLVAGHPNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          263 VSGYPPPSFTWLR----GEEVI-------------QLRSKKYSLLGGSNLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         206 -DIG--IYRCSARNPASSRTGNEAEVRILSDPGLHRQLYFLQRPSNVVAIEGKDAVLECC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       490 GNIKPEAMYTFRVVAYNEWGPGESS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  428 LPSAPRDVVPVLVSSRFVRLS--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                257 TLNHTDLVPCLCIQVWSLEPDSERVEFCPFREDPGAH-----RNLWHIARLRVLSPG 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 204 · V-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QWLQ-----ATGRYVGVYFD 616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PELOVPGPVENLOAVSTSPTSILITWEP---PAYANGPVQGYRLFCTEVSTGKEQNIEVD 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISNVTD-----
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                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----LPWLNVSTDGDNVLLTLDVSEEQDFSFLLYLRPVPDALKSLWYKNLTGPQNI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----AKGNIQTFTVFFSREGDNRERALNTTQPGSLQLTV 489
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----LGVVKSDEGFYQCVAENEAGNAQTSAQLIVPKPAIPSSSV 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----VAVDLWSRRELSAHGALAWFHHQRRRILQEGGVVILLFSPAAVAQCQ 574
3.0%; Score 111.5;
19.8%; Pred. No. 6;
Live 43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------DDSGMYTCVVTYKNENISASAELTVLVP- 330
                                                 DB 2;
    140;
                                               Length 2910;
    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -QPIKVA-TQ 522
  153;
  Gaps
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    19;
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hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Date: 03;Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C;Accession: D75564
R;White, 0; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, M.; Shen, M.; Vamathevan, Heidelberg, J.F.; McDonald, L.; Utterback, T.; Zalewski, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Génome sequence of the radioresistant bacterium Deinococcus radiodurans FA;Reference number: A75250; MUID:20036896
A;Accession: D75564
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                                                                                                                                                                                                                         C; Genetics:
A; Gene: DR0061
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A;Experimental source: strain R1
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                                                                                                               Query Match
Best Local Similarity
                                                                                          Matches
                         237 PVP---DALKSLWYKNLTGPQNITLNHTDLVPCLCIQVWSLEPDSERVEFCPFREDPGAH 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      961
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PVPGAGDVLVSLGNSEVVRQLARTLGDLLLLPGGAAQVWQA---LDRVEDDPFPPQPGDD 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RTALLLHSADGAGYERLVGALASALSQMPLRVAVDLWSRRELSAHGALAWFHHQRRRILQ 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LSRVL----EALWELLLQAILQAIG-ANRDVSADFYSRFHFTLEALVSFFH---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAHRNLW--HIARLRVLSPGVWQLDAPCCLPGKVTLCWQAPDQSPCQPLVPPVPQK--NA 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QNITLN----HTDLVPCLCIQVW-------SLEPDSERVEFCPFREDP 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H-QCMQLWNDDNMGSLWACPMDKYIHRRWVLVWLACLLLAAALFFFLLLKKDRRKAARGS 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MLLVEMKTGLNNTSVCALEPSGCTPLPSMASTRA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DSRSLALAGIHAPFLP--AVKLWFQVLRDQAKWRLQGAVDMDTLEP----VDASSRHSSS 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAKSPREQPG---PQRLP---GLVVLADAVYDDLQFCYSVYASLFHSILNVDVFTLTFRQ 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYTKPRYQKELNLTQQLPDCRGL----EVRDSIQSC-----
                                                                                                                                                                                                                                                                                                                 1-478 <WHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AATAGLCLSHIQEL-----W-----VRLAW--PDPAQAQGLGTQLGQDVCEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LERLVAEEAWVL-----TEELSPKMTLEVASG---LFELYL-TLAD-LQRFW-DSIPGR 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RCA-----LLEVQVPADLVQPGQSVGSAVFDC-FEASLGAEV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NSTAVHRLELLLKCLGKLQLFQPSFEI-----CPFESELNMDIAAALKRGNREWYDRIL 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----VNEPQDFQLVAG----HPNLCVQVSTWEKVQ-----LQACSWADSLGPFKDD 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----WVLPWLNVSTDGDNVLLTLDVSEEQDFSFLLYLRPVPDALKSLWYKNLTGP 253
                                                                                     2.8%; Score 106.5; llarity 23.2%; Pred. No. 1.5; Conservative 38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----ATGPEGVLPRPLLSCTQALDDDLQREAHTVTAHLTSKMVGDIRK 873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----QGLPLESLRDGSYKRL 978
                                                                                                                                 DB 2;
                                                                                       184;
                                                                                                                               Length 478;
                                                                                       Indels 169;
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                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4;Introns: 77/1; 136/2; 183/2; 232/3; 283/3; 386/3; 427/3; 527/3; 577/1; 699/3; 782/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    presynaptic activity regulator aex-3 - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_chance_revision 04-Dec-1999                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δõ
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ubmitted to the EMBL Data Library, February 1996
Description: The sequence of C. elegans cosmid CO2H7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Status: translated from GB/EMBL/DDBJ; Molecule type: DNA; Molecule type: DNA; Molecule type: DNA CAPPE: Box Status: 1-1409 CLEI>; Cross-references: EMBL:U49945; PIDN:AAC47926.1; GSPDB:GN00029; Experimental source: strain Bristol N2; clone C02H7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.8%; Score 106.5; Best Local Similarity 20.0%; Pred. No. 6; Matches 115; Conservative 77; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genetics:
Gene: aex-3; CESP:C02H7.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description: The sequence Reference number: Z20523 Accession: T37188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Accession: T37188
                                                                                                                                                                                                                                                                                                                                                                                                                                                        780 QQSKNQQTVREFCDQALVGQSVGMFSAPKLKR--LMEDESLRELV------CSK 825
254 -QNITLNHTD------LVPCLCIQVWSLEPDSERVEFCPFREDP--GAHRNIMHIARL 302
                                                                                                                            883 LEIAHTHYWAMGGGEVITPSSSAPSTMTTPSEHSNDILKESRPKLPA-STIDLRTPTKPL 941
                                                                                                                                                                                                                                                                                          826 LNLGLEVKL---SEDEYVKEVQLTKGQFKAYVKILKACLEGIEVSENTPGCCGFASVFHV 882
                                                                                                                                                                                                                                                                                                                                                  101 EAGKSDSELQESRNASIQAQVVLSFQAYFIARCALLEVQVFADLVQFGQSVGSAVFDCFE 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   400 VFPLGPDPLEVRLPGDRLLTLRPDYRAEL 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                645 DALQGGCSTSAGRPADRVERVTQALRSAL 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   348 ALLHLPP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      594 LSCVLPDFLQGRATGRYYGYYFDGLLHPDSVPSPFRVA---PLFSL---PTQLPA---FL 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6
                                                                                                                                                                                                         -----WVLPWLNVSTDGDNVLLTLDVSEEQDFSFLLYLRPVPDALKSLWYKNLTGP- 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADAAQTRHLARLAALGRACALLLLPAEQHGRLRLARTLARRLRGDP-----PRADDP 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OGLRL---SWR-SLGP--NWQLLVQQETSQPVSGGQLALLRPD----LP--ASER----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EKVQLQACSWADSLGPFKD8WLKYEMKTG--LNNTSVCALEPSGCTPLPSMASTRAARLG 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LARAPGQLPGTVPAHSVLYAQEEASALSAPAAGDGLTLH-----LGGPD---RLAHW 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QLDAPCCLPGKVTLCWQAPDQSPCQPLVPPVPQKNATVNEPQDFQLVAGHPNLCVQVSTW 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASGQVAFAQTPAECLAAARRSLQRLEPLLGRFSPAQVA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALFAQLAAIRQRGGSPHERAQLEEVLRAGAGPQSALRADPRERPLLREAAQRIRRWLARR 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EELLQDFRSHQCMQLWNDDNWGSLWACPMDKYIHRRWVLVWLACLLLAAALFFFLLLKKD 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----RRKAARGSRTALLLHSADGAGYERLVGALASALSOMPLRVAVDLWSRRELS 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --HYAAQVQQAAEHAASAAEPLREAATDPLVGREAGPPVLPATGHFI 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -VLSPGV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-Dec-1999 #text_change 18-Feb-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1409;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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RESULT 8
B39439
60K cysteine-rich outer membrane protein 1 precursor - Chlamydophila psittaci

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C; Accession: G83156
R; Stover, C.K.; Pham, X.Q.;
adman, S.; Yuan, Y.; Brody,
                                                                                                                               probable transcription regulator PA3921 [imported] - Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Species: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
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A; Title: Complete genome sea A; Reference number: A82950;
                                         .; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-44, A', 46-72, 'E', 74-557 <WAT>
A; Cross-references: GB: X53512; NID: g40625; PIDN: CAA37592.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Sequence analysis and lipid modification A;Reference number: A39439; MUID:91267949 A;Accession: B39439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: B39439; S12603
R;Everett, K.D.E.; Hatch, T.P.
J. Bacteriol. 173, 3821-3830,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: The nucleotide sequence of the 60kDa
A;Reference number: S12603; MUID:90384851
A;Accession: S12603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic Acids Res. 18, 5300, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:M61116; NID g144489;
A;Experimental source: strain 6BC (R. Natson, M.W.; Lambden, P.R.; Clarke, I.N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reywords: membrane protein; virulence; 1-22/Domain: signal sequence #status predicted <?; 23-40/Domain: propeptide #status predicted <PRO>; 41-557/Product: 60K cysteine-rich outer membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    be an important virulence factor. superfamily: 60K cysteine-rich outer membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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;Residues: 1-557 <EVE>
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Pate: 21-Feb-1992 #sequence_revision 27-Jun-1994 #text_change 31-Mar-2000
                                                                                                                                                                                                                                                                                                                        406 CALE 409
                                                                                                                                                                                                                                                                                                                                                         386 VWCIKEMCPGETLQFKVVAKAQSPGKFTNQVVVKTNSDCGTCTSCAEVTTHWKGLAATHM
                                                                                                                                                                                                                                                                                                                                                                                                        369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                158 CF-EASIGAEVQIWSYTKPRYQKELNLTQQLPDCRGLEVRDSIQSCWVLPWLNVSTDGDN
                                                                                                                                                                                                                                                                                   446 CVID 449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  217 VLLTLDVSEEQDFSFLLYLRPVPDALKSLWYKNLTGPQNITLNHTDLVP----CLCIQVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                   GADWSYVCKPVEYTIVVSNPGDLKLYDVVIEDTAPSGATI-----LEAAGAEICCNKA
                                                                                                                                                                                                                                                                                                                                                                                                        Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLEPDSERVEFCPFREDP------GAHRNLWHIARLRVLSPGVWQLDAPC-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -CLPGKVTLCWQAP-DQSPCQPLVPPVPQKNATVNEPQDFQLVAGHPNLCVQVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VEFCPQKRGKVTNVATVSYCGGHKCSANVTTV---
                                                                                                                                                                                                                                                                                                                                                                                                  -EKVQLQACSWADSLGPFKDDMLL-----
  sequence of Pseudomonas aeruginosa PA01, an 50; MUID:20437337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.8%;
                                                                       Erwin, A.L.; Mizoguchi, S.D.; Warrener, L.L.; Coulter, S.N.; Folger, K.R.; Kas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --NPVPDG----YTHASGQRVLSFNLGDMRPGDSKCFC----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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F;1271-1615/Domain: intracellular #status predicted <INT>
F;1353-1573/Domain: protein-tyrosine-phosphatase homology <PTP1>
F;1525/Active site: Cys (phosphocysteine intermediate) #status p
                                                       C;Keywords: alternative splicing; phosphoprotein; phospho F;1254-1270/Domain: transmembrane #status predicted <TMN>F;1271-1615/Domain: intracellular #status predicted <INT>
                                                                                                     A; Introns: 1605/3
C; Superfamily: protein-tyrosine-phosphatase, receptor type 4E; fibronectin
                                                                                                                                                      A;Cross-references: GB:L20894
C;Genetics:
A;Gene: FlyBase:Ptp4E
A;Cross-references: FlyBase:FBgn0004368
   F;1531/Binding site:
                                                                                                                                                                                                                                                                                           R;Oon, S.H.; Hong, A.; Yang, X.;
J. Biol. Chem. 268, 23964-23971,
A;Title: Alternative splicing in
A;Reference number: A49502; MUID.
                                                                                                                                                                                                                                                                                                                                                                                    protein-tyrosine-phosphatase (EC 3.1.3.48) receptor type 4E, C;Species: Drosophila melanogaster C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_char
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A; Residues: 1-1615 <00N>
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A;Residues: 1-906 <STO>
A:Cross-references: GB:AE004809; GB:AE004091;
A:Experimental source: strain PAO1
C;Genetics:
A:Gene: PA3921
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A; Status: prelimina
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substrate phosphate (Arg) #status predicted
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                                                                                                                                                                                                                                                                                                             novel tyrosine phosphatase gene (DPTP4E)
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;Date: 10 No. 2502

2;Accession: A49502

2;Accession: A49502

R;Con, S.H.; Hong, A.; Yang, X.; Chia, W.

R;Con, S.H.; Hong, A.; Yang, X.; Chia, W.

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                                                                                                                                                                                                                        ;Gene: ptp4E;Gene: rlyBase:FBgn0004368;Cross-references: FlyBase:FBgn0004368;Superfamily: protein-tyrosine-phosphatase, receptor type 4E; fibronectin type III repd;Superfamily: protein-tyrosine-phosphatase, receptor: monoester hydrolase; receptor: laternative splicing; phosphoprotein; phosphoric monoester hydrolase; receptor: 1270/Domain: transmembrane #status predicted <TWN>
F;1271-1767/Domain: intracellular #status predicted <TWN>
F;1273-1573/Domain: protein-tyrosine-phosphatase homology <PTP1>
F;1325/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1321/Binding site: substrate phosphate (Arg) #status predicted
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3.Title: Alternative splicing

3.Reference number: A49502; MI

3.Recession: A49502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Residues: I-1767 <00N>
Cross-references: GB:L20894
;Note: authors translated the codon ATA for residue 1715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Molecule type:
Residues: 1-170
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                                                                60 VLVPTRLQTELVLRC------PQKTDCALRVRVVVHL------AVHGHWAEPEEA 102
                                                                                                                                                                    Local Similarity
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      ILEPGRTY-EVVVKTIADNVNSWPASGEVTLRPRPVRSLGGFLDDRSNALHISW-EPAET 460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PQNLTLQTVHTNLV----VLHWQAPEGSDFSEYVVRYRTDASPW
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21.7%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----ITRYTRP----AAPLIQELRSIDQGLMLSWRSDVNSR 559
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MUID:94043220
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Pred. No. 18;
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                                                                                                                                                                                           Length 1767;
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                                                                                                                       SFQAYPIARCALLEVQVPADLVQPGQSVGSAVFDCFEASL----
                                                                                                                                                                                                                                           LVLRCPQKTDCALRVRVV----VHLAVHGHWAEPEEAGKSDSELQESRNASLQA--QVVL 123
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02; Conservative
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C; Superfamily: acyl carrier protein homology; acetate--CoA ligase homology (C; Keywords: carrier protein; phosphopantetheine; phosphoprotein F;511-951/Domain: acetate--CoA ligase homology <ACPl>
F;966-1034/Domain: acyl carrier protein homology <ACPl>
F;1563-2024/Domain: acyl carrier protein homology #status atypical <ACL2>
F;1563-2024/Domain: acyl carrier protein homology <ACP3>
F;2399-2467/Domain: acyl carrier protein homology <ACP3>
F;2399-2467/Domain: acyl carrier protein homology <ACP3>
F;2395-3427/Domain: acyl carrier protein homology <ACP3>
F;4043-4492/Domain: acyl carrier protein homology <ACP4>
F;407-4575/Domain: acyl carrier protein homology <ACP5>
F;407-4575/Domain: acyl carrier protein homology <ACP5>
F;407-4575/Domain: acyl carrier 
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C;Species: Streptomyces pristinaespiralis
C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 01-Dec-2000
C;Accession: T30289
F:998,2431,3473/Binding site: phosphopantetheine (Ser) (covalent) #status predicted
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                                                                                                                                                 QPGQSVGSAVFDCFEASLGAEVQIWSYTKPRYQKELNLTQQLPDC-RGLEVR-----DSI 199
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-GAEVQI---WSYTK 174

2.7%; Score 102; DB 22.5%; Pred. No. 67; tive 50; Mismatches

DB 2; Length 4848

Gaps

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A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Froh J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig, chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, A.Athors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y., F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasa A; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvei M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AE004030; GB:AE003849; NID:g9107292; PIDN:AAF84968.1; GSPDB:GN001A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, Eas-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
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A;Note: for a complete list of authors see reference number A59328 bel
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R; anonymous, The Xylella :
Nature 406, 151-157, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein xF2169 [imported] - Xylella fastidiosa (strain 9a5c) C;Species: Xylella fastidiosa (strain 9a5c) C;Date: 18-Aug.2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: XF2169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number:
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                                                                                                                                                                                                                                                                                                                                                           Query Match 2.7
Best Local Similarity 19.3
Matches 109; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1571 ALQLPRSLDLVTAV-LAVWKGĞAAYLPVDPD-----YPPER-----IAHNRADA 1613
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                                                                                                                                  307
                                                                                                                                                                                                                                                                                          176 RYQKELNLTQQLPDCRGLEVRDSIQSCW-----VLPWLNVSTDGDNVLLTLDV-- 223
364 AETVARQIVAIEPGRLSGEQRIVEALLQRDPPT
                                                                                                                                                                                                                                                     249
                                                    264 VPCLCIQVWSLEP----DSERVEFCPFREDPGAHRNLWHIARLRVLSPGVWQLDAPCCLP 319
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                                                                                                            DIKPRNHDLWLARLAVAPVGSDEARIVIERWLSAMPEHLPAL--ETLMSLHDIQ-NNPEA 363
                                                                                                                                                                                                                               RLTGEFELLAGHPD-RALTHLRQVLATWPEDPRTLEALLTAWKQLDMD-DDARITLDAAL 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LDVSEEQDFSFLL--YLRPVPDAL-----KSLWYKNL------TGPQNIT 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            \mathbf{x}_{\mathbf{y}} lella fastidiosa Consortium of the Organization for Nucleotide Sequence
                                                                                                                                                                                                                                                                                                                                                                                          2.7%; Score 101.5;
19.3%; Pred. No. 6.1;
                                                                                                                                                                       ----SEEQDFSFLLYLRPVPDALKSLWYKNLTGPQNITLNHTDL 263
                                                                                                                                                                                                                                                                                                                                                     66; Mismatches 197; Indels 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 698;
AVACL- 401
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GKVTILOMOAPDOSPCOPLYPPVPOKNATYNEP	Qy 187 LPDCR	RESULT 14 ROBOLT 14 RYPOTHETICAL PROTEIN F17 C;Species: Arabidopsis t C;Date: 30-Apr-1999 #seq C;Accession: T04018 R;Bevan, M. Murphy, G.; submitted to the Protein A;Accession: T04018 A;Accession: T04018 A;Molecule type: DNA A;Residues: 1-1274 CMBEV- A;Cross-references: EMEV- A;Cross-references: EMEV- A;Cross-references: EMEV- A;Introns: 55/3; 801/1 A;Note: F17A8.60 Query Match Best Local Similarity Matches 112; Conserv.	Oy 320 GKVTI Db 402 Oy 371 EKVOI Db 438 LOFOD OY 431 LLQDF Db 477 LL OY 491 KAARG OY 491 KAARG OY 491 KAARG OY 491 KAARG Db 503 -ADRY OY 544 -LAWF Db 555 WLLWW OY 596 CVLDD Db 613 Db 613 Db 667
	LPDCRGLEVRDSIQS	A8.60 - Arab hallana (mou uence_revisi Ridley, P.; Sequence Da 84 ALL049482 ultivar Colu ultivar Colu 2.7%; Scr 20.2%; Pro	GKVTLCWQAPDQSPCOPLVPPVPQKN.
	VLPWLNVSTDGDNVLLTLLDVSEEQDESFLLYL	opsis thaliana -ear cress) 30-Apr-1999 #text_change 30-Apr.1999 #text_change 30-Apr.1999 idson, S.; Bancroft, I.; Mewes, March 1999 base, March 1999 ia; BAC clone F17A8 ia; BAC clone F17A8	GLVQDRAG VCALEPSG VCA
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T26240
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;;Gene: CESP:W06F12.la
;;Gene: CESP:W06F12.la
;;Introns: 47/2; 87/1; 145/1; 179/1; 216/3; 255/2; 317/2; 353/1; 564/3; 634/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein W06F12.1a - Caenorhabditis elegans
C;$pecies: Caenorhabditis elegans
C;$pecies: Oot-1999  #sequence_revision 15-Oct-1999  #text_change 15-Oct-1999
C;Accession: T26240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.7
Best Local Similarity 23.0
Matches 45; Conservative
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Residues: 1-647 <WIL>
Cross references: EMBL: Z83244; PIDN:CAB05827.1; GSPDB:GN00021; CESP:W06F12.1a
Experimental source: clone W06F12
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SOFTWARE: FastSEQ for Windows Version 3.0
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TITLE OF INVENTION: Compositions Isolated
TITLE OF INVENTION: and Methods For Their
FILE REFERENCE: 11000.1011c1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Watson, James D. APPLICANT: Strachan, Lorna APPLICANT: Sleeman, Matthew APPLICANT: Onrust, Rene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              444
                                                            334
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                                                                                                                                                                                                                                                                                                                                                                                                                 175 PRYOKELNLTQQLPDCRGLEV-----RDSIQSC--WVLPWLNVSTDGDNVLLTLDVSEE 226
                                                                                                                                                                                                                                                                                                              182 ----
                                                                                                                                                                                                                                                        287 REDPGAH-RNLWHIARLRVLSPG---VWQLDAPCCLEGKYTLCWQAPDQSPCQPLVPPVP
                                                                                                                                                                                                                                                                                                                                        227 QDESFLLYLRPYPDALKSLWYKNLTGPQNITLNHTDLVPCLÇIQVWSLEPDSERVEFCPF 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
        WNDDNMGSLWACPMDKYIHRRWYLV-----WLACLLLAAALFFFLLLKKDRRKAARGS
                                                                                                                                  -PNATAQESEGWYILENVDLHPQLCFKFS-FENSSHVECPHQSGSLPSWTVSMDT-QAQQ 333
                                                                                                                                                                           QKNATVNEPQDFQLVAG---HPNLCVQVSTWEKVQLQAC-----SWADSLGPFKDDM 391
                                                                                                                                                                                                                    QSWPEAYGSDFWQSIRFTDYSQHNQMVMALTLRCPLKLEASLCWRQDPLTPCETL----
                                                     LTLHESSRTYATESAAWSDPGLGPDTPMPPVYSISQTQGSVPVTLDLIIPFLRQENCILV 393
                                                                                            LLVEMKTGLNNTSVCALEPSGC---TPLPSMASTRAARLGEELLQD----FRSHQCMQL 443
                                                                                                                                                                                                                                                                                                                                                                                     PEFSFDL-----LPEVQAVRVTIPAGFKASVRLCY@WALECEDLSSPFDT------ 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               134;
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US-08-488-346A-28
US-08-404-531B-6
US-08-476-900A-6
US-08-488-546A-6
US-08-488-546A-6
US-08-68-751-189-4
US-09-184-445-4
US-09-184-445-3
US-09-184-445-3
US-09-184-445-3
US-09-186-22
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US-08-445-640-10
US-08-170-558-10
US-08-447-314-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 312; DB 4;
Pred. No. 1.4e-24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 617;
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Qy 554 ILQEGGVVILLESPAAVAQC : :	394 497	•
INDEGOVILLESPANVACCOOMIGLOTEPHHALAAMISCVLEDEIGRATGRYCY 613 :	1 – × H	

	CLASSIFICATION: CLASSIFICATION: PRIOR APPLICATION DATA: APPLICATION NUMBER: USSN 08/620,694 FILING DATE: 21 MARCH 1996 APPLICATION NUMBER: USSN 08/538,765 FILING DATE: 7 AUGUST 1995 PRIOR APPLICATION DATA:	
	ER: Apple Power ING SYSTEM: Apple Power Apple Power Apple Power ING SYSTEM: Apple Power ING Powe	
	ZIP: 98101 COMPUTER READABLE FORM: MEDIUM TYPE: Florpy disk	
	WA	
	STREET: 51 University Street	
	DENCE ADDRESS	
	Fanslow, W	
	; APPLICANT: Yao, Zhengbin ; APPLICANT: Spriggs, Melanie	
	INFORMATION	
	LT 9-02 quen	
	Db 479 -GDLFTAAMNMILPDEKRPACEGTTVVCYESGICSERDVPDLFNITSRYPL 528	
	CVLP	
: KPA 478	Db 425 VGVMTWVSRQKQEMVESNSKIIILCSRGTQAKWKAILGWAEPAVQLRCDHW	
TVEPG 585	Qy 541 HGALAWFHHQRRRILQEGGVVILLESPAAVAQCQQWLQLQTVEPG	
42	Db 365 GILPVADLTPPPLRPRKVWIVYSADHPLYVEVYLKFAQFLITACGTEVALDLLEEQVISE	
RELSA 540	Qy 497	
 DSKIN 364	Db 314PVADYI-PLWYYGLITLIAILLYGSVIVLIICMTWRLSGADQEKHGDDSKIN	
3S 496	Qy 448 NMGSLWACPMDKYIHRRWYLVWLACLLLAAALFFFLLLKKDRRKAARG	
313	Db 275 WCCHHYQVQPFFSSCLNDCLRHAVTVPCPVISNTTVPK	
LWNDD 447	PSGC	
LSKFH 274	Db 219 VDFTLWNEST-PYQVLLESFSDSENHSCFDVVKQIFAPRQEEFHQRANVTFTLSKF	
405	Qy 375 LQACSWADSLGPFKDDMLLVEMKTGLNNTSV	
: :: TQHLR 218	Db 168IPDGDPNHKSKIIFVPDCEDSKMKMTTSCVSSGSLMDPNITVETLDTQHLR	
WEKVQ 374	QY 319 PGKVTLCWQAPDQSPCQPLVPPVPQKNATVNEPQDFQLVAGHPNLCVQVSTWEKVQ	
KP 167	Db 112 AELSVLQLNTNERLCVKF-QFLSNLQHHRKRWRFSFSHFVVDDFQEYEVTVHHLPKP-	
	QY 278 SERVEFCPFREDPGAHRNLWHIARLR-VLSPGVWQLDAPCCL	
LYLEG 111	Db 53 KNSTCLDDSWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVE-WTLQTDASILYLEG	
277	TGPQNITLNHTDLVPCLCIQVWSLEPD	
LSCRV 52	Db 2 AIRRCWPRVVPGPALGWLLLLLNVLAPGRASPRLLDEPAPVCAQEGLSCRV	
239	SCWVLPWLNVSTDGDNVLLT	

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Matches 121;
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Best Local Similarity
                                                                                                                                                                         09-022-696-2
                                                                                            APPLICANT: Yao, Z
                                                                                                                                        equence 2, Application US/09022696 atent No. 6072037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
-09-022-255-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 864 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                  479 -GDLFTAAMNMILPDFKRPACFGTYVVCYFSGICSERDVPDLFNITSRYPL 528
                                                                                                                                                                                                                                                                                                                                          425
                                                                                                                                                                                                                                                                                                                                                                          541 HGALAWFHHORRRILQEGGVVILLFS----
                                                                                                                                                                                                                                                                                                                                                                                                           365 GILPVADLTPPPLRPRKVWIVYSADHPLYVEVVLKFAQFLITACGTEVALDLLEEQVISE 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               319 PGKVTLCWQAPDQSPCQP----LVPPVPQKNATVNEPQDFQLVAGHPNLCVQVSTWEKVQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240 ---DALKSLWY--KNLT--GPQNITLN------HTDLVPCLCIQVWSLEPD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53 KNSTCLDDSWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVE-WTLQTDASILYLEG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 23 MAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 AIRRCWPRVVPGPALGWL------LLLLNVLAPGRASPRLLDFPAPVCAQEGLSCRV 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
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                                                                                                                                                                                                                                                                                        PHDALAAWLSCVLPDFLQGRATGRYVGVYFDGLLHPDSVPSPFRVAPLFSL 636
                                                                                                                                                                                                                                                                                                                                  VGVMTWVSRQKQEMVESNSKIIILCSRGTQAKWKAILGWAEPAVQLRCDHW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NMGSLWACPMDKYIHRRWY--LVWLACLLLAAALFFFL-----LLKKDRRKAARGS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WCCHHHVQVQPFFSSCLNDCLRHAVTVPCPVISNTTVPK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VDFTLWNEST-PYQ---VLLESFSDSENHSCFDVVKQIFAPRQEEFHQRANVTFTLSKFH 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AELSVLQLNTNERLCVKF-QFLSMLQHHRKRWRFSFSHFVVDPGQEYEVTVHHLPKP--- 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -CA-----LEP--SGC-----TPLPSMASTRAARLGEELLQDFRSHQCMQLWNDD
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NATION NUMBER: 34,695
              Spriggs, Melanie
Fanslow, William
INVENTION: NO. 60720
SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---PVADYI-PLWVYGLITLIAILLVGSVIVLIICMTWRLSGADQEKHGDDSKIN 364
                                                                                                Yao, Zhengbin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -IPDGDPNHKSKIIFVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLR 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -SER--VEFCPFREDPGAHRNLWHIARLR-VLSPG----VWQLDAPCCL
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20.5%;
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                             6072037el Receptor That Binds IL-17
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Pred. No. 1.1e-09;
55; Mismatches 189;
                                                                                                                                                                                                                                                                                                                                                                      -PAAVAQCQQWLQLQTVEPG 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 864;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 864 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: Apple Operating System SOFTWARE: Microsoft Word for Apple, Versi CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 23 MARCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                              314
                                                                                                                                                                                                                                                                                          168
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        497
                                                                                                                                                                                                  219 VDFTLWNEST-PYQ---VLLESFSDSENHSCFDVVKQIFAPRQEEFHQRANVTFTLSKFH
                                                                                                                                                                                                                                                                                                               319 PGKVTLCWQAPDQSPCQP----LVPPVPQKNATYNEPQDFQLVAGHPNLCVQVSTWEKVQ 374
                                                                                                                                                                                                                                                                                                                                                             112 AELSVLQLNTNERLCVKF-QFLSMLQHHRKRWRFSFSHFVVDPGQEYEVTVHHLPKP--- 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240 ---DALKSLWY--KNLT--GPQNITLN------HTDLVPCLCIQVWSLEPD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                198 SIQSCW-----VLPWLNVSTDGDNVLLTLDVSEEQDFSFLLYLRPVP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                             53 KNSTCLDDSWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVE-WTLQTDASILYLEG
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OPERATING SYSTEM: Apple Operati
SOFTWARE: Microsoft Word for Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 AIRRCWPRVVPGPALGWL------LLLLNVLAPGRASPRLLDFPAPVCAQEGLSCRV 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Perkins, Patricia REGISTRATION NUMBER: 34,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
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                                                                               NMGSLWACPMDKYIHRRWV--LVWLACLLLAAALFFFL--
                                                                                                                       WCCHHIVQVQPFFSSCLNDCLRHAVTVPCPVISNTTVPK--
                                                                                                                                                                                                                                        LQACSWADSLGPFKDDMLLVEMKTGLNNTSV-----
                                                                                                                                                                     -CA-
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51 University Street
                                                                                                                                                                                                                                                                                  ---IPDGDPNHKSKIIFVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLR
                                                                                                                                                                                                                                                                                                                                                                                                     ----SER--VEFCPFREDPGAHRNLWHIARLR-VLSPG-----VWQLDAPCCL 318
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                                       PVADYI-PLWVYGLITLIAILLVGSVIVLIICMTWRLSGADQEKHGDDSKIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.78;
RTALLLHSADGAGYERLVGALASAL-SQMPLRVAVDLWSRRELSA 540
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7R:
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CH 1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 177; DB 3;
Pred. No. 1.1e-09;
5; Mismatches 189
                                                                                                                                                             -TPLPSMASTRAARLGEELLQDFRSHQCMQLWNDD 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 864;
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239

29;

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319 PGKVTLCWQAPDQSPCQPLVPPVPQKNATVNEPQDFQLVAGHPNLCVQVSTWEKVQ 374	EYEVTVHHLPKP	278SERVEFCPFREDPGAHRNLWHIARLR-VLSPGVWQLDAPCCL 318	53 KNSTCLDDSWIHPKNLTPSSPKNIYINLSVSSTQHGELVFVLHVE-WTLQTDASILYLEG 111		198 SIQSCW VLPWLNVSTDGDNVLLTLDVSEEQDFSFLLYLRPVP 239 : :	Query Match Sest Local Similarity 20.5%; Pred. No. 1.1e-09; Matches 121; Conservative 65; Mismatches 189; Indels 216; Gaps 29;	ESULT 5 F-08-978-773-2 Sequence 2, Application US/08978773 Sequence 2, Application US/08978773 Fatent No. 6083906 GEMERRAL IMPORMATION: Method of Regulating Mitric Oxide Production APPLICANT: Troutt, Anthony TITLE OF INFORMATION: Method of Regulating Mitric Oxide Production APPLICANT: Stormers: S1 University Street CITY: Seattle STREET: 51 University Street CITY: Seattle STATE: WA COUNTRY: USA ZIP: 98101 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM: COMPUTER READABLE FORM: MEDIUM TYPE: JORDY disk COMPUTER READABLE FORM: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM: MEDIUM TYPE: JORDY disk	365 GILPVADLTPPPLRPRKVWIVYSADHPLYVEVVLKEAQFLITACGTEVALDLLEEQVISE 424 541 HGALAWFHHORRRILQEGGVVILLES

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RESULT 6
US-09-022-253-
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Patent No.
                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (206)587-0430
                                                                                                                                                     CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA: US/08/620,694
APPLICATION NUMBER: US/08/620,694
FILING DATE: 21-MARCH-1996
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0
CURRENT APPLICATION DATA:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 541 HGALAWFHHQRRRILQEGGVVILLES------PAAVAQCQQWLQLQTVEPG 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        365 GILPVADLTPPPLRPRKVWIVYSADHPLYVEVVLKFAQFLITACGTEVALDLLEEQVISE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         375 LOACSWADSLGPFKDDMLLVEMKTGLNNTSV-----
                                                                                            NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 98101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -GDLFTAAMNMILPDFKRPACFGTYVVCYFSGICSERDVPDLFNITSRYPL 528
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51 University Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spriggs, Melanie
Fanslow, William
WENTION: No. 6096305el Receptor That Binds IL-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                      (206)
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                                                                                                                                                                                                                                                                                                                                                                                                                US/09/022, 253
                  2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Version 6.0.1
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MOLECULE TYPE: protein s-09-022-253-2
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                                                                                                                                                                                                                                                                                                                                                                                      -09-022-260-2
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                  APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6100235el Receptor That Binds IL-17
                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                            UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240 ---DALKSLWY--KNLT--GPQNITLN------HTDLVPCLCIQVWSLEPD------
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating
                                                                                   COUNTRY: U
                                                                                                                                                              STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53 KNSTCLDDSWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVE-WTLQTDASILYLEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 864 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 AIRRCWPRVVPGPALGWL---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GILPVADLTPPPLRPRKVWIVYSADHPLYVEVVLKFAQFLITACGTEVALDLLEEQVISE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----PVADYI-PLWVYGLITLIAILLVGSVIVLIICMTWRLSGADQEKHGDDSKIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PGKVTLCWQAPDQSPCQP----LVPPVPQKNATVNEPQDFQLVAGHPNLCVQVSTWEKVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AELSVLQLNTNERLCVKF-QFLSMLQHHRKRWRFSFSHFVVDPGQEYEVTVHHLPKP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                            -GDLFTAAMNMILPDFKRPACFGTYVVCYFSGICSERDVPDLFNITSRYPL 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VGVNTWVSRQKQEMVESNSKIIILCSRGTQAKWKAILGWAEPAVQLRCDHW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NMGSLWACPMDKYIHRRWV--LVWLACLLLAAALFFFL-----LLKKDRRKAARGS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -CA-----LEP--SGC------TPLPSMASTRAARLGEELLQDERSHQCMQLWNDD 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----IPDGDPNHKSKIIFVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLR 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOACSWADSLGPFKDDMLLVEMKTGLNNTSV----
                                                                                                                                           Seattle
                                                                                                                        WA
                                                                                                                                                              E: Immunex Corporation
51 University Street
                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --SER--VEFCPFREDPGAHRNLWHIARLR-VLSPG-----VWQLDAPCCL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 177; DB 3; 1; Pred. No. 1.1e-09; 65; Mismatches 189;
System 7.5.5
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US-09-022-260-2
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Best Local Similarity

Matches 121; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: | PERKINS, PATTICLA ANNE
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Microsoft Word for Apple, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                     219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
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                479
                                                                                       425 VGVMTWVSRQKQEMVESNSKIIILCSRGTQAKWKAILGWAEPAVQLRCDHW-----KPA
                                                                                                                                                                  365 GILPVADLTPEPLRPRKVWIYYSADHPLYVEVVLKFAQFLITACGTEVALDLLEEQVISE
                                                                                                                                                                                                                    497
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                                                                                                                                                                                                                                                                                      448 NMGSLWACPMDKYIHRRWV--LVWLACLLLAAAERFIL----LLKKDRRKAARGS---
                                                                                                                                                                                                                                                                                                                                                                             406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        375 LQACSWADSLGPFKDDMLLVEMKTGLNNTSV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240 ---DALKSLWY--KNLT--GPQNITLN-----HTDLVPCLCIQVWSLEPD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 864 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53 KNSTCLDDSWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVE-WTLQTDASILYLEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 AIRRCWPRVVPGPALGWL------LLLLNVLAPGRASPRLLDFPAPVCAQEGLSCRV 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
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                                               PHDALAAWLSCVLPDFLQGRATGRYVGVYFDGLLHPDSVPSPFRVAPLFSL 636
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          -GDL#TAAMNMILPDFKRPACFGTYVVCYFSGICSERDVPDLFNITSRYPL
                                                                                                                                HGALAWFHHQRRRILQEGGVVILLFS-----
                                                                                                                                                                                                                                                                                                                                  WCCHHHVQVQPFFSSCLNDCLRHAVTVPCPVISNTTVPK-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Perkins, Patricia
                                                                                                                                                                                                                                        ---PVADYI-PLWVYGLITLIAILLVGSVIVLIICMTWRLSGADQEKHGDDSKIN
                                                                                                                                                                                                                                                                                                                                                                           ---LEP--SGC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----IPDGDPNHKSKIIFVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----SER--VEFCPFREDPGAHRNLWHIARLR-VLSPG-----VWQLDAPCCL 318
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                                                                                                                              -----PAAVAQCQQWLQLQTVEPG 585
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Query Match
Best Local Similarity 20.5
Matches 121; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS LENGTH: 864 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: PERKINS, PATTICLA Anne
REGISTRATION UNMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
375 LOACSWADSLGPFKDDMLLVEMKTGLNNTSV---
                                                168 -----IPDGDPNHKSKIIFVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLR 218
                                                                                                                         112 AELSVLQLNTNERLCVKF-QFLSMLQHHRKRWRFSFSHFVVDPGQEYEVTVHHLPKP--- 167
                                                                                  319 PGKVTLCWQAPDQSPCQP----LVPPVPQKNATVNEPQDFQLVAGHPNLCVQVSTWEKVQ 374
                                                                                                                                                                     278
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CITY: Seattle
STATE: WA
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                                                                                                                                                                                              53 KNSTCLDDSWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVE-WTLQTDASILYLEG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
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                                                                                                                                                                                                                                                                      2 AIRRCWPRVVPGPALGWL------LLLLNVLAPGRASPRLLDFPAPVCAQEGLSCRV 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Immunex Corporation STREET: 51 University Street
                                                                                                                                                            ------SER--VEFCPFREDPGAHRNLWHIARLR-VLSPG-----VWQLDAPCCL 318
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GY: linear
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Fanslow, William
NVENTION: No. 6191104el Receptor That Binds IL-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (206)587-0430
                                                                                                                                                                                                                                                                                                                                             4.7%; Score 177; DB 4; Length 864; 20.5%; Pred. No. 1.1e-09; ative 65; Mismatches 189; Indels 2
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		9-022-257	US-0
	YPE:	; MOLECULE	٠.
	Y: linear	TOPOLOGY	٠. ٠
	864 amino acids	TENGTH:	
	CHARACTERISTICS:	SEQUENCE	٠.,
	FOR SEQ ID NO: 2:	Õ	; I
	(206)	TELEFAX:	٠
	ATION INFORMAT	TELECOMMUNIC	
	r NUMBE	REFERENCE	٠.
	ATION NUMBER: 34,695	REGISTRATION	•• •
	INFORMATION:	ATTORNEY/AGENT	
	ON:	CLASS	٠.
	3 MARCH 1995	FILING	•••
	TION DATA:	APPLICATION	
		CLA	٠.
	: NOMBEN. 00	FILING	٠. ٠
	NIMBER: 08/620 6	PRIOR APPLICATION	
	CLASSIFICATION:	CLASS	٠.
	DATE:	FILING DATE	•• ••
	CATION DATA:	CURRENT	٠.
	RE: Microsoft Word for Apple, Version 6.0.1	SOFTWARE	٠. ٠
	Apple Power Macintosh	COMPUTER:	٠. ٠.
	YPE: Floppy di	MEDIUM	٠.
	READABLE FORM:	COMPUTER	٠. ٠
	98101 98101	ZIP: 9	
	WA	STATE	· ••
	seattle	CITY:	٠.
	51 University Street	STREET: 5	•• ••
	ADDRESS:	CORRESPONDENCE	
	ENCES: 10	NUMBER OF	••
	¥	TITLE OF	•••
	Spriggs, Mela	APPLICANT	
		APPLICANT	•••
	INFORMATION:	GENERAL I	
	Application US/09022257	വ	 Se
		9 022-3	RESULT
	GDLFTAAMMMILPDFKRPACFGTYVVCYFSGICSERDVPDLFNITSRYPL 528	479 -G	Db
	CVLPDFLQGRATGRYVGVYFDG	586 PH	Qγ
478	VGVMTWVSRQKQEMVESNSKIIILCSRGTQAKWKAILGWAEPAVQLRCDHWKPA	425 VG	Db
585	LQEGGVVILLESPAAVAQCQQWLQLQTVEPG	541 HG	ОУ
424	VYSADHPLYVEVVLKFAQFLITACGTEVALDLLEEQVISE	365 GI	В
540	RTALLHSADGAGYERLYGALASAL-SQMPLRVAVDLWSRRELSA	497	VΩ
364	TLIAILLVGSVIVLIICMTWRLSGADQEKHGDDSKIN	314	D
496	LWACPMDRYIHRRWYLYWLACLLLAAALFEFLLLKKDRRKAARGS	448 NMGS	γ
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447	LEPSGCTPLPSMASTRAARLGEELLQDFRSHQCMQLWNDD	406 -CA	γQ
274	VDFTLWNEST-PYQVLLESFSDSENHSCFDVVKQIFAPRQEEFHQRANVTFTLSKFH	219 VD	ф

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Query Match
Best Local Similarity
Matches 54; Conserv
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Best Local Similarity
Matches 121; Conserv
                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/188,930A CURRENT FILING DATE: 1998-11-09 NUMBER OF SEO ID NOS: 348 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 125 EQUID NO 125 EQUID NO 125 TYPE: PRT
                                                                                                                                                                                                                                                                                                                       APPLICANT: Watson, James D.
APPLICANT: Stemann, Matthew
APPLICANT: Sleemann, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                atent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                equence 125, Apparent No. 61505
                                                                                                                                    ORGANISM: mouse
09-188-930-125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240 ---DALKSLWY--KNLT--GPQNITLN------HTDLVPCLCIQVWSLEPD------ 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                198 SIQSCW------VLPWLNVSTDGDNVLLTLDVSEEQDFSFLLYLRPVP------ 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53 KNSTCLDDSWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVE-WTLQTDASILYLEG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 AIRRCWPRVVPGPALGWL------LLLLNVLAPGRASPRLLDFPAPVCAQEGLSCRV 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VGVMTWVSRQKQEMVESNSKIIILCSRGTQAKWKAILGWAEPAVQLRCDHW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------PVADYI-PLWVYGLITLIAILLVGSVIVLIICMTWRLSGADQEKHGDDSKIN 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NMGSLWACPMDKYIHRRWV--LVWLACLLLAAALFFFL-----LLKKDRRKAARGS--- 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PGKVTLCWQAPDQSPCQP----LVPPVPQKNATVNEPQDFQLVAGHPNLCVQVSTWEKVQ 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -GDLFTAAMNMILPDFKRPACFGTYVVCYFSGICSERDVPDLFNITSRYPL 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WCCHHHVQVQPFFSSCLNDCLRHAVTVPCPVISNTTVPK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LQACSWADSLGPFKDDMLLVEMKTGLNNTSV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----IPDGDPNHKSKIIFVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLR 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -CA-----LEP--SGC------TPLPSMASTRAARLGEELLQDFRSHQCMQLWNDD 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/09188930A
                               4.0%;
ilarity 23.2%;
Conservative 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---RTALLLHSADGAGYERLVGALASAL-SOMPLRVAVDLWSRRELSA 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.7%; Score 177; DB 4; I
20.5%; Pred. No. 1.1e-09;
tive 65; Mismatches 189;
                               36;
                           Score 150.5; DB 4;
Pred. No. 1.5e-07;
6; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 864;
                                                                    Length
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                             Indels
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                           65;
                         Gaps
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                           10;
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                                                                  Matches
                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10,
                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Microsoft Word for Apple, Version 6
CURRENT APPLICATION DATA:
APPLICATION NUMBER 1
                                                                                                                                                                                     TOPOLOGY: 1:
                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                  TYPE: amino acids
    55 SAPGP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                137 PEFSFDL-----LPEVQAVRVTIPAGPKASVRLCYQWALECEDLSSPFDT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            343 QKNATVNEPQDFQLVAG---HPNLCVQVSTWEKVQLQAC-----SWADSL 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    277 - PNATAQESEGWYILENVDLHPQLCFKFS-FENSSHVECPHQSGSLPSWTVSM 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   222 QSWPEAYGSDFWQSIRFTDYSQHNQMVMALTLRCPLKLEASLCWRQDPLTPCETL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         287 REDPGAH-RNLWHIARLRVLSPG---VWQLDAPCCLPGKVTLCWQAPDQSPCQPLVPPVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        227 QDFSFLLYLRPVPDALKSLWYKNLTGPQNITLNHTDLVPCLCIQVWSLEPDSERVEFCPF
                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 7 AUGU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 51 Uni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE
                                                               140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRYOKELNLTQQLPDCRGLEV-----RDSIQSC--WVLPWLNVSTDGDNVLLTLDVSEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   U,|Application US/08620694A
5869286
                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                              Perkins, Patricia Anne
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Immunex Corporation
51 University Street
                                                           3.9%; Score 147.5; DB 2; ilarity 19.3%; Pred. No. 1.7e-06; Conservative 78; Mismatches 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spriggs, Melanie
Fanslow, William
VENTION: No. 5869286el Receptor That Binds IL-17
                                                                                                                                                                                                                                                                                                                 (206)
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                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                    (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IUMBER: USSN 08/538,765
7 AUGUST 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 MARCH 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -VLVP----TRLQTELVLRCPQKTDCALRVRVVVHLAVHGHWAEPE 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10
                                                                                                                                                                                                                                                                                                                                                                                           34,695
                                                                                                                                                                                                                                                                                           10:
                                                           Indels
                                                                                                    Length 866;
                                                           269;
                                                           Gaps
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1 QY 5/5 QWL	Interest Contact of the Contact of t
, i	Operating System 7.5.
Db 397 KFAC	Power Macintosh
Qy 516 ALAS	COMPUTER READABLE FORM: MEDIUM TYPE: Floray disk
Db 338 -LL1	COUNTRY: USA ZIP: 98101
Qy 481 FFLI	Seattle WA
Db 308 DT	ADDRESSEE: Immunex Corporation STREET: 51 University Street
QY 421 STR	CE ADDRESS:
Db 273 LKG	Fanslow,
QY 361 PNLC	APPLICANT: Yao, Zhengbin APPLICANT: Spriggs, Melanie
Db 253	Patent No. 6072033 (GENERAL INFORMATION:
Qy 307 PGVI	9-022-255-10 Sequence 10, Application US/09022255
Db 200 GSL	SULT 12
Оу 269	567 LRAALD 572
Db 149 FVVI	669 LRSALD 674
Qy 210 VSTI	517 FGAAPRYPLMDRFEEVYFRIQDLEMFQPGRMHRVGELSGDNYLRSPGGRQ 566
Db 104	28
Qy 157 DCFI	
Db 67	575 QWLQLQTVEPGP-HDALAAWLSCVLPDFLQGRATGRXYGYYFDGLLHPDSVPSP 627
Qy 101 EAG	397 KFAQFLLTACGTEVALDLLEEQAISEAGVMTWVGRQKQEMVESNSKIIVLCSRGTRAKWQ 456
Db 10 AVP	
Qy 55 SAP	338 -LLIVCMTWRLAGPGSEKYSDDTKYTDGLPAADLIPPPLKPRKVWIIYSADHPLYVDVVL 396
Matches 14	
~	308 DTPEPIPDYMPLW
US-09-022-255	421 STRAARLGEELLQDFRSHQCMQLWNDDNMGSLWACPMDKYIHRRWVLVWLACLLLAAALF 480
; MOLECULE	273 LKGCCRHQVQIQPFFSSCLNDCLRHSATVSCPEMP 307
; LENGTH:	361 PNICVQVSTWEKVQLQACSWADSLGPFKDDMLLVEMKTGLNNTSVCALEPSGCTPLPSWA 420
; SEQUENCE	253PEEFHQRSNVTLTLRN 272
; TELEPH	307 PGVWQLDAPCCLPGKVTLCWQAPDQSPCQPLVPPVPQKNATVNEPQDFQLVAGH 360
; TELECOMM	200 GSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHMENHSCFEHMHHI 252
; NAME:	269IQVWSLEPDSERVEFC
; FILING ; ATTORNEY	149 FVVDDDQEYEVTVHHLPKPIPDGDPNHQSKNFLVPDCEHARMKVTTPCMSS 199
; PRIOR AP ; APPLIC	210 VSTDGDNVLLTLDVSEEQDFSFLLYLRPVPDALKSLWYKNLTGPQNITLNHTDLVPCLC- 268
; APPLIC ; FILING	
; APPLIC	V 157 DCFEASLGAEVQIWSYTKPRYQKELNLTQQLPDCRGLEVRDSIQSCWVLPWLN 209
; CLASSI PRIOR AP	NLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTD
; APPLIC	
·	b 10 AVPGPLLGLLLLLLGVLAPGGASLRLLDHRALVCSOPGLNCTVKNSTCIANSWIHDR 66

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: amino acid
LOGY: linear
LE TYPE: prot
55-10
                                                                                                                                                                                                                                                                                                                                        LCVQVSTWEKVOLQACSWADSLGPFKDDMLLVEMKTGLNNWSVCALEPSGCTPLPSMA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VDPD-----QEYEVTVHHLPKPIPDGDPNHQSKNFLVPDCEHARMKVTTPCMSS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TDGDNVLLTLDVSEEQDFSFLLYLRPVPDALKSLWYKNLTGPQNITLNHTDLVPCLC- 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PGP------VLVP----TRLQTELVLRCPQKTDCALRVRVVVHLAVHGHWAEPE 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Perkins, Patricia Anne STRATION NUMBER: 34,995
STRATION ET NUMBER: 2617-B
AMUNICATION INFORMATION:
1,206)587-0430
                                                  AQE;UTACGTEVALDLLEEQAISEAGVMTWVGRQKQEMVESNSKIIVLCSRGTRAKWQ 456
                                                                                                                                             RAARLGEELLQDFRSHQCMQLWNDDNMGSLWACPMDKYYHRRWVLVWLACLLLAAALF 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VWQLDAPCCLPGKVTLCWQAPDQSPCQPLVPPVPQKNATVNEPQDFQ-----LVAGH 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHMENHSCFEHMHHI----- 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEASL----GAEVQIWSYTKPRYQKELNLTQQLPDCRGLEVRDSIQ---SCWVLPWLN 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GKSDSELQESRNASLQAQVVLSF----QAYPIARCALLEVQVPADLVQPGQSVGSAVF 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CON FOR SEQ ID NO:
E CHARACTERISTICS:
B66 amino acids
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IG DATE: 7 AUGUST 1995
IPPLICATION DATA:
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CATION NUMBER: USSN 0
CATE: 21 MARCH 1996
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CATION NUMBER: US/09/022,255
                                                                                                AS-ALSOMPLRVAVDLWSRRELSAHGALAWFHHORRRILQEGGVVILLFSPAAVAQCO 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --ASILYLEGAELSY------LQLNTNERL--CVRFEFLSKLRHHHRRWRFTFSH 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PGPLLGLLLLLLGVLAPGGASLRLLDHRALVCSQP---GLNCTVKNSTCLDDSWIHPR 66
                                                                                                                                                                                                     LLKKDRRKAARGS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATION NUMBER:
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DATE: 23 MARCH 1995
AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --IQVWSLEPDSERVEFC-------PFREDPGAHRNLWHIARLRVLS 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --NLTPSSPKDLQIQLHFAHTQQGDLFPVAH---IEWTLQTD------- 103
---QLQTVEPGP-HDALAAWLSCVLPDFLQGRATGRYVGVYFDGLLHPDSVPSP 627
                                                                                                                                                                                                                                             PAPR -----PEEFHORSNVTLTLRN 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.9%; Score 147.5; DB 3; Length 866; ilarity 19.3%; Pred. No. 1.7e-06; Conservative 78; Mismatches 239; Indels 269; Gaps
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101 67	55 SAPGPVLVPTRLQTELVLRCPQKTDCALRVRVVVHLAVHGHWAEPE 100	atch 3.9%; Score 147.5; DB 3; Length 866; cal Similarity 19.3%; Pred. No. 1.7e-06; 140; Conservative 78; Mismatches 239; Indels 269; Gaps	TOPOLOGY: linear MOLECULE TYPE: protein +09-022-696-10	SEQUENCE CHARACTERISTICS: LENGTH: 866 amino acids TYPE: amino acid	TELEPHONE: (206) 587-0430 TELEPAN: (206)	ATTORNEY/AGENT INFORMATION: NAME: Perkins, Patricia Anne REGISTRATION NUMBER: 34,695 REFERENCE/DOCKET NUMBER: 3617-B TELECOMMUNICATION INFORMATION.	PRIOR APPLICATION DATA: PRIOR APPLICATION UNUBER: USSN 08/410,535 FILING DATE: 23 MARCH 1995 CLASSIFICATION:	PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/620,694 FILING DATE: CLASSFERMAN	LICATION DATA: ON NUMBER: US/09/022,696 ITE: ATTON.	MEDIOM TYPE: Floppy disk COMPUTER: Apple Power Macintosh OPERATING SYSTEM: Apple Operating System 7.5.5 SOFTWARE: Microsoft Word for Apple, Version 6.0.1	STATE: WA COUNTRY: USA ZIP: 98101 COMPUTER READABLE FORM:	Si	APPLICANT: IdO, Zhengbin APPLICANT: Spriggs, Melanie APPLICANT: Fanslow, William TITLE OF INVENTION: No. 6072037el Receptor That Binds IL-17 NUMBER OF SEQUENCES: 10	Applica 72037 RMATION	SULT 13	y 669 LRSALD 674 b 567 LRSALD 572	O 20 ENVAPUESLETQUEAFLDALQGGCSTSAGRPADRVERVTQ	ALLGRGAPVRLRCDHGKPVGD
		32;			; GENE	RESULT OS-08-97 Sequent Patent	Qy Db	Qy Db	. Oy	Qy Db	Db Qy	p by	Db Oy	Оу	Ωy Db	Db .	Оу	Qy
CLASSIFICATION: 530 PRIOR APPLICATION DATA: APPLICATION UMBER: USSN 60/052,525 FILING DATE: 27 NOVEMBER 1996	SUTTWAKE: MICTOSOIT WOID for POWERMACINTOSH, VERSION 6.0.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/978,773 FILING DATE:	ADABLE FORM: PE: Floppy disk Apple PowerMacintosh SYSTEM: Apple Operating System 7.5.5	CITY: Seattle STATE: WA COUNTRY: USA ZIP: 98101	ABER OF SEQUENCES: 4 RRESPONDENCE ADDRESS: NDDRESSEE: Immunex Corporation	Ĕĭž	T 14 -978-773-4 uence 4, Application US/08978773 ent No. 6083906	669 LRSALD 674 : 567 LRAALD 572	628 FRVAPLFSLPTQLPAFLDALQGGCSTSAGRPADRVERVTQ	5/5 QMLQLQTVEPGP-HDALAAWLSCVLPDFLQGRATGRYYGVYFDGLLHPDSVPSP 627	ALAS ALS	481 FFLLIKKDRKKAARGS		PNLCVQVSTWEKVQLQACSWADSLGPFKDDMLLVEMKTGLNNTSVCALEPSGCTPLPSMA	307 PGVWQLDAPCCLPGKVTLCWQAPDQSPCQPLVPPVPQKNATVNEPQDFQLVAGH 360	269	FVVDPD-	104 ASILYLEGAELSVLQLNTNERLCVREEFLSKLRHHHRRWRETESH 148 210 VSTDGDNVLLTLDVSEEQDESFLLYLREVEDALKSLWYKNLTGPQNITLNHTDLVPCLC- 268	157 DCFEASLGAEVQIWSYTKPRYQKELNLTQQLPDCRGLEVRDSIQSCWVLPWLN 209

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Best Local Similarity
Matches 140; Conser
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia
  567
                          669 LRSALD 674
                                                                                                                                                              457 ALLGRGAPVRLRCDHGKPVGDLFTAAMNNILPDFKRPACFGTYVVCYFSEVSCDGDVPDL
                                                                                                                                                                                                      575 QWL-----QLQTVEPGP-HDALAAWLSCVLPDFLQGRATGRYVGVYFDGLLHPDSVPSP 627
                                                                                                                                                                                                                                                  397 KFAQFLLTACGTEVALDLLEEQAISEAGVMTWVGRQKQEMVESNSKIIVLCSRGTRAKWQ 456
                                                                                                                                                                                                                                                                                         516 ALAS-ALSQMPLRVAVDLWSRRELSAHGALAWFHHQRRRILQEGGVVILLFSPAAVAQCQ 574
                                                                                                                                                                                                                                                                                                                                 338 -LLIVCMTWRLAGPGSEKYSDDTKYTDGLPAADLIPPPLKPRKVWIIYSADHPLYVDVVL 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                 517 FGAAPRYPLMDRFEEVYFRIQDLEMFQPG-
                                                                                                                                                                                                                                                                                                                                                                                 481 FFLLLKKDRRKAARGS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                            421 STRAARLGEELLQDFRSHQCMQLWNDDNMGSLWACPMDKYIHRRWVLVWLACLLLAAALF 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 PNLCVQVSTWEKVQLQACSWADSLGPFKDDMLLVEMKTGLNNTSVCALEPSGCTPLPSMA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               307 PGVWQLDAPCCLPGKVTLCWQAPDQSPCQPLVPPVPQKNATVNEPQDFQ-----LVAGH 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           149 FVVDPD------QEYEVTVHHLPKPIPDGDPNHQSKNFLVPDCEHARMKVTTPCMSS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    210 VSTDGDNVLLTLDVSEEQDFSFLLYLRPVPDALKSLWYKNLTGPQNITLNHTDLVPCLC- 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    157 DCFEASL----GAEVQIWSYTKPRYQKELNLTQQLPDCRGLEVRDSIQ----SCWYLPWLN 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 EAGKSDSELQESRNASLQAQVVLSF----QAYPIARCALLEVQVPADLVQPGQSVGSAVF 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      273 LKGCCR----HQVQIQ------PF-----FSSCLND----CLRHSATVSCPEMP 307
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REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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LRAALD 572
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                                                                                                                         FRVAPLFSLPTQLPAF-----LDALQGGCSTSAGRPADRVERVTQ------A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.9%; Score 147.5; DB 3; 19.3%; Pred. No. 1.7e-06; tive 78; Mismatches 239;
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                                                                               RMHRVGELSGDNYLRSPGGRQ 566
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US-09-022-253-10
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Yao, Z
                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: USSN 0
FILING DATE: 23 MARCH 1995
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                                   210
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     149 FVVDPD
                                                                                                                                                          101 EAGKSDSEIQESRNASIQAQVVLSF----QAYPIARCALLEVQVPADLVQPGQSVGSAVF 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF
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                                                                                                                                   67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/U,
APPLICATION NUMBER: US/U,
TIME DATE: 21-MARCH-1996
TIME DATE: USSN 08/538,765
                                                                                                                                                                                                                               55 SAPGP
                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System
SOFTWARE: Microsoft Word for Apple, Versi
                                                                                                                                                                                             10 AVPGPLIGHTHLIGVLAPGGASLRILDHRALVCSQP---GLNCTVKNSTCLDDSWIHPR 66
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                                                                                                                                                                                                                                                                                                                                                                                             TYPE:
                                                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                              VSTDGDNVLLTLDVSEEQDFSFLLYLRPVPDALKSLWYKNLTGPQNITLNHTDLVPCLC- 268
                                                                                              DCFEASL----GAEVQIWSYTKPRYQKELNLTQQLPDCRGLEVRDSIQ---SCWVLPWLN
                                                                   ----ASILYLEGAELSV-
                                                                                                                                                                                                                                                                 140;
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51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                            866 amino acids
                                                                                                                               -NLTPSSPKDLQIQLHFAHTQQGDLFPVAH---IEWTLQTD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (206)
                                                                                                                                                                                                                       -----VLVP----TRIQTELVLRÇEQKTDCÄLRVRVVVHLAVHGHWAEPE 100
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                                                                                                                                                                                                                                                                                                                                                           protein
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--QEYEVTVHHLPKPIPDGDPNHQSKNFLVPDCEHARMKVTTPCMSS 199
                                                                                                                                                                                                                                                          3.9%; Score 147.5; DB 3; 19.3%; Pred. No. 1.76-06; tive 78; Mismatches 239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US/09/022, 253
                                                               ----LQLNTNERL---CVRFEFLSKLRHHHRRWRFTFSH
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                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                           Length 866;
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몋	200 GS	GSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHMENHSCFEHMHHI
8	307 PG	PGVWQLDAPCCLPGKVTLCWQAPDQSPCQPLVPPVPQKNATVNEPQDFQLVAGH
₽	253	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
ទួ	361 PN	PNICVQVSTWEKVQLQACSWADSLGPFKDDMLLVEMKTGLNNTSVCALEPSGCTPLPSMA 420
멅	273 LR	273 LKGCCRHOVOTO
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Ş	421 ST	STRAARLGEELLQDFRSHQCMQLWNDDNMGSLWACPMDKYIHRRWVLVWLACLLLAAALF
	308 DT	DTPEPIPDYMPLWVYWFITGISILLVGSVI-
Ş	481 FF	FFLLLKKDRRKAARGS
D	338 -L	- LLIVCMTWRLAGPGSEKYSDDTKYTDGLPAADLIPPPLKPRKVWIIYSADHPLYVDVVL
Ş	516 AL	ALAS-ALSOMPLRVAVDLWSRRELSAHGALAWFHHORRRILQEGGVVILLFSPAAVAOCO
명	397 KF	397 KFAQFILITACGTEVALDILEEQAISEAGVMTWVGRQKQEMVESNSKIIVLCSRGTRAKWQ
Ş	575 QW	TQLQTVEPGP-HDALAAWLSCVLPDFLQGRATGRYVGVYFDGLLHPDSVP
문	457 AL	457 ALLGRGAPVRLRCDHGKPVGDLFTAAMNMILPDFKRPACFGTYVVCYFSEVSCDGDVPDL 516
Ϋ́	628 FR	FRVAPLESLPTQLPAFLDALQGGCSTSAGRPADRVERVTQA
문	517 FG	FGAAPRYPLMDRFEEVYFRIQDLEMFQPGRMHRVGELSGDNYLRSPGGRQ 566
Ş	669 LR	674
문	567 LR	: LRAALD 572

Search completed: September 28, 2002, 19:40:30

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Hery: US-09-894-471
Hery: US-09-894-471
Hery length: 674
Htabase: N.Geneseq
Mtabase sequences:
Mtabase length: 858
Gearch time (sec): 9
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-C-/C972_1/USP70_spool/US09899471/runat_27092002_142440_17943/app_query.fasta_1.2519
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-TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -THR_SCORE-pct
-TH_MAX-100 -THR_MIN-0 -ALIGN-15 -MODE-LOCAL -OUTFAYT-pfs
-NORM-ext -HEAPSIZE-500 -MINLEN-0 -MALEN-200000000
-USER-US0989471_@CGN1_1_926 -NCPU-6 -ICPU-3 -LONGLOG
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                                DS1/gcgdata/geneseq/geneseqn-emb1/NA1996_DAT:AAT33800 + DS1/gcgdata/geneseq/geneseqn-emb1/NA1998_DAT:AAV27591 + DS1/gcgdata/geneseq/geneseqn-emb1/NA1999_DAT:AAX01921 + DS1/gcgdata/geneseq/geneseqn-emb1/NA2000_DAT:AAAS1238 + DS1/gcgdata/geneseq/geneseqn-emb1/NA2000_DAT:AAAS1987 + DS1/gcgdata/geneseq/geneseqn-emb1/NA2000_DAT:AAAS1987 + DS1/gcgdata/geneseq/geneseqn-emb1/NA2000_DAT:AAAS1987 + DS1/gcgdata/geneseq/geneseqn-emb1/NA2000_DAT:AAAS2145 + DS1/gcgdata/geneseq/geneseqn-emb1/NA2000_DAT:AAAS2145 + DS1/gcgdata/geneseq/geneseqn-emb1/NA2000_DAT:AAAS2145 + DS1/gcgdata/geneseq/geneseqn-emb1/NA2000_DAT:AAAS2145 + DS1/gcgdata/geneseq/geneseqn-emb1/NA2000_DAT:AAAS2145 + DS1/gcgdata/geneseq/geneseqn-emb1/NA2000_DAT:AAAS2145 + DS1/gcgdata/geneseq/geneseqn-emb1/NA2000_DAT:AAAS2145 + DS1/gcgdata/geneseq/geneseqn-emb1/NA2000_DAT:AAAS2145 + DS1/gcgdata/geneseq/geneseqn-emb1/NA2000_DAT:AAAS2145 + DS1/gcgdata/geneseq/geneseqn-emb1/NA2000_DAT:AAAS2145 + DS1/gcgdata/geneseq/geneseqn-emb1/NA2000_DAT:AAAS2145 + DS1/gcgdata/geneseq/geneseqn-emb1/NA2000_DAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gcgdata/geneseq/geneseqn-embl/NA2002.DAT:AAS18131 + 1548
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LA.DAT: AAL02817
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- 291.00

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.2e-31
.1e-17
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.2e-52
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alignment_block:
US-09-899-471-2
                                                                                                                                                                                                                                                                                          alignment_scores:
                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                   Sequence 2314 BP; 411 A;
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Quality: Ratio:

3565.00 5.305 96.275

Percent

Identity:

96.132

Length: Gaps:

725

c; 705

G; 473 T; 0 other;

x AAS18132

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seq_documentation_block:
ID AAS18132 standard; cDNA; 2314 BP.
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/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:AAV27592
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:AAX01922
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:AAA61240
subunit (CRS) polypeptides and the polynucleotides encoding them. The receptors or their portions may be useful as phosphate labelling enzymes to label general or specific substrates. The subunits may also be functional immunogens to elicit recognising antibodies, or antigens capable of binding antibodies. A combination, e.g., including a DCRS can be used as an immunogen for the production of antisera or antibodies capable of distinguishing between other cytokine receptor family members. A purified DCRS can also be used as a reagent to detect antibodies generated in response to the presence encetted levels of expression, or immunological disorders which lead to antibody production to the endogenous receptor. This sequence represents cDNA encoding the mouse DCRS7 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated antigenic human or mouse DNAX receptor subunit-like polypeptide useful for detecting antibodies generated in response presence of increased protein levels or immunological disorders -
                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to primate and rodent DNAX cytokine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 17-20; 148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-106198/14.
P-PSDB; AAU11354.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse DNAX cytokine receptor subunit 7 (DCRS7) cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAR-2002
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Align seg 1/1 to: AAS18132 from: 1 to: 2314

860T	CCCCIICCGGGAAGAICCCGGTGCACACAGGAACCTCTGGCACATAGC	- 4
	ysProPheArgGluAspProGlyAlaHisArgAsnLeuTrpHisIleAla	260
260	uCysIleGlnValTrpSerLeuGluProAspSerGluArgValGluPheC	243
1048		999
243 998	ThrGlyProGlnAsnIleThrLeuAsnHisThrAspLeuValProCysLe	227 949
226	YTLeuArgProValProAspAlaLeuLysSerLeuTrpTyrLysAsnLeu	210
948		899
210	lLeuLeuThrLeuAspValSerGluGluGlnAspPheSerPheLeuLeuT	193
898		849
193 848	AGCTGCTGGGTCCTGGCCTGAATGTGTCTACAGATGGTGACAATGT	. 189 799
188 798	hrGlnGlnLeuPro	4- 00
184 · 748	lGlnIleTrpSerTyrThrLysProArgTyrGlnLysGluLeuAsnLeuT 	167 699
167	ValGlySerAlaValPheAspCysPheGluAlaSerLeuGlyAlaGluVa	151
698		649
15 <u>0</u>	laLeuLeuGluValGlnValProAlaAspLeuValGlnProGlyGlnSer	134
648		599
13 4	UGlnAlaGlnValValLeuSerPheGlnAlaTÿrProIleAlaArgCysA	117
598		549
117	GluAlaGlyLysSerAspSerGluLeuGlnGluSèrArgAsnAlaSerLe	101
548		499
100 498	alArgValValValHisLeuAlaValHisGlyHisTxpAlaGluProGlu 	449
84	nThrGluLeuValLeuArgCysProGlnLysThrAspCysAlaLeuArgV	67
448		399
67	GlySerLeuGlnSerAlaProGlyProValLeuValProThrArgLeuGl	51
398		349
50	erLeuGlyLeuSerCysHisLeuTrpAspGlyAspValLeuCysLeuPro	34
348		299
34 298	1ValValSerLeuGluArgLeuMetGluProGlnAspThrAlaArgCyss	17 249
17 248	MetProValSerTrpPheLeuLeuSerLeuAlaLeuGlyArgAsnProVa 	199

560	543	527	510	493	477	460	443	427	410	393	377	360	343	327	310	293	277
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0 roGlyProHisAspAlaLeuAlaAlaTrpLeuSerCysValLeuProAs 	3 OA1AA1aVa1A1AGInCYSGInGlnTrpLeuGlnILeuGlnThrVa1Glu 	7 ArgArgArgIleLeuGlnGluGlyGlyValValIleLeu 	0 erargargGluLeuSeralaHisGlyAlaLeuAlargph 										3 1SerThrTrpGluLysValGlnLeuGlnAlaCysSer 				
р 576	P 560	r 543	n 526	S 510	e 493	u 476	L 460	e 443	y 426	A 410	r 393	u 376	L 360	a 343	u 326	C 310	y 293
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Т 1998	1948	C 1898	G 1848	A 1798	1748	1698	C 1648	T 1598	A 1548	G 1498	C 1448	C 1398	T 1348	T 1298	1248		1148

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eq_name:
The invention relates to primate and rodent DNAX cytokine receptor subunit (DCRS) polypeptides and the polynucleotides encoding them. The receptors, or their portions may be useful as phosphate labelling enzymes to label general or specific substrates. The subunits may also be functional immunogens to elicit recognising antibodies, or antigens capable of binding antibodies. A combination, e.g., including a DCRS can be used as an immunogen for the production of antisera or antibodies capable of distinguishing between other cytokine receptor family members. A purified DCRS can also be used as a reagent to detect antibodies generated in response to the presence of elevated levels of expression, or immunological disorders which lead to antibody production to the endogenous receptor. This sequence represents mouse DCRS7 reverse
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New polypeptide encoding a human cytokine receptor Zcytor14,

for

treating inflammation e.g. rheumatoid arthritis

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lignment_scores:
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Ratio: 4.149
Percent Similarity: 83.628
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US-09-899-471-2 x AAC85027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention provides a new human cytokine receptor desinated Zcytor14. Exptor14 can be expressed by standard recombinant methodology. The encoding nucleic acid is useful for detecting the expression of a Zcytor14 gene in a biological sample. Anti-Zcytor14 antibodies can be used to screen biological samples in vitro for the presence of Zcytor14. Proteins, polypeptides and peptides in vitro for the presence of Zcytor14 administered to a subject who lacks an adequate amount of this polypeptide, for treating inflammation and conditions such as rheumatoid arthritis. In contrast, Zcytor14 antiponists (e.g. anti-Zcytor14 antibodies) can be used to treat a subject who produces an excess of Zcytor14. Zcytor14 nucleotide sequences can also be used to provide Zcytor14 to a subject. The present sequence represents a cDNA encoding
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                                                     CTGCCCGCTGCTGCTGGAGGTGCAAGTGCCTGCTGCCCTTGTGCAG
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uGlyAlaGluValGlnIleTrpSerTyrThrLysProArgTyrGlnLysG
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CGTGTCA CGTGTCA LIUGINAS	454 aLeuPhePhePheLeuLeuLysLysAspArgArgLysAla	38 HisargargTrpValLeuValTrpLeuAlaCysLeuLeuLeuA 	SPLY ACAA	404 yGluGluLeuLeuGlnAspPheArgSerHisGlnÖysMetGln ::::: ::: 1404 AGAGTACTTACTACAAGACCTGCAGTCAGGCCAGTGTCTCTGCAG	Alaa - - - GCTC	TGG	pAlaAspSerLeuGlyProPheLysAspAspMetLeu 	338 AsnLeuCysValGlnValSerThrTrpGluLysValGlnLeuG 	321 snAla [†] thrValAsnGluProGlnAspPheGlnLeuValAlaGl 	304 aProAspGlnSerProCysGlnProLeuValProProValPro	288 LeuAspAlaProCysCysLeuProGlyLysValThrLeuCysT 1054 CTGGACGCACCGTGCTCGCTGCCCGCAGAAGCGGCACTGTGCT	271 snLeuTrpHisIleAlaArgLeuArgValLeuSerProGlyVa ::: ::: ::: 1004 ACCTCTGGCAAGCCGGCCGACTGCGGCTGACCCTGCAGAC	254 rGluḥrgValGluPheCysProPheArgGluAspProGlyAla :::::::	238 AspLeuValProCysLeuCysIleGlnValTrpSerLeuGlui 	221 euTrṗTyrLysAsnLeuThrGlyProGlnAsnIleThrLeuAs ::: 	204 pPheSerPheLeuLeuTyrLeuArgProValProAspAlaLeu	189AspG1yAspAsnValLeuLeuThrLeuAspValSerGlu(180 luLeuAsnLeuThrGlnGlnLeuPro	
	rgArgLysAlaAlaArgG 4	YSLeuLeuLeuAlaAlaAl 4	SProMetAspLysTyrIle 4 	GlnČysmetGlnLeuTrpA 4 :::	hrargalaalaargLeuGl 4 	CTGTGCCTTGGAACCCAGT 1	AspAspMetLeuLeuVal ::: ::: GACGATGTGCTACTGTTG	SValGlnLeuGlnAlaC ::: CTGCAGCTGCAGGAGT	nLeuValAlaGlyHisPr ::: ATTGCTGAAAGGCCACCC	ProProValProGlnLys ::: CCACCGCTTTCCTGGGAG	alThrLeuCysTrpGln ::::: ::: :GGCACTGTGCTGGCGG	uSerProGlyValTrp ::: ACCCTGCAGAGCTGG	AspProGlyAlaHisArg ::: GACCCCCGCGCACACCAG	rpSerLeuGluProAspS GGCCTCTGGAACCTGACT	nIleThrLeuAsnHisTh 	ProAspAlaLeuLysSer CAGGGCCCCCAAAAACCC	.spValSerGluGluGln :: ATGTCTCTGAGGAGCAG	GCCCTGGCTCAACGTGTC	

GCTTTCCCTCATCCTCCTTCTCAAAAAGGATCACGCGAAAGCGGCCGCCA 1600

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AAS46223 standard; cDNA;
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                                                                                                             PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha; blood; chondrocyte cell; cell proliferation; cell differentiation; col adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorc
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Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR comparing the level of expression of a PRO polypeptides of the invention. The sequences of the comparing the level of expression of a PRO polypeptide in a test sample con comparing the level of expression in the test sample of normal cells, whereby a confidence in the manmal. Mammals include dogs, cats, cattle, horses, sheep, comparing the mammal. Mammals include dogs, cats, cattle, horses, sheep, comparing the mammal. Mammals include dogs, cats, cattle, horses, sheep, comparing the mammal. Mammals include dogs, cats, cattle, horses, sheep, comparing the mammals include dogs, cats, cattle, horses, sheep, comparing the mammals include dogs, cats, cattle, horses, sheep, comparing the contacted with it. A specific polypeptide can be used to stimulate tumour necrosis factor (NWP) alpha release from human comparing the proliferation or differentiation of chondrocyte cells. The comparing the proteins can be used to determine the presence of tumours and also comparing the proteins can be used to determine the presence of tumours and also comparing the proteins of tumour development, particularly adrenal, lung, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, colon, co
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21-MAR-2000;
28-MAR-2000;
29-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                            Novel nucleic acids encoding PRO polypeptides, presence of tumours, such as prostate and bread to screen for modulators of the compounds -
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ith V, Watanabe
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2000WO-US32678.
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st tumours, in mammals and
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Sequence 2380 BP; 411 A; 776 C; 743 <u>.</u> 450 T; 0 other;

PCR primer.

liver; genetic disorder;

colon; ss;

Homo sapiens.

WO200168848-A2

28-FEB-2001; 2001WO-US06520.

20-SEP-2001.

lignment_scores:
Quality: 2339.00
Ratio: 4.118
Percent Similarity: 82.081 lignment_block: US-09-899-471-2 x AAS46223 lign seg 1/1 to: AAS46223 from: 1 238 AspLeuValProCysLeuCysIleGlnValTrpSerLeuGluProAspSe 254 33 GATGAGGAAAAGTTTGGAGGAGCAGCTGACTCAGGGGTGGAGGAGCCTAG gAsnAlaSerLeuGlnAlaGlnValValLeuSerPheGlnAlaTyrProI 130 pPheSerPheLeuLeuTyrLeuArgProValProAspAlaLeuLysSerL 221 Glu.....AlaGlyLysSerAspSerGluLeuGlnGluSerAr 113 AACTCAACCACACAGCAGCTGCCTGCCCTGCCCTGGCTCAACGTGTCA 832 luLeuAsnLeuThrGlnGlnLeuPro...... Gaps: 7
Percent Identity: 66.329 to: 2380

524 HisHisGlnArgArgArgIleLeuGlnGluGlyGlyValValIleLeuLe 540

523 1876	507 spLeuTtpSerArgArgGluLeuSerAlaHisGlyAlaLeuAlaTrpphe:	16
507 1826	490 lGlyAlaLeuAlaSerAlaLeuSerGlnMetProLeuArgYalAlaYalA : 	117
490 1776	euLeuLeuHisSerAlaAspGlyAlaGlyTyrGluArgLeuVa ::: 	13
473 1726	468AlaAlaArgGlySerArg	۲,
467 1679	4 aLeuPhePhePheLeuLeuLeuLysLysAspArgArgLys	۲,
454 1629	438 HisArgArgTrpValLeuValTrpLeuAlaCysLeuLeuLeuAlaAlaAl -::	н.
437 1579	421 snaspåspasnmetGlySerLeuTrpalaCysProMetAspLysTyrIle ::::: :::	н.
421 1531	404 yGluGluLeuLeuGlnAspPheArgSerHisGlnCysMetGlnLeuTrpA 	<u>, </u>
404 1482	188 GlyCy\$ThrProLeuProSerMetAlaSerThrArgAlaAlaArgLeuGl 	14
387 1432	371 luMetLysThrGlyLeuAsnAsnThrSerValCysAlaLeuGluProSer 	<u>م</u>
371 1382	pAlaAspSerLeuGlyProPheLysAspAspMetI GCTGACTCCCTGGGGCCTCTCAAAGACGATGTGG	н
354 1332	338 ASDLeuCysValGlnValSerThrTrpGluLysValGlnLeuGlnAlaCy	<u> </u>
337 1282	321 snAlaThrValAsnGluProGlnAspPheGinLeuValAlaGlyHisPro 	۳
321 1232	304 aProAspGlnSerProCysGlnProLeuValProProValProGlnLysA ::: ::: 1183 TCCGGGTGGGGACCCCTGCCAGCCACTGGTCCCACCGCTTTCCTGGGAGA	_
304 1182	288 LeuAspAlaProCysCysLeuProGlyLysValThrLeuCysTrpGlnAl 	_
287 113;	271 snLeuTrpHisileAlaArgLeuArgValLeuSerProGlyValTrpGln :: :: ::: 	
271 108	254 rGluargValGluPheCysProPheArgGluAspProGlyAlaHisArgA 	–
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AASO9515 standard; cD
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AASO9515;

AASO9516;

Human; Interleukin-17
PRO20040; DNA 164625-
rheumatoid arthritis;
Altergic disease; ast
degenerative cartilag

AASO9515;

Human; Interleukin-17
PRO20040; DNA 164625-
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2000US-0175481.
2000WO-US04341.
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233..292
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21-MAR-2000;
21-MAR-2000;
21-MAR-2000;
02-JUN-2000;
22-JUN-2000;
22-AUG-2000;
24-AUG-2000;
24-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence (DNA 164625-2890) encodes a PRO polypeptide (PRO20040) which is the human Interleukin 17 receptor, II-17RH2. A composition containing ant/agonists to the PRO polypeptides or individual components are useful for treating a mammal with an immune related disease, e.g. systemic lupus erythematosus, rheumatoid arrthritis, osteoarthritis, systemic lupus erythematosus, rheumatoid arrthritis, osteoarthritis, juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, aridiopathic inflammatory myopathy, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
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                                                                                                                                                                             thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, a demyelinating disease, an autoLimnune or immune-mediated skin disease, contact dermatitis, an allergic disease e.g. food hypersensitivity, asthma, a transplantation associated disease, or a chronic inflammatory demyelinating polyneuropathy. Treating a degenerative cartillaginous disorder comprises administering a PRO1122 polypeptide agonist, or antagonist to the mammal. Numerous examples of the diseases and disorders are given in the specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diagnosis
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              GlySerLeuGlnSerAlaProGlyProValLeuValProThrArgLeuGl
                                                                           erLeuGlyLeuSerCysHisLeuTrpAspGlyAspValLeuCysLeuPro
                                                                                                                   GGTCCTTTCTCTGGAGAGGCTTGTGGGGCCTCAGGACGCTACCCACTGCT
                                                                                                                                              lValValSerLeuGluArgLeuMetGluProGlnAspThTAlaArgCysS
GGGGACATCGTGCCTGCTCCGGGCCCCGTGCTGCCCCTACGCACCTGCA
                                                           2001-451708/48.
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                                                                                                                                                                                                                                                                                                                                              Quality: 2339.00
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L, Li H, Hillan KJ,
CK, Williams PM, W
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                                                                                                                                                                                                                                                                                                                                 Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptides homologous to interleukin-17, useful for the and treatment of immune related disease e.g. rheumatoid and diabetes -
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2000US-02130B7
2000US-0644848
2000WO-US2332B
2000WS-0242837
2000WS-0242837
2000WS-0253646
                                                                                                                                                                                                                                                                                                                                                                                                         BP;
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2000US-0191007.
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                                                                                                                                                                                                                                                                                                                4.118
82.081
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Percent Identity:
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Wood WI, Ya
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lumas D, Van Lookeren M,
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Vandlen RL;
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or

	54 sSerTrpAlaAspSerLeuGlyProPheLysAspAspMetLeuLeuValG 37	S
	38 AsnLeuCysValGlnValSerThrTrpGluLysValGlnLeuGlnAlaCy 354	338 1283
		321 1233
	104 aProAspGlnSerProCysGlnProLeuValProProValProGlnLysA 321	304 L183
	188 LeuAspAlaProCysCysLeuProGlyLysValThrLeuCysTrpGlnAl 304	288 1133
	<pre>771 snLeuTrpHisIleAlaArgLeuArgValLeuSerProGlyValTrpGln 287</pre>	271 1083
	254 rGluArgValGluPheCysProPheArgGluAspProGlyAlaHisArgA 271 	
·	238 ASPLeuValProCysLeuCysIleGlnValTrpSerLeuGluProAspSe 254 	
	221 euTrpTyrLysAsnLeuThrGlyProGlnAsnIleThrLeuAsnHisThr 237 :::	221 933
	204 pPheSerPheLeuLeuTyrLeuArgProValProAspAlaLeuLysSerL 221 :::::: ::: 383 CTTCGGCCTCTCCCTGTACTGGAATCAGGTCCAGGGCCCCCAAAACCCC 932	204 883
	189AspGlyAspAsnValLeuLeuThrLeuAspValSerGluGluGlnAs 204 	189 833
	180 luLeuAsnLeuThrGlnGlnLeuPro	180 783
	163 uGlyAlaGluValGlnIleTrpSerTyrThrLysProArgTyrGlnLysG 180 ::: :::	
	47 ProGlyGlnServalGlySerAlavalPheAspCysPheGl 	147 683
	130 leAlaArgCysAlaLeuLeuGluValGlnValProAlaAspLeuValGln 146 	633
	113 gAsnAlaSerLeuGlnAlaGlnValValLeuSerPheGlnAlaTyrProI 130 	11; 58;
	101 GluAlaGlyLysSerAspSerGluLeuGlnGluSerAr 113 ::: :::: ::::: 533 GATGAGGAAAAGTTTGGAGGAGCAGCTGACTCAGGGGTGGAGGAGCCTAG 582	10: 53:
	84 alargValValValHisLeualaValHisGlyHisTrpAlaGluProGlu 100 	
	67 nThrGluLeuValLeuArgCysProGlnLysThrAspCysAlaLeuArgV 84	

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637		604 2127	587 2077	2 7	557 1977	540 1927	524 1877	507 1827	490 1777	474 1727	468 1680	454 1630	. 438 1580	421 1532	404 1483	388 1433	371 1383	1333
gValG1 :::	AspAla	heArgV : TCCGCA	1Glyva :: GGGGGG	SerCys	hrVald	uPhese CTTCTC	HisHis	spLeuf	1G1yA1	Thral	GGCTC	aLeup GCTTT	Hisarg	snAsp 	yGluĞluL AGAĞTACT	GLYCYS	luMetL : AGACAC	CTTGTG
uArgVa	LeuGlnG CTGCAGC	ValAlap :::::: ACCGTGC	TTY:	CysValLeui	luPro. GCCCG	SerProAl	GlnArg CAGCGG	rpSer# GAGCC	aLeu/ 	ThralaLeuLeus:::	TTGAAAC	hePhePh ::::: CCCTCAT	JArgTrpV : : GCGCTGGG	PASPASNI	luLeuL ACTTAC	SThrPro ACTTCA	ysThr :: GAGGC	GCTG
lThrGln	lygly Agcci	roLeuP ::: CCGTCT	rPheAspG1 TTCGACAG	ProAs		AlaAlaValA] ::: :GTGCGGTGGC	ArgArg ::: CGCCAG	rgArgG GTCGTG	AlaserAla CGTCGGCC	PuLeuHis ::: CCTCTAC	AGGACG	hePheLeuLeuLysLy ::::: TCATCCTCCTTCTCAAAAA	ValLet ::: GCCCTC	AsnMetGlys ::::: : SACTTGGGAG	LeuLeuGlnAspi TACTACAAGACO	DLeuPro ACTACCO	GlyLeuA CCCCAGG	HIIIIIII
nAlaLeuA : :	CysSer:	heSerLe	lyLeuLeuHi GCTGCTCCA	spPheLeuG \CTTCTTGC	Glyp ACGGCC	LaG1	TleLeuG ACCCTGC	luLeus AACTG#	Leuse CTGTG	SerAla CAGCC	TCCG	uLeuLy TCTCAA	ValLeuValTrpLeu ::: GCCCTCGTGTGGCTG	SerLeuTr ::: SCGCTATG	hea	DSerMetal DAGCAAAGO	ASNASNT : : : BACAACA	reeecc
ArgSer :::	ThrserA: CCGCGTT	uProj :	uHisPro CACCCG	lngly AGGGG	TOHISA CGCACG	nCysGl :: GTGCAG	GlnGluG CAGGAGG	SerAlaH : GCGCGC	rGlnMe :: CCAGCT	AspGly GATGAC	ନ୍ଧ :	SAS	LeuAlaCy: CTGGCCTG	rpalac GGGCCT	rgSerHis :: AGTCAGGC	aSeI	hrserv : GATCCC	TCTC
AlaLe	laGly :: cceee	hrGlnLe :: CCCAACT	Asps III:	Argala CGGGG	SPALaL : ACGCCW	nGlnTr :::: :CGAGTG	lyGly GCGGC	TisGlyAl :: :AGGGGCC	tProfe : GCCGCT	Alagly ::: TCGGGT	Ala CGGCC	PArgAr ::: TCACGC	CysLeuLe TGCCTACT	ysPro GCCCC	Glncy CAGTG	Thrarg	alcys! :: TCTGTG	AAGACGA
uAspSer 	ArgProA CGGCTCC	uPro#	Serval Pro :: \H ::ccgraccc	AlaThrGlyA	laLeuAlaAla: ::: CCMMCCGCGCCC	PLeuGln GCTACAG	ValValIle ::: GTGGTGGTC	laLeuAlaTı ::: CCGTGGCTT	Arg\	.yTyrGluAr : : : !TTCGAGCG	AlaArgGly GCCAGGGGC	gLys GAAAGG	LeuLeuA : : : CTCTTTG)MetAspLys ATGGACAAA	SMetG1 ::: TCTGCA	AlaAlaA GCAGCTC	laLeuG CCTTGG	::: ATGTGCT
Cys	Alaaspar ::: Caagagag	laPheLe ACTTCCT	SerProP ::: GCCCTTT	ArgTyrV AGCTACG	CGC LTPL	LeuG1	TTC Leu	ig II g	/alalava TGGCCGT	gLeu CCTG	lyserAr GCCG	GTGGCT	AlaAlaAl GCCGCTGC	Tyr] []]]	nLeuTr GCTATG	rgLe IIII	LuPros AACCCA	::
6	N 6	ი — ნ	νο	H - p' N 5	0 - E	n¶ 5 GG 1	CT 1	he 5	7alA 5	Va 4 H GT 1	C 1	GA 1	6C 1	TC 1	Б. 1	uGl 4	Ser 3	ର <u>-</u>
52 ·	37 226	20 176	04 126	87 076	026	976	926	.876	826	190	173 1726	167 1679	154 1629	137 1579	421 1531	404 1482	387 1432	1382

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1)19nment_scores:
Quality: 2339.00
Ratio: 4.118
                                                                                                                                                                                             AAF92138 standard; cDNA; 2380 BP.

AAF92138;

C AAF92138;

TY

15-MAY-2001 (first entry)

E Human PRO20040 cDNA.

No

Human; PRO protein; mapping; ss.

Homo sapiens.

24-Aug-2000; 2000Wo-US23328.

20-DEC-1999; 99W-US20111.

15-SEP-1999; 99W-US20111.

15-SEP-1999; 99W-US20111.

16-FEB-2000; 2000Wo-US04342.

20-DEC-1999; 99W-US04444.

11-AAR-2000; 2000Wo-US04341.

18-FEB-2000; 2000Wo-US04341.

18-FEB-2000; 2000Wo-US04441.

22-FEB-2000; 2000Wo-US04414.

23-APR-2000; 2000Wo-US04441.

24-AAR-2000; 2000Wo-US04441.

25-APR-2000; 2000Wo-US04441.

26-APR-2000; 2000Wo-US04441.

27-FEB-2000; 2000Wo-US04441.

28-CO-USO4342.

29-FEB-2000; 2000Wo-US04441.

20-HAR-2000; 2000Wo-US04442.

20-HAR-2000; 2000Wo-US04442.

20-HAR-2000; 2000Wo-US04441.

20-HAR-2000; 2000Wo-US04441.

20-HAR-2000; 2000Wo-US04442.

20-HAR-2000; 2000Wo-US04442.

20-HAR-2000; 2000Wo-US04442.

20-HAR-2000; 2000Wo-US0444.

20-HAR-2000; 2000Wo-US0444.

20-HAR-2000; 2000Wo-US0444.

20-HAR-2000; 2000Wo-US0444.

20-HAR-2000; 2000Wo-US0444.

20-HAR-2000; 2000Wo-US0444.

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20-HAR-2000; 2000Wo-US0444.

20-HAR-2000; 2000Wo-US0444.

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20-HAR-2000; 2000Wo-US0444.

20-HAR-2000; 2000Wo-US0444.

20-HAR-2000; 2000Wo-US0444.

20-HAR-2000; 2000Wo-US0444.

20-HAR-2000; 2000Wo-US0444.

20-HAR-2000; 2000Wo-US0444.

20-HAR-2000; 2000Wo-US0444.

20-HAR-2000; 2000Wo-US0444.

20-HAR-2000; 2000Wo-US0444.

20-HA
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                                                                                                                                                                                                                                                                                                  The present sequence is the coding sequence for a human PRO polypeptide (secreted and transmembrane). The PRO protein, and PRO agonists, PRO antagonists or anti-PRO antibodies are useful for preparation of a medicament useful in the treatment of a condition which is responsive to the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO protein may also be employed as molecular weight markers for protein electrophoresis. The PRO coding sequence has applications in molecular biology, including use as hybridisation probes, and in chromosome and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eighty four nucleic acids encoding PRO polypeptides, useful in molecular biology, including use as hybridization probes, and chromosome and gene mapping. -
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Watanabe
                    Percent
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             Identity: 66.329
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alignment_block:
US-09-899-471-2 x AAF92138
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GASNALASETLEUGINALAGINVALVALLEUSETPHEGINALATYTPTOI 130
                                                      pPheScrPheLeuLeuTyrLeuArgProValProAgeAlaBeuLysSerL
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                                                                                                                                                                   CTTCGGCCTCTCCCTGTACTGGAATCAGGTCCAGGGCCCCCAAAAACCCC
                                                                                                                                                                                                                            GCAGATGGTGACAACGTGCATCTGGTTCTGAATGTCTCTGAGGAGCAGCA
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                                                       HisHisGlnArgArgIeLeuGlnGluGlyGlyValValIleLeuLe 540
                                                                                                                                                                         hrValGluPro.
                             uPheSerProAlaAlaValAlaGlnCysGlnGlnTrpLeuGlnLeuGlnT
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                                                                                              ACCTGTGGAGCCGTCGTGAACTGAGCGCGCAGGGGCCCCGTGGCTTTGGTTT
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                                                                                                                                              lGlyAlaLeuAlaSerAlaLeuSerGlnMetProLeuArgValAlaValA
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The invention relates to primate and rodent DNAX cytokine receptor subunit (DCRS) polypeptides and the polynucleotides encoding them. receptors, or their portions may be useful as phosphate labelling to label general or specific substrates. The subunits may also be

enzymes The Disclosure; Page 12-15; 148pp; English.

Isolated antigenic human or mouse DNAX receptor subunit-like polypeptide useful for detecting antibodies generated in respensence of increased protein levels or immunological disord

in response disorders -

នដ្ឋក្នុកក្នុកក្នុកក្នុក្ lignment_scores: Quality: 2235.00 lignment_block: US-09-899-471-2 x AAS18130 Ratio: 4.042 Percent Similarity: 78.218 Align seg 1/1 to: AAS18130 from: 1 to: 2308 functional immunogens to elicit recognising antibodies, or antigens capable of binding antibodies. A combination, e.g., including a DCRS can be used as an immunogen for the production of antisera or antibodies capable of distinguishing between other cytokine receptor family members. A purified DCRS can also be used as a reagent to detect antibodies generated in response to the presence of elevated levels of expression, or immunological disorders which lead to antibody production to the endogenous receptor. This sequence represents cDNA encoding the human 681 631 581 130 leAlaArgCysAlaLeuLeuGluValGlnValProAlaAspLeuValGln 146 531 113 481 GATGAGGAAAAGTTTGGAGGAGCAGCTGACTTAGGGGTGGAGGAGCCTAG 530 101 431 281 189 731 180 163 147 381 331 231 Sequence 2308 BP; 384 A; DCRS7 polypeptide. 67 84 51 34 17 1ValValSerLeuGluArgLeuMetGluProGlnAspThrAlaArgCyss 34 CTGCCCGCTGCGTCCTGCTGGAGGTGCAAGTGCCTGCTGCCCTTGTGCAG gAsnAlaSerLeuGlnAlaGlnValValLeuSerPheGlnAlaTyrProI 130 Glu.....AlaGlyLysSerAspSerGluLeuGlnGluSerAr 113 GATCCTTTCTCTGGAGAGGCTTGTGGGGCCTCAGGACGCTACCCACTGCT 280 luLeuAsnLeuThrGlnGlnLeuPro..... AACTCAACCACACAGCAGCTGCCTGACTGCAGGGGGCTCGAAGTCTGG 780 GAATGCCTCTCCAGGCCCAAGTCGTGCTCTCCTTCCAGGCCTACCCTA 580 757 C; 731 G; 434 T; 2 other; Gaps: 8
Percent Identity: 62.942 707 As 188 630 430 380

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475	AlaAlaArgGlySerArgThrA	468
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456 1576	gArgTrpvalLeuValTrpLeuAlaCysLeuLeuLeuAl 	439 1527
439 1526	AspasmetGlySerLeuTrpAlaCysPrometAsplysT :::::: :::	423 1477
422 1476	6 luLeuLeuGlnAspPheArgSerHisGlnCysMetdinLeuTrpAsnAsp 	40 143
406 1429	9 sThrProLeuProSerMetAlaSerThrArgAlaAlaArgLeuGlyGluG 	38 138
389 1379	3 LYSThredyLeuAsnAsnThrSerValCysAlaLeuGluProSerGlyCy ::: 0 CGAGGCCCCCAGGACAACAGATCCCTCTGTGCCTTGGAACCCCAGTGGCTG	37 133
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289 1130	3 TrpHisIleAlaArgLeuArgValLeuSerProGlyValTrpGlnLeuAs :: ::: :::	27 108
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256 1030	9 uValproCysLeuCysIleGlnValTrpSerLeuGluProAspSerGluA 	23 98
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222 930	rovalp	88
206 880	9 pGlyAspAsnValLeuLeuThrLeuAspValSerGluGluGlnAspPheS 	18 83
830	1 AACAGCATCCCGAGCTGCTGGGCCCTGCCCTGGCTCAACGTGTCAGCAGA	78

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11-JAN-2000; 2000JP-0118775
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                                                                                                                                           Human; secretory protein; membrane protein;
rheumatoid arthritis; diabetes; ss.
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                                                                   10-JAN-2001
                                                                                                                                                                           Human cDNA encoding a membrane or secretory protein clone PSEC0233
                                                                                                                                                                                                       23-MAY-2001
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                                                                                                                                                                                                                                                                                      /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAF93875
                                          2000EP-0114090
                                                                                                                                                                                                     (first entry)
                                                                                                                                                  gene therapy,
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alArgValValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu 100
                      nThrGluLeuValLeuArgCysProGlnLysThrAspCysAlaLeuArgV 84
                                                                                                                                                                                                                                                                                                                                                                                                             2499 BP; 418 A; 821 C;
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764 G; 496 T; 0 other,

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(e.g. polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples. They may also be used to study the expression and function of secretory proteins/membrane polypeptides and their role in metabolism. The polypeptides may be used as antigens in the production of antibodies against them and in assays to identify modulators (agonists and antagonists) of expression and activity. The antibodies and antagonists may also be used as therapeutic agents to down regulate expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of the polypeptides in samples (e.g. by enzyme linked immunosorbant assay (ELISA). Examples of diseases which may be treated include rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the production of antibodies directed against the proteins, and cDNA sequences, which can be used in vaccines. The polynucleotide sequences can be used in gene therapy. The polynucleotide sequences and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate secretory protein/membrane protein expression. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            which encode human secretory or membrane proteins represented by AAB88317 - AAB88419. Included in the invention are primers AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the
arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA sequences of the invention. The invention also includes methods for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention relates to nucleic acid sequences AAF93744 - AAF93916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID 263; 609pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding secretory proteins/membrane proteins, useful gene therapy or as candidate target molecules in drug development -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-MAY-2000; 2000JP-0183766.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sugiyama T,
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alignment_scores:
Quality: 2182.00
Ratio: 3.974
Percent Similarity: 71.953
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                                                                                 51 GlySerLeuGlnSerAlaProGlyProValLeuValProThrArgLeuGl
                                                                                                                          erLeuGlyLeuSerCysHisLeuTrpAspGlyAspVaLLeuCysLeuPro
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Gaps: 10
Percent Identity: 58.060
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407 67

117	CysTrpGlnAlaProAspGlnSerProCysGlnProLeuValProProVa 3	301
.357	GAGCTGGCTGGACGCACCGTGCTCGCTGCCCGCAGAAGCGGCACTG 1	Ö
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œ i	YAlaHisArgAsnLeuTrpHisIleAlaArgLeuArgValLeuSerProG	267
257	GluProAspSerGluArgValGluPheCysProPheArgGluAspProGl 2	251 1208
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234	CAACCTCCTTCCTT	0 1
1107	CTTCCTGGTTTCCTTGACTTTGGCCTCCTCCTCTTCCTCCT	Ū
225		
1057	TTGAAGAGGACTCACCCCAAGCAAGGGAAAATTGGTGGGGGAAC	1008
225		225
1007	TGTAGGCCGATGCCTGTGCAAAGGACGCAGTGCCATATCAGAGAGG	958
225		225
957		908
225	euTrpTyrLysAsn	221
907	CTTCGGCCTCTCCCTGTACTGGAATCAGGTCCAGGGCCCCCAAAACCCC	5 6
	DPheSarPheIonI enteriorate Date To December 1987 December	204
ö	AspGlyAspAsnValLeuLeuThrLeuAspValSerGluGluGlnAs	0
807	AACTCAACCACACACAGCAGCTGCCTGCCCTGCCCTGGCTCAACGTGTCA	UT.
188	ThrGlnGlnLeuPro	. 18
757		0
o d	uGlvAlaGluValGlnIleTrpSerTvrThrIvsProArcTvrThrIvsCroCT	σ (
5 65	7 ProGlyGlnSerValGlySerAlaValPheAspCysPheGluAlaSerLe	65
657		60
	eAlaArgCysAlaLeuLeuGluValGlnValProAlaAspLeuValGln	13
130	3 9AsnAlaSerLeuGlnAlaGlnValValLeuSerPheGlnAlaTyrProI 	. 55
557	GATGAGGAAAAGTTTGGAGGAGCAGCTGACTCAGGGGTGGAGGAGCCTAG	0 0
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500 2241	584 GlyArg†yrValGlyValTyrPheAspGlyLeuLeuHisProAspSerVa 6	
583 2191	567 laAlaTipLeuSerCysValLeuProAspPheLeuGlnGlyArgAlaThr 5	
567 2141	553 uGlnLeuGlnThrValGluProGlyProHisAspAlaLeuA 5	
553 2091	537 VallleLeuLeuPheSerProAlaAlaValAlaGITCYsGlnGlnTrpLe 5	
536 2041	520 euAlaTrpPheHisHisGlnArgArgArgIleLeuGTMGluGlyGlyVal 5 ::	
520 1991	aHisGlyAlaL ::: CAGGGGCCCG	
503 19 41	487 GluArgLeuValGlyAlaLeuAlaSerAlaLeuSerGlnMetProLeuAr (
486 1891	470 rgGlyŚerArgThrAlaLeuLeuLeuHisSerAlaAspGlyAlaGlyTyr (
470 1844	7 s Alaalaa	
467 1794	PhePhePheLeuLeuLysLysAspArgArgLy :::::: ::: TCCCTCATCCTCCTTCTCAAAAAGGATCACGCGAA	
450 1744	YrIleHisArgArgTrpValLeuValTrpLeuAlaCysLeuLeu ::: :::	
434 1694	nAspAspAsnMetGlySerLeuTrpAlaCysProMetA :::::: ::: GACGATGACTTGGGAGCGCTATGGGCCTGCCCCATGG	
165]		
417	lyGluGluLeuLeuGlnAspPheArgSerHisGlnCysMe	
400 1651	384 euGluproSerGlyCysThrProLeuProSerMetAlaSerThrArgAla	
384 1607	367 tLeuLeuValGluMetLysThrGlyLeuAsnAsnThrSerValCysAlaL 	
367 155	351 LeuGlnAlaCysSerTrpAlaAspSerLeuGlyProPheLysAspAspMe 	
350 150	334 laGlyHisProAsnLeuCysValGlnValSerThrTrpGluLysValGln	
334 145	317 lProGlnLysAsnAlaThrValAsnGluProGlnAspPheGlnLeuValA ::: ::: ::::::::::::::::::::::::	
140	58 recreecesecrees	

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292 17

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The invention provides a new human cytokine receptor desinated 2cytor14.

The zcytor14 can be expressed by standard recombinant methodology. The C cytor14 can be expressed by standard recombinant methodology. The C zcytor14 gene in a biological sample. Anti-Zcytor14 antibodies can be CC used to screen biological samples in vitro for the presence of Zcytor14.

CC proteins, polypeptides and peptides having 2cytor14 activity can be CC administered to a subject who lacks an adequate amount of this recumatoid CC polypeptide, for treating inflammation and conditions such as rheumatoid polypeptide, for treating inflammation and conditions such as rheumatoid cc arthitis. In contrast, Zcytor14 antagonists (e.g. anti-Zcytor14 CC arthitis. Can be used to treat a subject who produces an excess of cc antibodies) can be used to treat a subject who produces an excess of cytor14. Zcytor14 nucleotide sequences can also be used to provide antibodies. Cc zcytor14 to a subject. The present sequence represents a cDNA encoding 2cytor14 to a subject. The present sequence represents a cDNA encoding a variant of the human cytokine receptor Zcytor14, designated Zcytor14. Cc The variant is a truncated form of the receptor polypeptide and lacks cross the condition of the receptor polypeptide and lacks cross the condition of the receptor polypeptide and lacks cross the condition of the receptor polypeptide and lacks cross the condition of the receptor polypeptide and lacks cross the condition of the receptor polypeptide and lacks cross the condition of the receptor polypeptide and lacks cross the condition of the receptor polypeptide and lacks cross the condition of the receptor polypeptide and lacks cross the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of
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AAC85029 standard; cDNA; 1753 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytokine receptor; Zcytor14; human; inflammation; rheumatoid antiinflammatory; gene therapy; vaccine; variant; Zcytor14-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human variant Zcytor14 protein Zcytor14-1 encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ZYMO ) ZYMOGENETICS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                p-PSDB; AAB61881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
                                                                                                                                                                                                                                                                                                                                                                                                            New polypeptide encoding a human cytokine receptor 2cytor14, for treating inflammation e.g. rheumatoid arthritis .
                                                                                                                                                                                                                                                                                                                                                                pisclosure; Page 95-98; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /SIDS1/gcgdata/geneseg/geneseqn-embl/NA2001A.DAT:AAC85029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Burkhead SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9908-0348854
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pownder
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alignment_scores:
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US-09-899-471-2
                                                                                                                                                                                                                                                                                                                                                                         percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1753 BP;
                                                                                                                                                                                                                                                                                                                             110 GlnGluSerArgAsnAlaSerLeuGlnAlaGlnValValLeuSerPheGl
                                                                                                                                                                                                                                                                                                           126 nAlaTyrProlleAlaArgCysAlaLeuLeuGluValGlnValProAlaA 143
                                                                                                                                                                                                                                                                          143 spLeuvalGlnProGlyGlnSerValGlySerAlaValPheAspCysPhe
                                                                                                                                                                                                                                                   2 GAGGAGCCTAGGAATGCCTCTCCAGGCCCAAGTCGTGCTCCTTCCA 51
                                                                                                                                                                                                      201 GluGluGlnAspPheSerPheLeuLeuTyrLeuArgProValProAspAl 217
                                                                                                           284 lyvalTrpGlnLeuAspAlaProCysCysLeuProGlyLysValThrLeu 300
                                      Quality:
                                                                                                                                                                                334
                                                              Ratio:
                           lproGlnLysAsnAlaThrValAsnGluProGlnAspPheGlnLeuValA 334
laGlyHisProAsnLeuCysValGlnValSerThrTrpGluLysValGln 350
                  TTCCTGGGAGAACGTCACTGTGGAC.....
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percent Identity: 64.249
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GTGAACAGCTCGGAGAAGCTGCAG 700
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:::|||||||||||::: ||
TTTGCCGCTGCGCTTTCCCTCATCCTCCTCAAAAAGGATCACGCGAA
                                                          lProSerProPheArgValAlaProLeuPheSerLeuProThrGlnLeuP
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| ACCCGCCTTTTCCGCACCGTGCCCGTCTCACACTGCCCTCCCAACTGC
                                                                                                                                     GlyArgTyrValGlyValTyrPheAspGlyLeuLeuHisProAspSerVa
                                                                                                                                                                                  GCGCCTCGCTCAGCTGCGTGCTGCCCGACTTCTTGCAGGGCCCGGCGCGCCC 1444
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                                                                                                                                                                                                                                                                                                                          ValIleLeuLeuPheSerProAlaAlaValAlaGlnCysGlnGlnTrpLe 553
                                                                                                                                                                                                                                                                                                                                                                                                                                 GluArgLeuValGlyAlaLeuAlaSerAlaLeuSerGlnMetProLeuAr 503
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CAGACTTCCTGGGGGCCCTGCAGCAGCCTCGCGCCCCCGCGTTCCGGGCGG
                roAlaPheLeuAspAlaLeuGlnGlyGlyCysSerThrSerAlaGlyArg
                                                                                                                        GGCAGCTACGTGGGGGCCTGCTTCGACAGGCTGCTCCACCCGGACGCCGT
                                                                                                                                                                                                                                                                                                           GTGGTCTTGCTCTCTCCCGGTGCGGTGGCGCTGTGCAGCGAGTGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                              gValAlaValAspLeuTrpSerArgArgGluLeuSerAlaHisGlyAlaL 520
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Seq_documentation_block:
ID AAZ65269 standard; D)
XX AAZ65269;
XY 23-MAR-2000 (first 6
XX Human; secreted protest
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                                                                                                                                                                                                                                                                                                                                      New isolated human genes and the secretary polypeptides they encode, useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
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Shi Y, Young
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ng PE, Wei F, Brewer
A, Ebner R;
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pet DR;
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US-09-899-471-2 x AAZ65269
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                                                                                 AGGGAGTGAGGTACGAATCTGGTCCTATACTCAGCCCAGGTACGAGAAGG
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Ratio: 4.157
nilarity: 81.048
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456 he.PhePheLeuLeuLysLysAspArgArgLys 467	439 gArgTrpValLeuValTrpLeuAlaCysLeuLeuLeuAla 	423 ASPASNMETGLYSETLEUTTPALACYSPTOMETASPLYSI	406 luLeui.euGlnAspPheArgSerHisGlnCysMetGlnLe :::::	389 SThrProLeuProSerMetAlaSerThrArgAlaAlaArg 	373 LysThrGlyLeuAsnAsnThrSerValCysAlaLeuGluP: ::: ::: :::	356 rpAlaaspSerLeuGlyProPheLysAspAspMetLeuLk 	339 uCysValGlnValSerThrTrpGluLysValGlnLeuGlnAlaCysS 	323 ThrValAsnGluProGlnAspPheGlnLeuValAlaGlyi :::::: ::: ::: 176 ACTGTGGACAAGGTTCTCGAGTTCCCATTGCTGAAAGGCC	306 spGlnSerProCysGlnProLeuValProProValProG::::	289 pAlaproCysCysLeuProGlyLysValThrLeuCysTr	273 TrpHisIleAlaArgLeuArgValLeuSerProGlyVal	256 rgValGluPheCysProPheArgGluAspProGlyAlaHisA 	239 uValproCysLeuCysIleGlnValTrpSerLeuGluPro	223 TyrLysAsnLeuThrGlyProGlnAsnIleThrLeuAsnF ::: 977 CACA AAACCTGACTGGACCGCAGATCATTACCTTGAACC	206 erPheLeuLeuTyrLeuArgProValProAspAlaLeuLyss :::: :: 927 GCCTCTCCCTGTACTGGAATCAGGTCCAGGGCCCCCCAAAA	189 pGlyÅspAsnValLeuLeuThrLeuAspValSerGluGl 	827 AACACCATCCCGAGCTGCTGGGCCCTGCCCTGGCTCAAC
gLys 4	uLeuA ::: CTTTG	શ≐⊄	SMetGlnLeuTrpAsnAsp 422 :::	AlaAlaArgLeuGlyGluG 406 	laLeuGluProSerGlyCy 389 	pMetLeuLeuValGluMet 372 ::: ::: TGTGCTACTGTTGGAGACA 1425	GlnLeuGlnAlaCysSerT 356 CAGCTGCAGGAGTGCTTGT 1375	alAlaGlyHisProAsnLe 339 :: TGAAAGGCCACCCTAACCT 1325	oValProGlnLysAsnAla 322 ::: :: ::: CTTTCCTGGGAGAAYGTC 1275	euCysT GTGCT	oGly GCAG	OGlyAlaHisArgAsnLeu 272 	LeuGluProAspSerGluA 256	hrLeuAsnHisThrAspLe 239	pAlaLeuLysSerLeuTrp 222 CCCCCCAAAACCCCGGTGG 976	SerGluGluGlnAspPheS 206 	GGCTCAACGTGTCAGCAGA 876

seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAC85028

1670 TCCCTCATCCTCCTTCTCAAAAAGGATCACGCGAAA 1705

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S-09-899-471-2 x AAC85028
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AAC85028 standard; cDNA; 2076 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention provides a new human cytokine receptor desinated Zcytor14. Eavytor14 can be expressed by standard recombinant methodology. The encoding nucleic acid is useful for detecting the expression of a Zcytor14 gene in a biological sample. Anti-Zcytor14 antibodies can be used to screen biological samples in vitro for the presence of Zcytor14. Proteins, polypeptides and peptides having Zcytor14 activity can be administered to a subject who lacks an adequate amount of this polypeptide, for treating inflammation and conditions such as rheumatoid arthritis. In contrast, Zcytor14 antagonists (e.g. anti-Zcytor14 antibodies) can be used to treat a subject who produces an excess of Zcytor14. Zcytor14 nucleotide sequences can also be used to provide Zcytor14 to a subject. The present sequence represents the human cytokine receptor Zcytor14 degenerate nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2076 BP; 232 A; 273 C; 399 G; 265 T; 907 other;
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              101
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SNCCNGGNYTNWSNTGYMGNYTNTGGGAYWSNGAYATHYTNTGYYTNCCN 150
                                     lValValSerLeuGluArgLeuMetGluProGlnAspThrAlaArgCysS 34
                                                                                                              NGTNYTNWSNYTNGARWGNYTNGTNGGNCCNCARGAYGCNACNCAYTGYW 100
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337 1050	1 snalathrvalasnGluProGlnAspPheGlnLeuValAlaGlyHisPro ::: :::::: aYGTNACNGTNGAYAARGTNYTNGARTTYCCNYTNYTNAARGGNCAYCCN	32 100
321 1000	4 aProAspGlnSerProCysGlnProLeuValProProValProGlnLysA ::: 1 HCCNGGNGGNGAYCCNTGYCARCCNYTNGTNCCNCCNYTNWSNTGGGARA	30 95
304 950	8 LeuAspAlaProCysCysLeuProGl	90
287 900	1 snleutrphisilealaargleuargValleuSerProGlyValtrpGln 	27 85
271 850	4 rGluargValGluPheCysProPheArgGluAspProG	25 80
25 4 800	8 AspLeuValProCysLeuCysIleGlnValTrpSer	23 75
237 750	1 euTrpTyrLysasnLeuThrGlyProGlnasnII ;::	70
221 700	4 pPheSerPheLeuLeuTyrLeuArgProValProAspAlaLeuLysSe ::	20 65
204 650	9AspGlyAspAsnValLeuLeuThTLe 	18 60
188	luLeuAsnLeuThrGlnGlnLeuPro	180 551
180 550	UG1yAlaGluValGlnIleTrpSerTyrT ::: ::: NGGINGSNGARGT!NJGNATHTGGWSNTAYA	163 501
163 500	47 ProGlyGlnSerValGlySerAlaValPheAspCysPheGluAlaSerLe	45
146 450	30 leAlaArgCysAlaLeuLeuGluValGlnValProAlaAspLeuValGln	130 401
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                                                    AYTTYYTNGGNGCNYTNCARCCNMGNGCNCCNMGNWSNGGNMGNYTN
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                                                                                                                                                                                                                                The invention relates to primate and rodent DNAX cytokine receptor subunit (DCRS) polypeptides and the polynucleotides encoding them. The receptors, or their portions may be useful as phosphate labelling enzymes to label general or specific substrates. The subunits may also be functional immunogens to elicit recognising antibodies, or antigens capable of binding antibodies. A combination, e.g., including a DCRS can be used as an immunogen for the production of antisera or antibodies capable of distinguishing between other cytokine receptor family members. A purified DCRS can also be used as a reagent to detect antibodies
                                                                                                            generated in response to the presence of elevated levels of expression, or immunological disorders which lead to antibody production to the endogenous receptor. This sequence represents human DCRS7 reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated antigenic human or mouse DNAX receptor subunit-like polypeptide useful for detecting antibodies generated in response presence of increased protein levels or immunological disorders -
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                                                                                       generic cDNA.
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alignment_scores 234 A; 267 Ç 415 G; Length: 269 924

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ATGCCNGTNCCNTGGTTYYTNYTNWSNYTNGCNYTNGGNWGNWSNCARTG 50

GGCARGCNGCNMGNYTNMGNYTNYTNACNYTNCARWSN	TGGCA	901
rpHisIleAlaArgLeuArgValLeuSerProGlyValTrpGlnLeuA	rpHi	273
NACNAAYATHTGYCCNTTYMGNGARGAYCCNMGNGCNCAYCARAAYYTN 9	NACN	851
gValGluPheCysProPheArqGluAspProGlyAlaHisArqAsnLeu 27	Val	256
AVAIPTOCYSLEUCYSIIEGINVAITTPSETLEUGIUPTOASPSETGIUA 256	uValP NGTNC	239 801
YAARAAYYTNACNGGNCCNCARATHATHACNYTNAAYCAYACNGA	YA.	751
yrLysAsnLeuThrGlyProGlnAsnIleT ::	<u>:</u> ::	223
: :: :: : NYTNWSNYTNTAYTGGAAYCARG	н	701
rPheLeuLeuTyrLeuArgProValProAspAlaLeuLysSerLeuT	н	206
GGNGAYAAYGTNCAYYTNGTNYTNAAYGTNWSNGARGARCARCA	g =	651
GlyAspAsnValLeuLeuThrLeuAspValSerGluGluGlnAspPh	ξŢ	189
YWSNATHCCNWSNTGYTGGGCNYTNCCNTGGYTNAAYGTN		601
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nAlaSerLeuGlnAlaGlnValValLeuSerPheGlnAlaTyrPr	. 3	113
:: AYGARGARAARTTYGGNGGN	െ	301
luAlaGlyLysSerAspSerGluLeuGlnGl	lu.	101
NMGNGTNGCNGTNCAYYTNGCNGTNCAYGGNCAYTGGGARGARCCNG	TNMG	251
lArgValValValHisLeuAlaValHisGlyHisTrpAlaGluProGl	₽.	84
CNGARYTNGTNYTNMGNTGYCARAARGARACNGAYTO	RACNO	201
hrGluLeuValLeuArgCysProGlnLysThrAs	: 목	67
GNGAYATHGTNCCNGCNCCNGGNCCNGTNYTNGCNCCNACNCAYYTNCA 2	ลี	151
lySerLeuGlnSerAlaProGlyProValLeuValProThrArgLeuGl 6	lys	51
NCCNGGNYTNWSNTGY	S.	101
TI AND UT AND CONTROLLED TO THE PROPERTY OF TH	er[e	יי. א
lvalvalSerLeuGluArgLeuMetGluProGlnAspThrAlaArgCysS	1Val' ::: GATH	17 51

951		100
306 1001	spGlnSerProCysGlnProLeuValProProValProGlnLysAsnAla :::	322 105
323	ThrValAsnGluProGlnAspPheGlnLeuValAlaGlyHisProAsnLe 3	339
1051	ACNGTNGAY	105
339 1060	uCysValGlnValSerThrTrpGluLysValGlnLeuGlnAlaCysSerT ::::: ::: 	356 109
356 1100	rpAlaAspSerLeuGlyProPheLysAspAspMetLeuLeuValGluMet 3 	372
373	LysThrGlyLeuAsnAsnThrSerValCysAlaLeuGluProSerGlyCy 3	00 i
1150	MGNGGNCCNCARGAYAAYMGNWSNYTNTGYGCNYTNGARCCNWSNGGNTG 1	<u> </u>
389	SThrProLeuProSerMetAlaSerThrArgAlaAlaArgLeuGlyGluG 4	24
406 1250	luLeuLeuGlnAspPheArgSerHisGlnCysMetGlnLeuTrpAsnAsp 	422 129
423 1297	AspasnMetGlySerLeuTrpAlaCysProMetAspLysTyrIleHisAr 4 ::: :::	.39 .34
439 1347	GATGT:pValLeuValTrpLeuAlaCysLeuLeuLeuAlaAlaAlaLeuP 4 :	.39
456 1397	hePhePheLeuLeuLeuLysLysAspArgArgLys4 ::: ::: SNYTNÄTHYTNYTNYTNAARAARGAYCAYGCNAARGGNTGGYTNMGNYTN 1	67
468 1447	YTNAARCARGAYGTNMGNWSNGGNGCNGCNGCNMGNGGNMGNGCNGCNYT 1	476 1496
476 1497	uLeuLeuHisSerAlaAspGlyAlaGlyTyrGluArgLeuValGlyAlaL 4	93
493 1547	euAlaSerAlaLeuSerGlnMetProLeuArgValAlaValAspLeuTrp 50 	965
510 1597	SHISG1 5	26
526 1647	LeuPheSerP 5	43 696
543 1697	roAlaAlaValAlaGlnCysGlnGlnTrpLeuGlnLeuGlnThrValGlu 5 ::: ::: ::: CNGGNGCNGTNGCNYTNTGYWSNGARTGGYTNCARGAYGGNGTNWSNGGN 1	59 746
560 1747	ProGlyProHisAspAlaLeuAlaAlaTrpLeuSerCysVa 5:	73 796
573	lLeuProAspPheLeuGlnGlyArgAlaThrGlyArgTyrValGlyValT 5	90

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eq_documentation_block:
D AAC85030 standard; cDNA; 1725 BP
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                                                                                                                                         The invention provides a new human cytokine receptor desinated Zcytor14. Caytor14 can be expressed by standard recombinant methodology. The encoding nucleic acid is useful for detecting the expression of a Zcytor14 gene in a biological sample. Anti-Zcytor14 antibodies can be used to screen biological samples in vitro for the presence of Zcytor14. Proteins, polypeptides and peptides having Zcytor14 activity can be administered to a subject who lacks an adequate amount of this polypeptide, for treating inflammation and conditions such as rheumatoid arthritis. In contrast, Zcytor14 antagonists (e.g. anti-Zcytor14 antibodies) can be used to treat a subject who produces an excess of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2047 GGNACNWSNGCNCCNGGN 2064
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                         Zcytor14. Zcytor14 nucleotide sequences can also be used to provide Zcytor14 to a subject. The present sequence represents a degenerate nucleotide sequence of a variant of the human cytokine receptor Zcytor14, designated Zcytor14-1. The variant is a truncated form of the receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytokine receptor; Zcytorl4; human; inflammation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 101; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polypeptide encoding a human cytokine receptor Zcytor14, treating inflammation e.g. rheumatoid arthritis -
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residues 1-113 of Zcytor14.
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                                                                                                                                             AYTTYYTNGGNGCNYTNCARCARCCNMGNGCNCCNMGNWSNGGNMGNYTN 1596
                                                                                                        oSerProPheArgValAlaProLeuPheSerLeuProThrGlnLeuProA 618
                                                                                                                                                                                                                     RGAYGGNGTNWSNGGNCCNGGNGCNCAYGGNCCNCAYGAYGCNTTYMGNG
                                                                                                                                                                                                                                                                                                                               nLeuGlnThrValGluPro......GlyProHisAspAlaLeuAlaA 568
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                                laPheLeuAspAlaLeuGlnGlyGlyCysSerThrSerAlaGlyArgPro 634
                                                                                                                                                                                ArgTyrValGlyValTyrPheAspGlyLeuLeuHisProAspSerValPr 601
                                                                                                                                                                                                                                                    laTrpLeuSerCysValLeuProAspPheLeuGlnGlyArgAlaThrGly 584
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                                                                       NGCNYTNTTYMGNACNGTNCCNGTNTTYACNYTNCCNWSNCARYTNCCNG
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21-JAN-2000;
25-APR-2000;
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AAH99805 standard;
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                                                                                                                                                                                                                                                          human polynucleotides encoding polypeptides, useful for and diagnosis of e.g. cancer, ulcers and HIV infection
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2000US-0552317.
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antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; antiparkinsonian; and immunostimulant. The proteins and polynucleotides encoding them can be used in gene therapy, antisense therapy and vaccine production, The proteins and polynucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,

AAH99166 to AAH99904 encode the human proteins given in AAM25225 to AAM25963. The proteins can have activities based on the tissues and cells they are expressed in, such as: antiinflammatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; central nervous system; virucide; anti-HIV; fungicide; antimatagen; cardiovascular; antianaemic; antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; dermatological; antiallergic; antiasthmatic; antiaither; cardiovascular; osteopathic; dermatological; antiallergic; antiasthmatic;

Page 659-660; 1217pp; English

neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, haematopoietic disorders, anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers, osteoporosis, severe combined immunodeficiency, eczema, allergic rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression, Alzhelmer's disease, Parkinson's disease, neurodegenerative and

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alignment_scores:
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                                                                                                                                                                                                                                                         GlySerLeuGlnSerAlaProGlyProValLeuValProThrArgLeuGl 67
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                                                   luLeuAsnLeuThrGlnGlnLeuPro.....
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                                                                                                                              TTTGGTCAGTCTGGGCTCTGTGGTATATGACTGCTTCGAGGCTGCCCT
AACAGCATCCCGAGCTGCTGGGCCCTGCCCTGGCTCAACGTGTCAGCAGA
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11-JUL-2000; 07-JUL-2 07-JUL-2000

2000US-0217487 2000US-0217496 2000US-0216647 2000US-0216880 2000US-0215135 2000US-0209467

14-AUG-2000,

2000US-0218290. 2000US-0220963. 2000US-0220964. 2000US-0224519. 2000US-0224519. 2000US-0225213. 2000US-0225214.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; reproductive system related antigen; reproductive system disorder;
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                                                                                                                                       The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention.
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298 ValThrLeuCysTrpGlnAlaProAspGlnSerProCysGlnProLeuVa
                                                                                                                       Sequence 16491 BP; 3837 A; 4251 C; 4180 G; 4223 T; 0 other:
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                                                                                                                                                                                        Disclosure; SEQ ID NO 5505; 1297pp + Sequence Listing; English.
                                                                                                                                                                                                          Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                      WPI; 2001-465570/50.
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467		467
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467 15608	YSASPATGAÖLYS	463 15559
463 15558	uAlaCysLeuLeuLeualaalaAlaLeuPhePhePheLeuLeuLeuLysL (446 15509
5 4		15474
4	AlaCysProMetAspLysTyrIleHisArgArgTrpValLenValTrpLe	430
429 15473		421 15430
ū	ATGAGCCACCGCACCCGGCCCAATTCATTTCTGTTAAGTCTCAGTTTTTC	15380
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413 15379	ThrargalaalaargLeuGlyGluGluLeuLeuGlnaspPheargSer::::::::::::::::::::::::::::::::::	398 15330
397 15329	AGGATGGTCTTGAT	15307
15306	TTTGTATTTTTAGTAGAGACGGGGTTTCACCGTGTTAGCC	15267
υ	saspaspmetLeuLeuVa]G];;metLvsThrG]vIenaspaspmhrsorv	w
64	LysValGlnLeuGlnAlaCysSerTrpAlaAspSerLeuGlyProPheLy ::: TAGCTGGGATTACAGGCGTGT	348 15225
347 15224	InLeuValAlaGlyHisProAsnLeuCysValGlnValSerThrTrpGlu ::	331 15196
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15145	GTTTTGTTTTGTTTTGA	وت د

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657 16405	rgSerAlaLeuAspSerCysThrSerSerSerg1 :: AGCCAGCCTGGATAGCTACTTCCATCCCCGGGGACTCC	643 16356
642 16355	lyCysSerThrSerAlaGlyArgProAlaAspArgValGluArgValThr	. 626 16306
626 16305	uPhéSerLeuProThrGlnLeuProAlaPheLeuAspAlaLeuGlnGlyG: ::: :::	609 16256
609 16255	GlyLeuLeuHisProAspSerValProSerProPheArgValAlaProLe	593 16206
592 16205	spPheLeuGlnGlyArgAlaThrGlyArgTyrValGlyValTyrPheAsp 	576 16156
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560 16105	ValAlaGlnCysGlnGlnTrpLeuGlnLeuGlnThrValGluPro	546 16056
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529 16005	gGluLeuSerAlaHisGlyAlaLeuAlaTrpPheHisHisGlnArgArgA 	512 15956

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69815 ! ACO96599 Rattus norvegicus cl
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145435 ! ACO26685 Homo sapiens chrom
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94 | AX350978 Sequence 12 from Pater

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2314 bp
Sequence 10 from Patent W00190358.
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627 C	610 h 2099 T	593 y 1 2049 G	577 P 1 1999 T	560 r 1949 c	543 q 1 1899 c	527 A 1849 C	510 e 	493 u 1749 G	477 I 1699 C	460 e 1 1649 T	443 ບ 1599 ສ	427 S 1549 T	410 s 1 1499 a	393 c	377 F 1 1399 F	360 e 1 1349 T	343 1 1299 G	9 -
ysserT	eSerLe	YLeuLeuHisF	heLeug	oglypr :cgggco	AlaAla GCGGCC	rgarga :Gacccc	rArgAr CCGCCG	uAlaSer	euLeuH	PuLeuLy	ValTrp	SerLeuT	SPPheAr	SerMet AGCATG	ASDASDT ACAACA	euGlyPr GGGCC	SerThr	CAÇAAG
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aGlyAr	GlnLeul CAGCTG	ProAspSerValProSerProPheArgValAlaPro 	galaTh	AlaLeui GCCCTC	lnCysG	uGlnGl GCAGGA	SerAla AGCGCG	LeuSerGlnMetProLeuArgValAlaValAspLeuTrpS 	aAspG1	ArgArg CGCAGG	ysLeuL GCCTAC	SProMe	GlnCys CAGTGT	Chrarga CGAGAG	Alcysal	SASPASP GATGAT	ysValG	 GTTGGT
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ValGluAr	spalaLe aTGCACT	eArgval	GlyVali GGGTCI	ercysva ccrace	nLeuGlr GCTCCAC	IleLeuI ATCCTT	laTrpPl CCTGGTT	IAlaval GCCGTO	ArgLeu\ CGCCTG	lyserA	aLeuPho CTTTT	Hisargi CACAGG	snAspA: ACGATG	yGluGlu AGAGGA	Glycys' GCTGT/	luMetLy AGATGA	SSerTr	HIIIII
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SFERENCE
AUTHORS
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$OCUS BC004759
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 6 Row: c Column: 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., I
A.M., Holloway, M., Telford, B, Hodgson, A., Bouck,
Muzny,D.M., Gibbs,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia De cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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Institute, 31 Center Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (21-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
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Strausberg, R.
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                    YrLeuArgProValProAspAlaLeuLysSerLeuTrpTyrLysAsnLeu
                                                                           CCTTCTGACACTGGATGTCTCTGAGGAGCAGGACTTTAGCTTCTTACTGT
                                                                                             lLeuLeuThrLeuAspValSerGluGluGlnAspPheSerPheLeuLeuT
                                                                                                                                                                                                                                uGlnAlaGlnValValLeuSerPheGlnAlaTyrProIleAlaArgCysA
ACCTGCGTCCAGTCCCGGATGCTCTCAAATCCTTGTGGTACAAAAACCTG
                                                                                                                                                         AGCTGCTGGGTCCTGGCCTCAATGTGTCTACAGATGGTGACAATGT
                                                                                                                                                                                                                                                                                                             ValGlySerAlaValPheAspCysPheGluAlaSerLeuGlyAlaGluVa-167
                                                                                                                                                                                                                                                                                                                                                    lGlnIleTrpSerTyrThrLysProArgTyrGlnLysGluLeuAsnLeuT
                                                                                                                                                                                                                                                                                                                                                                                             GTGGGTTCTGCGGTATTTGACTGTTTCGAGGCTAGTCTTGGGGCTGAGGT
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.....AspGlyAspAsnVa

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101 GluAlåGlyLysSerAspSerGluLeuGlnGluSerArgAsnAlaSerLe
                                                                                                                                                84 alargyalvalvalHisLeualavalHisGlyHisTrpAlaGluProGlu 100
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                                                                                                 GACGGAGCTGGTGCTGAGGTGTCCACAGAAGACAGATTGCGCCCCTCTGTG
                                                                                                              nThrGluLeuValLeuArgCysProGlnLysThrAspCysAlaLeuArgV
                                                                                                                                                                                                                                                   GTCGTCTCTGGAGAGACTGATGGAGCCTCAGGACACTGCACGCTGCT
                                                 TCCGTGTGGTGGTCCACTTGGCCGTGCATGGGCACTGGGCAGAGCCTGAA.
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	510	llaLeuSerGlnMetProLeuArgValAlaValAspLeuTr	
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	493	sSerAlaAspGlyAlaGlyTyrGluArgLeu	
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	476	uLeuLysLysAspArgArgLysAlaAlaArgGlySerArgTh	
·	460 1626	443 uValTrpLeuAlaCysLeuLeuLeuAlaAlaAlaLeuPhePhePheLeuL 	ב
	443 1576	427 SerleuTrpAlaCysProMetAspLysTyrIleHisArgArgTrpValle	سر
	(U F	7	<u></u>
	26	PheArqSerHisGlnCvsMetGlnLeuTrpAsnAspAspAsnMet	
	410 1476	393 oSerMetAlaSerThrArgAlaAlaArgLeuGlyGluGluLeuLeuGlnA 	ш
	393 1426	377 AsnAsnThrSerValCysAlaLeuGluProSerGlyCysThrProLeuPr	₽
	376 1376	360 euGlyProPheLysAspAspMetLeuLeuValGluMetLysThrGlyLeu 	μ'
	360 1326	343 1SerThrTrpGluLysValGlnLeuGlnAlaCysSerTrpAlaAspSerL 	
	343 1276	327 ProGlnAspPheGlnLeuValAlaGlyHisProAsnLeuCysValGlnVa 	L
	326 1226	310 ysGlnProLeuValProProValProGlnLysAsnAlaThrValAsnGlu 	<u>_</u>
	310 1176	293 SLEUPrOGIYLYSVAIThrLeuCySTrpGlnAlaProAspGlnSerProC 	ם
	293 1126	277 ArgLeuArgValLeuSerProGlyValTrpGlnLeuAspAlaProCysCy	H
	276 1076	260 ysProPheArgGluAspProGlyAlaHisArgAsnLeuTrpHisIleAla 	_
	260 1026	243 uCysIleGlnValTrpSerLeuGluProAspSerGluArgValGluPheC 	
	243 976	227 ThrGlyProGlnAsnIleThrLeuAsnHisThrAspLeuValProCysLe	

1 MetPro	Align seg 1/1	alignment_block US-09-899-471-	alignment_scores: Quality: Ratio: Percent Similarity:	BASE COUNT ORIGIN	Ö	REFERENCE 1 AUTHORS GOY TITLE Manual JOURNAL Pat	MS	seq_documentation LOCUS AX350 DEFINITION Seque ACCESSION AX350 VERSION AX350 KEYWORDS	seq_name: gb_pa	660 lycysc 1935 gcrgcr	643 nAlaLe 1885 GGCGCT	627 CysSer 1835 TGCTCC	610 heSerL 1785 TCTCCC	593 yLeuLe 1735 GCTGCT	577 PheLew 1685 TTCCTG	560 rogiyP 1637	1636	543 oAlaAl	1636	527 ArgArg
ValSerTrpPheLeuLeuSe	to: AX350978 from:	2 x AX350978	2637.00 4.938 76.504 Perc	/db_xref="taxon:32644" /note="rodent; surmised Mu 247 a 251 c 393 g 285 247 a 251 c 393 g 285	ERING CORPORATION (US) Location/Qualifiers 1. 2094 /organism="unidentif	1 (sites) Gorman,D.M. Mammalian receptor protection Patent: WO 0190358-A 12	dentified. dentified lassified.	tation_block: Ax350978 Sequence 12 from Patent Ax350978 1 GI:18616354	_Pat:AX350978	lyCysCysGluGluTrpAspLeuGlyProCysThrThrLeuGlu 	uArgSerAlaLeuAspSerC 	ThrSerAlaGlyArgProAl ACTTCCGCGGGGCGACCCGC	euProThrGlnLeuProAla ::: GCCCTCGCAGCTGCCGGCT	JHisProAspSerValProS 	31nGlyArgAlaThrGlyAr CAAGGCCGGGCGACCGGCCG	roHisAspAlaLeuAlaAla 		aValAlaGlnCysGlnGlnTr		rgIleLeuGlnGluGlyGl
rLeuAlaLeuGlyArgAsnProVa	1 to: 2094		Length: 698 Gaps: 1 ent Identity: 69.198	s musculus t * 918 c		eins; related reagents 29-NOV-2001;		2094 bp DNA li WC0190358.		67 4 197	nAlai-uArgSerAlai.euAspSerCysThrSerSerSerGluAlaProg 	CysSerThrSerAlaGlyArgProAlaAspArgValGluArgValThrGl 	heSelLeuProThrGlnLeuProAlaPheLeuAspAlaLeuGlnGlyGly :::	YLeuLeuHisProAspSerValProSerProPheArgValAlaProLeuP 	PheLeuGinGlyArgAlaThrGlyArgTyrValGlyValTyrPheAspGl 	GlyProHisaspAlaLeuAlaAlaTrpLeuSerCysValLeuProAsp 		rpLeuGlnLeuGlnThrValGlu		ArgÅrgArgIleLeuGlnGluGlyGlyValValIleLeuLeuPheSerPr
7a 17				thers		and methods		near PAT 06-FEB-2002		8	og 660 	31 643 11 2A 1884	1y 626 	1P 610 	31 593 11 3G 1734	sp 576 	1636	1P 560	1636	Pr 543

0 3	ArgValLeuSerProGlyValTrpGlnLeuAspAlaProCysCy 293 	ArgLeu	277 901
0 6	PProGlyAlaHisArgAsnLeuT CCNGGNGCNCAYMGNAAYYTNT	YSProp GYCCNT	260 851
0 0	uGluProAspSerGluArg NGARCCNGAYWSNGARMGN	uCysIl NTGYAT	243 801
0 3	LeuAsnHisThrAsj YTNAAYCAYACNGA	ThrGly	227 751
0 0	gProValProAspAlaLeuLysSerLeu NCCNGTNCCNGAYGCNYTNAARWSNYTI	yrLeuAr AYYTNMG	210 701
0 0	ThrLeuAspValSerGluGluGlnAspPheSerPheLeu ::: 	lLeuLe NYTNYT	193 651
ο ω	GGGTNYTNCCNTGGYTNAA	K .	189 601
0 8	LeuPio ! #TNCCNGAYTGYMGNGGNYTNGARGTNNGN	hrGlnG CNCARC	184 551
0 4	LysProArgTyrGlnLysGluLeuA ARCCNMGNTAYCARAARGARYTNA	IG1nI1 NCARAT	167 501
7	eralaValPheAspCysPheGluAlaSerLeuGlyAlaGluVa 16 ::	ValGlyS : GTNGGNW	151 451
	uGluValGlnValProAlaAspLeuValGlnProGlyGlnSer 15 	laLeuLe CNYTNYT	134 401
4 0	uSerPheGlnAlaTyrProTleAlaArgCysA 13 :::	uGlnAl NCARGO	117 351
0	euGlnGluSerArgAsnAlaSerLe 11 ::: ::: TNCARGARWSNMGNAAYGCNWSNYT 35	GluAla GARGCN	301
0 0	eualaValHisGlyHisTrpAlaGluProGlu 10 	alargv TNMGNG	84 251
ò	SPTOGInLySThrAspCysAlaLeuArgV 84 	nThrGl RACNGA	67 201
ō	euGlnSerAlaProGlyProValLeuValProThrArgLeuGl 67 ::: 	GlySerL ::: GGNWSNY	51 151
	YLeuSerCysHisLeuTrpAspGlyAspValLeuCysLeuPro 50 	erLeuGl :: [] SNYTNGG	34 101
Ō	uGluArgLeuMetGluProGlnAspThrAlaArgCyss 34 	lvalva GTNGT	17 51
-	50 SHASALGGALAXALAGANALAGANALAXALAXALAXALAXALAXALAXALAXALAXALAXAL	ATGCCNG	_

593	7 PheLeudinGlyArgAlaThrGlyArgTyrValGlyValTyrPheAspGl	57
1850		180
576	DHISASPAlaLeuAlaAlaTrpLeuSerCysValLeuProAsp	56
1800	:::	175
560 1750	ValGluP GTNGARC	54 170
543 1700	euPheSerPr ::: TNTTYWSNCC	52 165
526	0 erargargGluLeuSeralaHisGlyalaLeualaTzpPheHisHisGln	51
1650	:: :::	160
510	3 uAlaSerAlaLeuSerGlnmetProLeuArgValAlaValAspLeuTrpS	49
1600		155
493	7 LeuleuhisSeralaaspGlyAlaGlyTyrGluargLeuValGlyAlaLe	47
1550	:::	150
476	0 euleulyslysaspargarglysalaalaargGlySerargThralaleu	46
1500		145
460 1450	3 uValTrpLeuAlaCysLeuLeuLeuAlaAlaAlaLeuPhePhePheLeuL 1 NGTNTGGYTNGCNTGYYTNYTNYTNGCNGCNGCNYTNTTYTTYYTNY	44 140
443 1400	7 SerleuftpalaCysProMetAspLysTyrIleHisArgArgTrpValle :::	42 135
426 1350	0 spPheArgSerHisGlnCysMetGlnLeuTrpAsnAspAspAsnMetGly :::	'41 130
410	3 oSermetalaSerThrargalaalaargLeuGlyGluGluLeuLeuGlna	39
1300	::: :::	125
393 1250	7 ASNASNThrSerValCysAlaLeuGluProSerGlyCysThrProLeuPr	37 120
376 1200	0 euGlyProPheLysAspAspMetLeuLeuValGluMetLysThrGlyLeu 1 TNGGNCCNTTYAARGAYGAYATGYTNYTNGTNGARATGARAACNGGNYTN	36 115
360	3 lSerThrTrpGluLysValGlnLeuGlnAlaCysSerTrpAlaAspSerL	34
1150	:::	110
343	7 ProglnaspPheGlnLeuValAlaGlyHisProAsnLeuCysValGlnVa	32
1100		105
326 1050	0 ysginProLeuValProProValProGinLysAsnAlaThrValAsnGlu 	100
310	3 sLeuProGlyLysValThrLeuCysTrpGlnAlaProAspGlnSerProC	29
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AUTHORS
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ercent Similarity: 83.628
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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GLSLYWNQVOGPPKPRWHKNLTGPQ1ITLNHTDLVPCLCIQVWPLEPDSVRTN1CPFR
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                                                                                                                                                                                                                            DGVSGPGAHGPHDAFRASLSCVLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPV
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1gn seg 1/1 to: AX073993

from: 1

to: 2255

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271 100	rGluargValGluPheCysProPheArgGluAspProGlyAlaHisArgA	254 954
254 953	roCysLeuCysIleGlnValTrpSerLeuGftproAspSe 	် ပိ
237 903	euTrpTyrLysAsnLeuThrGlyProGlnAsnIleThrLéuasmHisThr :::	221 854
221 853	pPheSerPheLeuLeuTyrLeuArgProValProAspAlaLeuLysSerL	204 804
204 803	AspValSer ::: AATGTCTCT	189 754
188 753	luLeuAsnLeuThrGlnGlnLeuPro	180 704
180 703	uGlyAlaGluValGlnIleTrpSerTyrThrLysProArgTyrGlnLysG ::: :::	163 654
163 653	ProGlyGlnSerValGlySerAlaValPheAspCysPheGluAlaSerLe	147 604
146 603	leAl CTGC	130 554
130 553	gAsn GAAT	113 504
500	5× ⋅	101 454
100	alargValValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu:: ::	404
403	nThrigluLeuValLeuArgCysProGlnLysThrAspCysAlaLeuArgV	354
67 353	CI	304
303	erLeuGlyLeuSerCysH1sLeuTrpAspGlyAspValLeuCysLeuPro 	34 254
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                                                                                                                                         GTCTTGCTCTTCTCCCGGTGCGGTGGCGCTGTGCAGCGAGTGGCTACA
ArgTyrValGlyValTyrPheAspGlyLeuLeuHisProAspSerValPr
                                                                                        GATGGGGTGTCCGGGCCCGGGCCCACGCCCGCACGACGCCTTCCGCG
                                                                                                                                                                                           CTTGGTTTCACGCGCAGCGGCGCCAGACCCTGCAGGAGGGCGGCGTGGTG
                                                                                                                                                                                                                                                                                                                                                  CCTCGCTCAGCTGCCTGCCCGACTTCTTGCAGGGCCGGGCGCCCGGC
                                                                                                                                                                                                                                              GGCCGTAGACCTGTGGAGCCGTCGTGAACTGAGCGCGCAGGGGCCCCGTGG
                                                                                                                                                                                                                                                                                                 CGCCTGGTGGGCGCCTGGGCGTGTGCCAGCTGCCGCTGCGCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      laTrpLeuSerCysValLeuProAspPheLeuGlnGlyArgAlaThrGly 584
                                                                                                                nLeuGlnThrValGluPro......GlyProHisAspAlaLeuAlaA
                                                                                                                                                                IleLeuLeuPheSerProAlaAlaValAlaGlnCysGlnGlnTrpLeuGl
                                                                                                                                                                                                                                                          lAlaValAspLeuTrpSerArgGluLeuSerAlaHisGlyAlaLeuA 521
                                                                                                                                                                                                                                                                                                              ArgLeuValGlyAlaLeuAlaSerAlaLeuSerGlnMetProLeuArgVa 504
                                                                                                                                                                                                                                                                                                                                                                                                   GCTTTCCCTCATCCTCCTTCTCAAAAAGGATCACGCGAAAGCGGCCGCCA 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGAGTACTTACTACAAGACCTGCAGTCAGGCCAGTGTCTGCAGCTATGG. 1452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     yGluGluLeuGlnAspPheArgSerHisGlnCysMetGlnLeuTrpA 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlyCysThrProLeuProSerMetAlaSerThrArgAlaAlaArgLeuGI 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AACCTCTGTGTTCAGGTGAACAGCTCGGAGAAGCTGCAGCTGCAGGAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AsnLeuCysValGlnValSerThrTrpGluLysValGlnLeuGlnAlaCy 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SnAlaThrValAsnGluProGlnAspPheGlnLeuValAlaGlyHisPro 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aProAspGlnSerProCysGlnProLeuValProProValProGlnLysA 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       laTrpPheHisHisGinArgArgIleLeuGlnGluGlyGlyValVal 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGCTGTACTTCACTACCCAGCAAAGCCTCCACGAGGGCAGCTCGCCTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACGTCACTGTGGACAAGGTTCTCGAGTTCCCATTGCTGAAAAGGCCACCCT
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Align seg 1/1 to: AX092430

from: 1

to: 2380

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283

34 erLeuGlyLeuSerCysHisLeuTrpAspGlyAspValLeuCysLeuPro

17 282 34 332 332 382

nThrGluLeuValLeuArgCysProGlnLysThrAspCysAlaLeuArgV

432 84 GlySerLeuGlnSerAlaProGlyProValLeuValProThrArgLeuGl 67

GGGGACATCGTGCCTGCTCCGGGCCCCCGTGCTGGCGCCCTACGCACCTGCA

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BASE COUNT
ORIGIN
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Source
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LOCUS Axnaว/יים
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Ratio:
Percent Similarity:
                                                                                                                                                                                                                             TITLE
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Quality: 2339.00
Ratio: 4.118
milarity: 82.081
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AVOORANA
                                                                                                                                                                                 Genentech, Inc.
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                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                         411
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                                                                                                                                                  Location/Qualifiers
1. .2380
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/db_xref="taxon:9606"
776 c 743 g 450
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Percent Identity:
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	371	354 sSerTrpAlaAspSerLeuGlyProPheLysAspAspMetLeuLeuValG
	354 1332	338 ASnLeuCysValGlnValSerThrTrpGluLysValGlnLeuGlnAlaCy
	337 1282	321 snAlaThrValAsnGluProGlnAspPheGlnLeuValAlaGlyHisPro ::: ::::: ::: ::::: 1233 ACGTCACTGTGGACAAGGTTCTCGAGTTCCCATTGCTGAAAGGCCACCCT
	321 1232	304 aProAspGlnSerProCysGlnProLeuValProProValProGlnLysA :::
	304 1182	288 LeuAspAlaProCysCysLeuProGlyLysValThrLeuCysTrpGlnAl
	287 1132	271 snLeuTrpHisIleAlaArgLeuArgValLeuSerProGlyValTrpGln
•	271 1082	254 rGluArgValGluPheCysProPheArgGluAspProGlyAlaHisArgA
	254 1032	238 ASPLeuValProCysLeuCysIleGlnValTrpSerLeuGluProAspSe
,	237 982	221 euTrpTyrLysAsnLeuThrGlyProGlnAsnIleThrLeuAsnHisThr :::
	221 932	204 pPheSerPheLeuLeuTyrLeuArgProValProAspAlaLeuLysSerL :::::: ::: 883 CTTCGGCCTCTCCCTGTACTGGAATCAGGTCCAGGGCCCCCCAAAACCCC
·	204 882	189AspGlyAspAsnValLeuLeuThrLeuAspValSerGluGluGlnAs
	188 832	180 luLeuAsnLeuThrGlnGlnLeuPro
	180 782	163 uGlyAlaGluValGlnIleTrpSerTyrThrLysProArgTyrGlnLysG ::: :::
	163 732	147 ProGlyGlnSerValGlySerAlaValPheAspCysPheGluAlaSerLe
	146 682	130 leAlaArgCysAlaLeuLeuGluValGlnValProAlaAspLeuValGln :::
	130 632	113 gAsnAlaSerLeuGlnAlaGlnValValLeuSerPheGlnAlaTyrProI
	113 582	101 GluAlaGlyLysSerAspSerGluLeuGlnGluSerAr :::
	100 532	84 alargvalvalvalhisLeualavalhisGlyHisTrpAlaGluProGlu
	482	

2226 652 2276	1// GGGGCCCTGCAGCAGCCTCGCGCCCCCGGGTTCCGGGCGGCTCCAAGAC 637 gValGluargValThrGlnAlaLeuArgSerAlaLeuAspSerCys ::: :::: :::::
37	21 AspAlaLeuGlnGlyGlyCysSerThrSerAlaGlyArgPro
620 2176	604 heargyalalaproLeupheSerLeuproThrGlnLeuproAlapheLeu
60 4 2126	587 1G1yValTyrPheAspG1yLeuLeuHisProAspSetValProSerProP
587 2076	PheLeuGlnGlyArgA]
570 2026	557 hrvalGluProGlyProHisAspAlaLeuAlaAlaTrpLeu ::
557 1976	540 uPheSerProAlaAlaValAlaGlnCysGlnGlnTrpLeuGlnLeuGlnT
540 1926	524 HisHisGlnArgArgArgIleLeuGlnGluGlyGlyValValIleLeuLe
523 1876	507 spLeuTrpSerArgArgGluLeuSerAlaHisGlyAlaLeuAlaTrpPhe
507 1826	490 1G1yAlaLeuAlaSerAlaLeuSerGlnMetDroLeuArgValAlaValA
490 1776	474 ThralaLeuLeuLeuHisSerAlaAspGlyAlaGlyTyrGluArgLeuVa ::: :::
473 1726	468
467 1679	454 aLeuPhePhePheLeuLeuLysLysAspArgArgLys
454 1629	438 HisargargTrpValLeuValTrpLeuAlaCysLeuLeuLeuAlaAlaAl
4 ³ 7	421 snaspaspasnmetGlySerLeuTrpalaCysPrometAspLysTyrIle
421 1531	404 yGluGluLeuLeuGlnAspPheArgSerHisGlnCysMetGlnLeuTrpA
404 1482	388 GlyCysThrProLeuProSerMetAlaSerThrArgAlaAlaArgLeuGl
387 1432	371 luMetLysThrGlyLeuAsnAsnThrSerValCysAlaLeuGluProSer
1382	1333 CTTGTGGGCTGACTCCCTGGGGCCTCTCAAAGACGATGTGCTACTGTTGG

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alignment_scores:
Quality: 2339.00
Ratio: 4.118
Percent Similarity: 82.081
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ORIGIN
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OCUS AX180776
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                                                                                                                                                                                                                                                                                                                                                                           113 gAsnAlaSerLeuGlnAlaGlnValValLeuSerPheGlnAlaTyrProI 130
                             533 GATGAGGAAAAGTTTGGAGGAGCAGCTGACTCAGGGGTGGAGGAGCCTAG
                                                                                        483
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                                                                                                                   84
                                                                                                                                                         67 nThrGluLeuValLeuArgCysProGlnLysThrAspCysAlaLeuArgV 84
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                                                                                  Glu.....AlaGlyLysSerAspSerGluLeuGlnGluSerAr 113
                                                                                                                                          Homo sapiens
Eukaryota; Mettazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2380)
Chen, J., Filvaroff, E., Fonq, S., Goddard, A., Godowski, P.J.,
Grimaldi, C.J., Gurney, A.L., Li, H., Hillan, K.J., Tumas, D., van
Lookeren, M., Vandlen, R.L., Watanabe, C.K., Williams, P.M., Wood, W.I.
and Yansura, D.G.
Il-17 and il-17r homologous polypeptides and therapeutic uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2380 bp
Sequence 13 from Patent WO0146420.
AX180776
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent: WO 0146420-A 13 28-JUN-2001;
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776 c 743 g 450
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                               582
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37 13	AlaAspSerLeuGlyProPheLysAspAspWetLeuValG 	354 1333
35 13	ASnLeuCysValGlnValSerThrTrpGluLysValGliLeuGlnAlaCy 	338 1283
33 12	snAlathrValAsnGluProGlnAspPheGlnLeuValAlaGlyHisPro ::: :::	321 1233
32 12	pGlnSerProCysGlnProLeuValProProValProGlnLysA ::: ::: ::: rggggaCCCCTgCCAGCCACTGGTCCCACCGCTTTCCTGGGAGA	304 1183
30 11	LeuAspAlaProCysCysLeuProGlyLysValThrLeuCysTrpGlnAl	288 1133
28 11	snLeuTrpHisIleAlaArgLeuArgValLeuSerProGlyValTrpGln	271 1083
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25 10	ASPLeuValProCysLeuCysIleGlnValTrpSerLeuGluProAspSe	983
23 98	TyrLysAsnLeuThrGlyProGlnAsnIleThrLeuAsnHisThr :::	221 933
22 93	erPhéLeuLeuTyrLeuArgProValProAspAlaLeuLysSerL ::::: :: GCCTCTCCCTGTACTGGAATCAGGTCCAGGGCCCCCAAAACCCC	204 883
20 88	.pG1yAspAsnValLeuLeuThrLeuAspValSerGluGluGlnAs 	. 189 833
18 83	CTGCCCTGGCTCAACGTGTCA	180 783
18 78	lnLysG :: AGAAGG	163 733
16 73	lyGlnSerValGlySerAlaValPheAspCysPheGluAlaSerLe ::: :::	147
14 68	euValGln TGTGCAG	,130 633
63		583

404 yGluGlüLeuLeuGlnAspPheArgSerHisGlnCysMetGlnLeuTrpA 421

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VERSION
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                                             BC006411 2507 bp mRNA linear PRI 12-JUL-2
Homo sapiens, clone MGC:10763 IMAGE:3606276, mRNA, complete cds.
  BC006411
BC006411.1 GI:13623590
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                                           US-09-899-471-2 x BC006411
                                                                                                          Percent Similarity:
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                                                                                                        Quality: 2316.50
Ratio: 4.071
nilarity: 78.591
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This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticla Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Lisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC Project URL: http://mgc.nci.nih.gov
contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
rissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada
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Direct Submission
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37 .	221 euTrpTyrLysAsnLeuThrGlyProGlnAsnIleThrLeuAsnHisThr 2 :::
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.88	180 luLeuAsnLeuThrGlnGlnLeuPro
180 747	163 uGlyAlaGluValGlnIleTrpSerTyrThrLysProArgTyrGlnLysG 1 ::: :::
163 697	147 ProGlyGlnSerValGlySerAlaValPheAspCysPheGluAlaSerLe 1
146 647	130 leAlaArgCysAlaLeuLeuGluValGlnValProAlaAspLeuValGln 1
30	113 9AsnAlaSerLeuGlnAlaGlnValValLeuSerPheGlnAlaTyrProI 1
113 547	101 GluAlaGlyLysSerAspSerGluLeuGlnGluSerAr 1 ::::::::::::::::::::::::::::::::::
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47	67 nThrGluLeuValLeuArgCysProGlnLysThrAspCysAlaLeuArgV 8
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.7	1 MetProValSerTrpPheLeuLeuSerLeuAlaLeuGlyArgAsnProVa 1

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526 1942	509 1892	492 1842	476 1792	468 1745	1695	1645 467	46	454 1595	438 1545	421 1497	404 1448	388 1398	371 1348	354 1298	338 1248	321 1198	304 1148	288 1098
GlnArgArgArgIleLeuGlnGluGlyGlyValValIleLeuLeuPheSe :::	rpSerAtgArgGluLeuSerAlaHisGlyAlaLeuAlaTrpPheHisHis 	aLeuAlàSerAlaLeuSerGlnMetProLeuArgValAìaValAspLeuT	LeuLeuLeuHisSerAlaAspGlyAlaGlyTyrGluArgLauValGlyAl ::: 	CTCCCCATCTGTTTCTCCGGCAGCGCCCAGGGGCCGCGCGGCT	GCGGAGGGCCGCCCCCGGGGAGCCAGGCCTGTGCCAGCTCACCTCTTC	GGGGGGTGAGTGG		aLeuPhePheLeuLeuLeuLysLysAspArg.ArgLys	HisargargTrpValLeuValTrpLeuAlaCysLeuLeuLeuAlaAlaAl :: :::	SnåspåspåsnmetGlySerLeuTrpålaCysPrometAspLysTyrIle ::::: :::	yGludluLeuLeuGlnAspPheArgSerHisGlnCysMetGlnLeuTrpA 	GlyCysThrProLeuProSerMetAlaSerThrArgAlaAlaArgLeuGl 	lumetLysThrGlyLeuAsnAsnThrSerValCysAlaLeuGluProSer :: 	SSETTPAlaAspSerLeuGlyProPheLysAspAspMetLeuLeuValG 	AsnLeuCysValGlnValSerThrTrpGluLysValGlnLeuGlnAlaCy 	snālaThrValAsnGluProGlnAspPheGlnLeuValAlaGlyHisPro ::: ::::	aProAspGlnSerProCysGlnProLeuValProProValProGlnLysA 	LeuAspAlaProCysCysLeuProGlyLysValThrLeuCysTrpGlnAl
542 1991	525 1941	509 1891	492 1841	475 1791	7	1694 467	467	467 1644	454 1594	437 1544	421 1496	404 1447	387 1397	371 1347	354 1297	337 1247	321 1197	304 1147

542 rProAlaAlaValAlaGlnCysGlnGlnTrpLeuGlnLeuGlnThrValG 559

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REFERENCE
AUTHORS
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JOURNAL
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Sequence 7 from Patent WO0190358.
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Location/Qualifiers
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/note="primate; surmised Homo sapiens"
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gb_pat:AX136341
                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 2499)
Ota, T., Isogai, T., Nishikawa, T., Kawai, Y., Sugiyama,
                                                                                                                                                                                                                                                      Secretory protein or membrane protein Patent: EP 1067182-A 263 10-JAN-2001; Helix Research Institute (JP)
                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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221 908 225	500	58	147 658 163 708	113 558 130 608	84 458 101 508	51 358 67 408	34 308	8 7	ignment S-09-89 lign se	.ignmen ercent
euTrpTyrLysAsn			ProGlyGlnSerValGlySerAlaValPheAspCysPheGluAlaSerLe	gAsnAlaSerLeuGlnAlaGlnValLeuSerPheGlnAlaTyrProI	alArgValValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu :: ::	GlySerLeuGlnSerAlaProGlyProValLeuValProThrArgLeuG1 :::::: :::	TCTTTCTCTGGGGGGGCTTGTGGGGCCTCAGGACGCTACCCACTG LeuGlyLeuSerCysHisLeuTrpAspGlyAspValLeuCysLeuf	MetProValSerTrpPheLeuLeuSerLeuAlaLeuGlyArgAsnProVa	t_block: 99-471-2 x AX136341 eg 1/1 to: AX136341 from: 1 to: 2499	t_scores: Quality: 2182.00 Length: 763 Ratio: 3.974 Gaps: 10 Similarity: 71.953 Percent Identity: 58.060
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. 467 1794	LeuAlaAlaAlaAlaLeuPhePhePheLeuLeuLeuLysLysAspArgArgLy::::	451 1745
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1651	vravr Amena v Antonine menine	1651
9 0	euGluProSerGlyCysThrProLeuProSerMetAlaSerThrArgA	384 1608
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1107	CTTCCTGGTTTCCTTGACTTTGGCCTCCTCCTCTTCCTCCTTATCTTCTC	1058
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225		225
1007	TGTAGGCCGATGCCTGTGCAAAGGACGCAGTGCCATATCAGAGAGGATCC	958

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AUTHORS
TITLE
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                                                                  FEATURES
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                                                                                                                                                                             SOURCE
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                                                                                        JOURNAL
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||||::: |||||::::|||:::||||:::||||||||
|ACCCGCCCTTTTCCGCACCGTGCCCGTCTTCACACTGCCCTCCCCAACTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProAlaAspArgValGluArgValThrGlnAlaLeuArgSerAlaLeuAs
                                                                                                                                                                                                                                                                                                                                                                                                          roAlaPheLeuAspAlaLeuGlnGlyGlyCysSerThrSerAlaGlyArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ValIleLeuLeuPheSerProAlaAlaValAlaGlnCysGlnGlnTrpLe
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                                                                                                                                                                                                                                                                                               TAGCTACTTCCATCCCCGGGGACTCCCGCGCCGGGA 2428
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                                                                                                                                                                                                                                                                                                                                              CAGACTTCCTGGGGGCCCTGCAGCAGCCTCGCGCCCCGCGTTCCGGGCGG
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                                                                                                                                                                                                             1753 bp
Sequence 4 from Patent WO0104304.
AX073996
                                                                                     Human cytokine receptor Patent: WO 0104304-A 4 18-JAN-2001;
                                                                              ZymoGenetics,
                                                                                                             Presnell, S.R., Burkhead, S.K. and Pownder, S.L.
                                                                                                                                                                            human.
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       584 c
548 g
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US-09-899-471-2 x AX073996 Percent Similarity: 217 aLeuLysSerLeuTrpTyrLysAsnLeuThrGlyProGlnAsmileThrL 102 CCCTTGTGCAGTTTGGTCAGTCTGTGGGCTCTGTGGTATATGACTGCTTC 110 GlnGluSerArgAsnAlaSerLeuGlnAlaGlnValValLeuSerPheGl 2 GAGGAGCCTAGGAATGCCTCTCTCCAGGCCCAAGTCGTGCTCTCCTTCCA GluGluGlnAspPheSerPheLeuLeuTyrLeuArgProValProAspAl gTyrGlnLysGluLeuAsnLeuThrGlnGlnLeuPro....... GluAlaSerLeuGlyAlaGluValGlnIleTrpSerTyrThrLysProAr spLeuvalGlnProGlyGlnSerValGlySerAlaValPheAspCysPhe TCAACGTGTCAGCAGATGGTGACAACGTGCATCTGGTTCTGAATGTCTCT GTACGAGAAGGAACTCAACCACACAGCAGCTGCCTGCCCTGCCCTGGC GAGGCTGCCCTAGGGAGTGAGGTACGAATCTGGTCCTATACTCAGCCCAG Quality:AspGlyAspAsnValLeuLeuThrLeuAspValSer to: 1851.50 4.051 78.929 from: 1 Length: 579
Gaps: 7
Percent Identity: 64.249 : : 579 7 176 217 251 159 126 250 401 234 351 301 200 201 151 188 51

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DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
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AUTHORS
TITLE
JOURNAL
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US-09-899-471-2 x AX073995
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Percent Similarity:
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101 SNCCNGGNYTNWSNTGYMGNYTNTGGGAYWSNGAYATHYTNTGYYTNCCN 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
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                               34 erLeuGlyLeuSerCysHisLeuTrpAspGlyAspValLeuCysLeuPro 50
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                                                                                                                                       1 ATGCCNGTNCCNTGGTTYYTNYTNWSNYTNGCNYTNGGNMGNWSNCCNGT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCCGCCTTTTCCGCACCGTGCCCGTCTTCACACTGCCCTCCCAACTGC 1544
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Ratio: 3.764
milarity: 64.749
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synthetic construct
artificial sequence.
1 | (bases 1 to 2076)
| Presnell, S.R., Burkhead, S.K. and Pownder, S.L.
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Sequence 3 from Patent W00104304.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZymoGenetics, Inc. (US)
Location/Qualifiers
1. .2076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human cytokine receptor Patent: WO 0104304-A 3 18-JAN-2001;
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273 c 399 g 265 t
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304 951 321 1001	288 901	271 851	254 801	238 751	221 701	20 4 651	189 601	180 551	163 501	147 451	130 401	113 351	101 301	84 251	67 201	51 151
arcoaspiliberprocysGliproLeuValProproValProGlinLysA	LeuAspAlaProCysCysLeuProGlyLysValThrLeuCysTrpGlnAl	SnLeuTrpH1sT1eAlaArgLeuArgValLeuSerProGlyValTrpGln ::: AYYTNTGGCARGCNGCNMGNYTNMGNYTNYTNACNYTNCARWSNTGGYTN	rGluargValGluPheCysProPheArgGluAspProGlyAlaHisArgA ::::::::::: 	AspLeuValProCysLeuCysIleGlnValTrpSerLeuGluProAspSe 	euTrpTyrLysAsnLeuThrGlyProGlnAsnIleThrLeuAsnHisThr ::: 	PPheSerPheLeuLyrLeuArgProValProAspAlaLeuLysSerL 	AspGlyaspasnValleuLeuThrLeuAspValSerGluGluGlnas 	luLeuAsnLeuThrGlnGlnLeuPro	uGlyAlaGluValGlnIleTrpSerTyrThrLysProArgTyrGlnLysG ::: ::: ::: 	ProglyGlnSerValGlySerAlaValPheAspCysPheGluAlaSerLe ::: :::: :::	lealaargCysalaLeuLeuGluValGlnValProAlaAspLeuValGln 	9AsnalaSerLeuGlnalaGlnValLeuSerPheGlnAlaTyrProI ::: NAAYGCNWSNYINCARGCNCARGINGINYINWSNTIYCARGCNTAYCCNA	GluAlaGlyLysSerAspSerGluLeuglnGluSerAr::: ::: ::: ::: ::: GAYGARGARAARTTYGGNGGNGCNGCNGAYWSNGGNGTNGARGARCCNMG	alargValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu :::	nThrGluLeuValLeuArgCysProGlnLysThrAspCysAlaLeuArgV 	GlySerLeuGlnSerAlaProGlyProValLeuValProThrArgLeuGl ::::: :::: GNGAYATHGTNCCNGCNCCNGGNCCNGTNYTNGCNCCNACNCAYYTNCA
321 1000 337 1050	304 950	287 900	271 850	254 800	237 750	221 700	204 650	188	180 550	163 500	146 450	130 400	113 350	100 300	84 250	67 200

618 lapheleuAspalaLeuGlnGlyGlyCysSerT	601 OSerProPheArgValAlaProLeuPheSerLeuProThrGlnLeuProArgl	585 Argtyrvalgyvaltyrpheaspglyleuleuhisproaspgervalpr ::: 1798 WSNTAYGTNGGNGCNTGYTTYGAYMGNYTNYTNCAYCCNGAYGCNGTNCC	568 laTrpLéuSerCysValLeuProAspPheLeuGlnGlyArgaläThrGly	554 nLeuGlnThrValGluProGlyProHisAspAlaLeuAlaA	538 IleLeuLeuPheSerProAlaAlaValAlaG1 ::: :: ::	521 laTrpPheHisHisGlnArgArgArgIleLeuGlnGluGlyGlyValVal 	504 lalavalaspleuTrpSerargArgGluLeuSeralaHisGlyAlaLeuA 	488 argleüvalglyalaleualaseralaleuse 	471 lySerÅrgThrålaLeuLeuLeuHisSerAlaAspGlyAlaGlyTyrGlu ::: ::: :::: ::::	454 aLeuPhePhePheLeuLeuLeuLysLysAspArgArgLysAlaAlaAr 	438 HisargargtrpvalleuvaltrpLeualacysLeuLeuLeualaalaal 	421 snaspassmetGlySerLeuTrpalaCysPrometaspLysTyrIle ::: :::	404 yGluGluLeuLeuGlnAspPheArgSerHisGlnCysMetGlnLeuTrpA	388 GlyCysThrProLeuProSermetAlaSerTh	371 lumetLysThrGlyLeuAsnAsnThrSerValCysAlaLeuGluPr 	354 sSertrpalaaspserLeuglyProPhéLysaspaspmetLeuLeuValg ::: :::	1051 AAYYTNTGYGTNCARGTNAAYWSNWSNGARAARYTNCARYTNCARGARTG
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635 AlaAspArgValGluArgValThrGlnAlaLeuArgSerAlaLeuAspSe 651

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alignment_scores
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US-09-899-471-2 x AX350975
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Ratio: 3.625
Percent Similarity: 60.482
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                                                                                                                                            113 gAsnAlaSerLeuGlnAlaGlnValValLeuSerPheGlnAlaTyrProI 130
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351 NAAYGCNWSNYTNCARGCNCARGTNGTNYTNWSNTTYCARGCNTAYCCNA 400
                                                                        301 GAYGARGARARTTYGGNGGNGCNGCNGAYYTNGGNGTNGARGARCCNMG 350
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                                                                                                                                                                                                                                           67 nThrGluLeuValLeuArgCysProGlnLysThrAspCysAlaLeuArgV 84
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                                                                                                 Glu......AlaGlyLysSerAspSerGluLeuGlnGluSerAr 113
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Sequence 9 from Patent W00190358
AX350975
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Patent: WO 0190358 A 9 29-NOV-2001;
SCHERING CORPORATION (US)
Location/Qualifiers
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/db_xref="taxon:32644"
/note="primate; surmised Homo sapiens"
267 c 415 g 269 t 924 others
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Gaps: 7
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30 01 47 51	AlaArgCysAlaLeuLeuGluvalGlnvalProAlaAspLeuValG 	14 16 16
63	uGlyAlaGluValGlnIleTrpSerTyrThrLysProArgTyrGlnLysG ::: ::: ::: ::: ::: ::: NGGN#SNGARGTNMGNATHTGGWSNTAYACNCARCCNMGNTAYGARAARG	55
80 51	1uLeuAsnLeuThrGlnGlnLeuPro	18
01	AAYWSNATHCCNWSNTGYTGGGCNYTNCCNTGGYTNAAYGTNWSNGCNGA	55
51	pGlyAspAsnValLeuLeuThrLeuAspValSerGluGlnGlnAspPheS YGGNGAYAAYGTNCAYYTNGTNYTNAAYGTNWSNGARGARCARCAYTTYG	20
21 6	erPheLeuLeuTyrLeuArgProValProAspAlaLeuLysSerLeuTrp ::	7 2
23 51	TYrLysasnLeuThrGlyProGlnasnIleThrLeuAsnHisThrAspLe :::	23
10	uValProCysLeuCysIleGlnValTrpSerLeuGluProAspSerGluA 	85
51	rgValGluPheCysProPheArgGluAspProGlyAlaHisArgAsnLeu:::::::::::::	27 90
73	TrpHis1leAlaArgLeuArgValLeuSerProGlyValTrpGlnLeuAs	9 2
89 51	PAlaProCysCysLeuProGlyLysValThrLeuCysTrpGlnAlaProA 	μ ω
06	SpGlnSerProCysGlnProLeuValProProValProGlnLysAsnAla :::	32 10
23	ThrValAsnGluProGlnAspPheGlnLeuValAlaGlyHisProAsnLe	33
50	uCysValGlnValSerThrTrpGluLysValGlnLeuglnAFacysSerT	1 13
9 %	rpalaaspSerLeuGlyProPheLysAspAspMetLeuLeuValGluMet ::: ::: 	μ ω
50	LysThrelyLeuAsnAsnThrSerValCysAlaLeuGluProSerGlyCy:: :::	36
5 °6	SThrProLeuProSerMetAlaSerThrArgAlaAlaArgLeuGlyGluG 	4 6

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Seg_documentation_block:
LOCUS AX073998'
DEFINITION Sequence 6 f
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AX073998 1725 bp
Sequence 6 from Patent WO0104304.
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality: 1291.50
| Ratio: 3.628
| Percent Similarity: 61.592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1
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                                                                                                                                                               201 GluGluGlnAspPheSerPheLeuLeuTyrLeuArgProValProAspAl
                                                                                                                                                                                                             251 TNAAYGTNWSNGCNGAYGGNGAYAAYGTNCAYYFNGNYTNAAYGTNWSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                143 spLeuValGlnProGlyGlnSerValGlySerAlaValPheAspCysPhe 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 nAlaTyrProIleAlaArgCysAlaLeuLeuGluValGlnValProAlaA 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GARGARCCNMGNAAYGCNWSNYTNCARGCNCARGTNGTNYTNWSNTTYCA
                    euAsnHisThrAspLeuValProCysLeuCysIleGlnValTrpSerLeu
TNAAYCAYACNGAYYTNGTNCCNTGYYTNTGYATHCARGTNTGGCCNYTN
                                                                     NCCNAARCCNMGNTGGCAYAARAAYYTNACNGGNCCNCARATHATHACNY
                                                                                           aLeuLysSerLeuTrpTyrLysAsnLeuThrGlyProGlnAsnIleThrL
                                                                                                                                                                                                                                                                              NTAYGARAARGARYTNAAYCAYACNCARCARYTNCCHGCNYTNCCNTGGY
                                                                                                                                                                                                                                                                                                      gTyrGlnLysGluLeuAsnLeuThrGlnGlnLeuPro......
                                                                                                                                                                                                                                                                                                                                                        GARGCNGCNYTNGGNWSNGARGTNMGNATHTGGWSNTAYACNCARCCNMG
                                                                                                                                                                                                                                                                                                                                                                                       GluAlaSerLeuGlyAlaGluValGlnIleTrpSerTyrThrLysProAr 176
                                                                                                                                           GARGARCAYTTYGGNYTNWSNYTNTAYTGGAAYCARGTNCARGGNCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RGCNTAYCCNACNGCNMGNTGYGTNYTNYTNGARGTNCARGTNCCNGCNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  synthetic construct artificial sequence.
1 (bases 1 to 1725)
1 (pases 1 to 1725)
1 (pases 1 to 1725)
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AX073998.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human cytokine receptor
Patent: WO 0104304-A 6 18-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZymoGenetics, Inc. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ynthetic construct.
                                                                                                                                                                                                                                  .....AspGlyAspAsnValLeuLeuThrLeuAspValSer 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to: AX073998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="This degenerate sequence encodes
sequence of SEQ ID NO:5."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="N is any nucleotide."
226 c 332 g 216 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="n = A,T,C or G"
1. .1725
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/db_xref="taxon:32630"
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Gaps: 6
Percent Identity: 45.502
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251 GluProAspSerGluArgValGluPheCysProPheArgGluAspProGl

554 1346	Valalac GTNGCNY	538 .297
537 1296	LaTrpPheHisHisGlnArgArgArgIleLeuGlnGluGlyGlyValVal	521 247
521 1246	lalavalaspleutrpserargargGluLeuseralaHisGlyalaLeua 	504 197
504 1196	ArgLeuVaiGlyAlaLeuAlaSerAlaLeuSerGlnMetProLeuArgVa	488 147
487 1146	laLeuLeuHisSerA 	471 097
471 1096	YTNMGNYTNYTNAARCARGAYGTNMGNWS	467 047
467 1046	aAlaAlaLeuPhePhePheLeuLeuLys 	451 997
450 996	SPLYSTYTIleHisArgArgTrpValLeuValTrpLeuAlaCysLeuLeu ::: ::: AYAARTAYATHCAYAARMGNTGGGCNYTNGTNTGGYTNGCNTGYYTNYTN	434 947
434 946	tGlnLeuTrpAsnAspAspAsnMetGlySerLeuTrpAlaCysProMetA :: ::	417 900
417 899	GlyGluGluLeu GGNGARTAYYTN	401 850
4 00 849	GlyCysThrProle GNTGYACNWSNYT	384 800
384 ⁻ 799	uValGluMetLysThrGlyLeuAsnAsnThrSer ::::: NYTNGARACNMGNGGNCCNCARGAYAAYMGNWSN	367 750
367 749	uGlyProPhe NGGNCCNYTN	351 700
350 699	yHisProAsnLeuCysVal	334 676
334 675	OGIDLYSASDALATDIVALASDG LUPTOGIDASPPheGID :: :: ::: ::: NTGGGARAAYGTNACNGTNGAY	651
5 1	ysTrpGlnAlaProAspGlnSerProCysGlnProLeuValProProV	301
300 600	Leuaspalaprocyscysle YTNGAYGCNCCNTGYWSNYT	284 551
284 550	yAlahisArgAsnLeuTrphisIleAlaArgLeuArgValLeuSerProG ::: ::: ::: ::: NGCNCAYCARAAYYTNTGGCARGCNGCNHGNYTNHGNYTNYTNACNYTNC	267 501
000	GAINCHGAI MGNGANGAI CUNNG	

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VERSION
KEYWORDS
                                             COMMENT
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TITLE
                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   618 laPheLeuAspAlaLeuGlnGlyGlyCysSerThrSerAlaGlyArgPro 634
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                                                                                                                                                                      Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, Br., Heaford, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lakocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Lockak, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurt, A., McKernan, K., McPheeters, R., McCarthy, M., McEwan, P., McGurt, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., & Cennor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Fisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Stonge-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfave, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassillev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zalnoun, J., Zimmer, A., and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARGARMGNGCNGARCARGINWSNMGNGCNYINCARCCNGCNYINGAYWS 1646
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F., Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Colge,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dogdge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            166620 bp DNA linear. HTG 06-MAY-2001
Hómo sapiens chromosome 3 clone RP11-481H17 map 3, WORKING DRAFT
SEQUENCE, 22 unordered pieces.
Submitted (01-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 26, 2000 this sequence version replaced gi:7132995. All repeats were identified using RepeatMasker:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 | (bases 1 to 16620)
Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens chromosome 3, clone RP11-481H17
                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens chromosome 
Unpublished
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reads
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http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently consists of 22 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality co.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Consensus quality: 156369 bases at least Q40 Consensus quality: 161786 bases at least Q30 Consensus quality: 163606 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing vector: M13; M77815; 95% of reads
Sequencing vector: Plasmid; n/a; %-0.f%% of reads
5.05173463177115Chemistry: Dye-terminator Big Dye; 100% of
                                                                                                                       100511 100610: gap of 100 bp 100611 111192: contig of 10582 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insert size: 156000; agarose-fp
Insert size: 164520; sum-of-contigs
                                                                                     111193 111292: gap of 100 bp
1111293 124816: contig of 13524 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality coverage: 4.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center clone name: 481_H_17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center project name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                         66774 66873: gap of 100 bp
66874 76191: contig of 9318 bp in length
                                                                      24817 124916: gap of
                                                                                                                                                              76192 76291: gap of 100 bp 76292 100510: contig of 24219 bp in
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15281 25380: qa
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5555 5654: gap of 100 bp
5655 6844: contig of 1190 bp in length
6845 6944: gap of 100 bp
6945 8557: contig of 1613 bp in length
8558 8657: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                      26 33525:
                                                                                                                                                                                                                                                                   8 59897:
                                                                                                                                                                                                                                                                             1 52610: gap of 100 bp
1 59797: contig of 7187 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13527: gap of 1
17090: contig of
                                                                                                                                                                                                                                                                                                                                                                                                                            29666: gap of 100 bp
33425: contig of 3759
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                                                                                                                                                                                                                                                                                                                    179: gap of 100 bp 52510: contig of 7631 l
                                                                                                                                                                                                                     66773: contig of 6876 bp in length
                                                                                                                                                                                                                                                                                                                                                      79: gap of 100 bp
44779: contig of 7400 bp in
                                                                                                                                                                                                                                                                                                                                                                                     25: gap of 100 bp
37279: contig of 3754 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90: gap of 1
20876: contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47: gap of 1
13427: contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7: gap of 100 bp
11247: contig of 2590 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29566
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                                                                                                       alignment_block
                                                                                                                                        Quality:
Ratio:
Percent Similarity:
                                            Align seg 1/1
                                                                                    US-09-899-471-2 x AC024612
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alignment_scores:	BASE COUNT 42182 ORIGIN	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature		misc_feature		-	FEATURES	
	CLONE_end:!/ vector_side:right" 82 a 40159 c 39756 g 424@ t 2102 others	U 4- U	"assembly_f	"assembly_fragment 142057	e="assembly_fragment 93124816	"assembly_f	"assembly_fragment .100510	e="assembly_fragment 476191	"assembly_fragment .66773	"assembly_fragment .59797	.52510	"assembly_fragment .44779	.37279	.33425	.29566	/note≈"assembly_tragment 2097725280	/note="assembly_r 1719120876	/note="assembly_tragment 1352817090	/note="assembly_tragment" 1134813427	/note="assembly 8658. 11247	/note="assembly_tragment 69458557	vector_side:left" 56556844	"assembly_end:SP6		/chromosome="3" /map="3"	/organism="Homo sapiens" /db_xref="taxon:9606"	158044 166620: contig of 8577 bp in length. Location/Qualifiers	

298 ValThrLeuCysTrpGlnAlaProAspGlnSerProCysGlnProLeuVa

to: AC024612

from: 1

to: 166620

692.50 2.663 55.319

Length: 470
Gaps: 14
Percent Identity: 39.574

	o − ≥
uAlaSe GGCGTC	479 isSerAlaAspGlyAlaGlyTyrGluArgLeuValGlyAlaLeuAlaSer
LeuLeuH { : CTCCTCT	468AlaAlaArgGlySerArgThrAlaLeuLeuLeuH
CCCATCT	AGCCAGGCCTGTGCCAGCTCACCTCTTCCCT
	467
	72663 ACAGGACGTCCGCTCGGGGGGGGTGAGTGGGGAGCAAGCGTTGGGGGGGG
TCTTGA	13 ACTGGCTGCCTCCGCCCCTCTCCCCTAACAGGGTGGC
:	467
CGAGCTC	72563 GGACCAGAGTGGCTGTGGGAGTTCTCCGAGGGAAAGCGGCGGCCG
:	467
TGGGGGA	463 ysaspargarglys
LeuLys CTCAAA	446 uAlaCysLeuLeuLeuAlaAlaAlaLeuPhePhePheLeuLeuLeuLysL
alTrpI TGTGGC	430 AlaCysProMetAspLysTyrIleHisArgArgTrpValLeuValTrpLe
rLeuTr	421ASDASPASDASMETGlySerLeuTr
LeuTrp :::::: GTTTTT	414HisGlnCysMetGlnLeuTrp.
rgSer. ::: TAAAGG	398 ThrargalaalaargLeuGlyGluGluLeuLeuGlnaspPheargSer. ::: 2284 TCGTGATCTGCCCGCCTCGGCCTCCCGAAGTGCTGGGATTATATAAAGG
rMetAlaSer ::: ::: .GTCCTGACC	381 alCysAlaLeuGluProSerGlyCysThrProLeuProSerMetA
ThrSerV::: 	364 SASPASPMETLEULEUVALGLUMETLYSThrGlyLeuAsnAsnThr ::::::
roPheLy	348 LysValGlnLeuGlnAlaCysSerTrpAlaAspSerLeuGlyProPhe :::
rTrpGlu GAG	331 lnLeuValAlaGlyHisProAsnLeuCysValGlnValSerThrT
AspPheG CGAGTTC	314 1ProProValProGlnLysAsnAlaThrValAsnGluProGlnAspPheG ::: ::::::: :::::::::::::::::::::::
CAGGCT	72050 GTTTTGTTTTGTTTTGAGAGGAGTCTCACCCTGTCGCCCAGGCTG

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REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
LOCUS AC007783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: gb_pr:AC007783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73260 CTCGCGCCCCGCGTTCCGGGCGGCTCCAAGAGAGAGCGGAGCAAGTGTCC 73309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               643 GlnAlaLeuArgSerAlaLeuAspSerCys.....ThrSerSerSerGl 657
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                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 16865)

Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,

Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J.,

Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J.,

Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C.,

Burich, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F.,

Carter, M., Cavazos, S.R., Chacko, J., Chaevez, D., Chen, G., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C.,

Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C.,

Dany, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H.,

Dugan, Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C.,

Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J.,

Foster, P., Frantz, P., Gabisl, A., Gao, J., Garcia, A., Garner, T.,

Garba, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S.,

Hamilton, K., Harris, C., Harris, K., Hart, M., Haves, A.,

Hernandez, J., Hernandez, O., Hongson, A., Hongs, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCACGGCCCGCACGACGCCTTCCGCCTCGCCTCAGCTGCTGCTGCCCG 73109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGCGCCGGGA 73369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTTCACACTGCCCTCCCAACTGCCAGACTTCCTGGGGGCCCTGCAGCAGC 73259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGGCTGCTCCACCCGGACGCCGTACCCGCCCTTTTCCGCACCGTGCCCGT 73209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlyLeuHisProAspSerValProSerProPheArgValAlaProLe 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTTCTTGCAGGGCCGGCGCCCGGCAGCTACGTGGGGGCCTGCTTCGAC 73159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTGGCGCTGTGCAGCGAGTGGCTACAGGATGGGGTGTCCGGGGCCCGGGGC 73059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ValAlaGlnCysGlnGlnTrpLeuGlnLeuGlnThrValGluPro.... 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gGluLeuSerAlaHisGlyAlaLeuAlaTrpPheHisHisGlnArgArgA 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lyCysSerThrSerAlaGlyArgProAlaAspArgValGluArgValThr 642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens 3 BAC CTB-140019 complete sequence. AC007783
He,X., Hernandez,J., Hernandez,O., Hodgson,A., Holloway,C., Hollins,B., Homsi,F., Howard,S., Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Jol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC007783.26 GI:16572920
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            op DNA linear PRI 03-NOV-2001
(Cal Tech Human BAC Library B)
   ., Huber,J.,
Johnson,R.,
                                                                                                                    Gunaratne, P., Hale, S.
                                                                Hogues, M.,
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                             Hulyk, S.,
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Nelson,D., Newtson,J., Newtson,N., Nguyen,A., Nguyen,N., Nguyen,N., Nguyen,A., Nguyen,N. Direct Submission
Submitted (03-NOV-2001) Human Genome of Molecular and Human Genetics, Bayl Baylor Plaza, Houston, TX 77030, USA Submitted (01-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA Direct Submission
Submitted (11-JUN-1999) Molecular and Human Genetics, Baylor
College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
(bases 1 to 168665) Worley, K.C. gc-help@bcm.tmc.edu On Nov 1, 2001 this sequence version replaced gi:16519453. INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email Direct Submission Worley, K.C. Worley, K.C Unpublished Direct Submission Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, L., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Moore,S., Morgan,M., Moorish,T., Morris,S., Moser,M., Neal,D., Joudah, S., Karlsson, E., (bases 1 to 168665) nome Sequencing Baylor College Center, Department of Medicine, One

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are o sequenced and submitted once, so the sequence for the remainder the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing clones are only

COMMENT

REFERENCE

AUTHORS

TITLE JOURNAL

REFERENCE

AUTHORS TITLE

JOURNAL

AUTHORS

TITLE

JOURNAL

TITLE JOURNAL

ANNOTATION OF FEATURES:
STSs are identified using ePCR (Genome of a local database that includes entries local mapping efforts. from 7:541-550) searches dbSTS, GDB, and

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

cccgcctnnc(a)ncccaaggnn ccgcctnnca(n)cccaaggnnt nncancccaa(g)gnntngggnt

nccccgcctn(n)cancccaagg

nnccccgcct(n)ncancccaag tcggnnnnnn(c)cccgcctnnc

ancccaaggn(n)tngggntann

cacccaaagt(g)ctgggattac tgccacccaa(a)gtgctgggatcccacccaaag(t)gctgggatta ccgccttgcc(a)cccaaagtgc

cancccaagg(n)ntngggntan

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality

Reports quality at URL: standards of lowest quality individual bases and measures of base are listed below. Description of the metrics can be found http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation. estimated error rate less than 1 per 10,000 bases

Contig length: Phrap values in estimate: QUALSTAT-REPORT-----Summary Statistics

Average error rate (BCM-Phrap estimate): Fraction of Phrap values less than 40 : Number of consensus changing edits: Number of consensus changing Number of N's in consensus:

166919 9.71965e-05 0.0295473 168665

ition ccgnnctcgg(n)nnnnncccgc cgnnctcggn(n)nnnncccgcctn gnnctcggnn(n)nnncccgctn nnctcggnnn(n)nncccgcctn nctcggnnnn(n)ncccgcctn ctcggnnnn(n)ccccgcctnn nccccgnnct(c)ggnnnnnnccc gtctccannc(c)ccgnnctcgg nngtctccan(n)ccccgnnctc ncnannnngt(c)tccanncccc canannntna(n)cnannnngtc
nannntnanc(n)annnngtctc tgcacaccac(n)acgcccggnt cnacgcccgg(n)taattttttg nnccccgnnc(t)cggnnnnnnc canneceegn(n)eteggnnnnn ccannececg(n)neteggnnnn nnngtctcca(n)nccccgnnct nannnngtct(c)cannccccgn cnannnngtc(t)ccannccccg ancnannnng(t)ctccannccc ntnancnann(n)ngtctccann nntnancnan(n)nngtctccan nnntnancna(n)nnngtctcca gntttcanan(n)ntnancnann cgggntttca(n)annntnancn cgcntcccgg(n)ttcatgccat tcatgccatt(n)tcntgcctca tccanncccc(g)nnctcggnnn tnancnannn(n)gtctccannc ttcanannnt(n)ancnannnng nttcanann(n)tnancnannn tagagacggg(n)tttcanannn agtagcnggg(n)ctacaggtgc tcccagtagc(n)gggnctacag ctggagtgca(n)tggcgcgatc Original+Context edits cctgacctcg(t)gatctgcccgc ctcgtgatct(g)cccgccttgcctgcccgcct(t)gccacccaaa acctcgtgat(c)tgcccgccttgcctcgtgatc(t)gcccgccttg tgacctcgtg(a)tctgcccgcc gacctcgtga(t)ctgcccgcct caatctcctg(a)cctcgtgatc atctcctgac(c)tcgtgatctg tctcctgacc(t)cgtgatctgc ctcctgacct(c)gtgatctgcc ggtctcaatc(t)cctgacctcg
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ggtttcacag(t)gttagccaag ccacgcccgg(c)taattttttg
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657 uAlaProGly 660 ||||||||| 98638 CGCGCCGGGA 98629

98688 CGGGCCCTTCAGCCAGCCCTGGATAGCTACTTCCATCCCCGGGGACTCC 98639

Page 25

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; ORGANISM: Mouse
US-09-188-930-226
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-103-840A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A:
CURRENT FILING DATE: 1998-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             224 LysasnLeuThrGlyProGlnAsnIleThrLeuAsnHisThrAspLeuVa
                                                                                                                                                                                                                                                                                                                               240 lProCysLeuCysIleGlnValTrpSerLeuGluProAspSerGluArgV :||||||:::||||||::: |||
                                Lys \texttt{AsnAlaThrValAsnGluProGlnAspPheGlnLeuValAlaGly}...
                                                                       GGCAGGACCCACTCACACCCTGCGAAACCCTT.........
                                                                                                                                                   pGlnLeuAspAlaProCysCysLeuProGlyLystelThrLeuCysTrpG
                                                                                                                                                                                                                                                           TrpHisIleAlaArgLeuArgValLeuSerProGly......ValTr
                                                                                                                                                                                                                                                                                              GCAAAAAGTGTCCCTTCCAGAGCTGGCCTGAAGCTTATGGCTCAGACTTC
                                                                                                                                                                                                                                                                                                                                                                                        GCCCTGCATGTGCATAGAGGCCTCCTACCTGCAAGAGGACACTGTGAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAAATTGTGTCTGGAGGCCACACTGTAGACCTGCCTTATGAATTCCTTCT
CCCAACGCCACAGCACAGGAGTCAGAAGGATGGTATATCCTGGAGAATGT
                                                                                                              lnAlaProAspGlnSerProCysGlnProLeuValProProValProGln
                                                                                                                                                                                                                                 TGGCAGTCAATACGCTTCACTGACTACAGCCAGCACAATCAGATGGTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
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Identity:
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	634	lnGlyGlyCysSerThrSerAla	624
	624 1765	7 aProLeuPheSerLeuProThrGlnLeuProAlaPheLeuAspAlaLeuG 	607 1716
	607 1715	PheAspGlyLeuLeuHisProAspSerValProSerProPheArgValAl :::	591 1666
	590 1665	euProAspPheLeuGlnGlyArgAlaThrGlyArgTyrValGlyValTyr ::: ::: CTCCACGTCCGCTG	574 1640
	574 1639	rvalGluProGlyProHisAspAlaLeuAlaAlaTrpLeuSerCysValL:	557 1590
	557 1589	PheSerProAlaAlaValAlaGlnCysGlnGlnTrpLeuGlnLeuGlnTh :::::: :::	541 1564
•	540 1563	isHisGlnArgArgArgIleLeuGlnGluGlyGlyValValIleLeuLeu ::: ::: 	524 1514
	524 1513	PLEUTIPSETATGATGGluLeuSeTAlaHisGlyAlaLeuAlaTipPheH	507 1464
	507 1463	AlaSerAlaLeuSerGlnMetProLeuArgValAlaValAs ::	494 1414
	493 1413	PeuLeuHisSerAlaAspGlyAlaGlyTyrGluArgLeuValGlyAlaLeu :::	477 1364
	477 1363	ULEULYSLYSASPARGARGLYSAlaAlaArgGlySerArgThrAlaLeuL	460 1327
	460 1326	5TrpLeuAlaCysLeuLeuLeuAlaAlaAlaLeuPhePhePheLeuLe ::: :: 6 CCTTACCCTACTCAGCTGTTGCTC	445 1303
	444 1302	spLysTyrIleHisArgArgTrpValLeuVal	434 1261
	434 1260	7 tGlnLeuTrpAsnAspAspAsnMetGlySerLeuTrpAlaCysProMetA : ::: ::::: CCTGGTGTGGAGGTCAGAT	417 1242
	417 1241	5 GluLeuLeuGlnAspPheArgSerHisGlnCysMe :::	406 1192
	405 1191	ThrProLeuProSerMetAlaSerThrArgAlaAlaArgLeuGlyGlu :::	390 1142
	389 1141	5 yLeuAsnAsnThrSerValCysAlaLeuGluProSerGlyCys	375 1092
	375 ·	9 SerLeuGlyProPheLysAspAspMetLeuLeuValGluMetLysThrGl	359 1045
	358 1044	0 InLeuGlnAlaCysSerTrpAlaAsp :: ::: 5 GCCACGTTGAATGTCCCCACCAGAGTGGCTCTCTCCCATCCTGGACTGTG	350 995

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seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-620-694A-1
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                                                                                                                                                                                                                                                                          TELEFAX: (206)
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1866 TGCCAAAGATGACTACCAAGGCTCAACCAATAGTCCC 1902
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CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/620,694A
FILING DATE: 21 MARCH 1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          647 rAlaLeuAspSerCysThrSerSerSerGluAlaPro 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        635 AlaaspargValGluargValThrGlnAla.....LeuArgSe 647
                                          FEATURE:
                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 3288 base pair
TYPE: nucleic acid
                                                                                                ORIGINAL SOURCE:
                                                                                                                    MOLECULE TYPE: CI
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 51 Unit CITY: Seattle STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/538,765
EILLING DATE: 7 AUGUST 1995
CLASSIFICATION: 435
                                                               STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 98101
                                                                                                                                                                              STRANDEDNESS: Si
                                                                                                                                                                                                                                                                                                                                                                      NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION:
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|5869286
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                                                             HVS13 receptor
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51 University Street
CDS
121..2715
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alignment_scores: Quality:

174.50

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402 ArgLeuGlyGluGluLeuLeuGlnAspPheArgSerHisGlnCysMetGl 418	
387SerGlyCysThrProLeuProSerMetAlaSerThrArgAlaAla 401 ::: :::	
778 778 372 tLysThrGlyLeuAsnAsnThrSerValCysAlaLeuGluPro 386	
56 TrpAlaAspSerLeuGlyProPheLysAspAspMetLeuLeuValGluMe 3 76 mcc	
346TrpGluLysValGlnLeuGlnAlaCysSer 355	~ (.)
676 GAGGACAGCAAGATGAAGATGACCTCATGCGTGAGCCTCAGGCAGCCT 725	
ProGinAspPheGinLeuValAlaGlyHisProAsnLeuCysValGlnVa 3 :::::: :::	
	. .
294 LeuProGlyLysValThrLeuCysTrpGlnAlaProAspGlnSerProCy 310 ::: ::: 583 CAGGAGTATGAAGTGACTGTT	(D. N.
278 euArgValLeuSerProGlyValTrpGlnLeuAspAlaProCysCys 293 ::: ::::: 560 GCCACTTTGTGGTAGATCCTGGC	10. 1
261 oPheArgGluAspProGlyAlaHisArgAsnLeuTrpHisIleAlaArgL 278 ::: ::::::::::::::::::::::::::	(7. A)
254ValGluPheCysPr 261 :::	
248 rpSerLeuGluProAsp	
66	
224 LysasnLeuThrGlyProGlnAsnIleThrLeuAsn 235	
lgn seg 1/1 to: US-08-620-694A-1 from: 1 to: 3288	Align
lignment_block: US-09-899-471-2 x US-08-620-694A-1	align
Ratio: 0.687 Gaps: 28 rcent Similarity: 43.643 Percent Identity: 20.619	Perc

	6 rgSerÅlaLeuAspSerCysThrSerSerSerGluAlaPro 659	64
646 1835	9 rSeralaGlyArgProAlaAspArgValGluArgValThrGlnAlaLeuA :	629 . 1786
629 1785	3 LeuGln	623 1736
,622 1735	6 lAlaproLeuPheSerLeuPro.ThrGlnLeuProAlapheLeuAspAla :::: 7H	606 1686
606 1685	TyrPheAspGlyLeuLeuHisProAspSerValProSerProPheArgVa ::: ::: T :::: T :::: T :::: T ::::: T ::::::::	590 1636
589 1635	3 alleuProAspPheLeuGlnGlyArgAlaThrGlyArgTyrValGlyVal ::	573 1586
573 1585	nThrValGluProGlyProHisAspAlaLeuAlaAlaTrpLeuSerCysV ::: ::: ::::: :::::::::::::::	556 1546
556 1545	TGGGCTGAGCCTGCTGT	543 1507
542 1506	8 leLeuleupheSer	538 1457
538 1456	1 aTrpPheHisHisGlnArgArgArgIleLeuGlnGluGlyGlyValValI	521 1407
521 1406		505 1357
504 1356	euValGlyAlaLeuAlaSerAlaLeu ::: ::: TGGTCCTAAAGTTCGCCCAGTTCCTG	489 1307
489 1306		473 1257
1256	ATCAATGGCATCTTGCCCCGTAGCAGACCTGACTCCCC	1207
472	2	472
472 1206	0LeuLeuLysLysAspArgArgLysAlaAlaArgGlySer	460 1157
459 1156	6 uAlaCysLeuLeuLeuAlaAlaAlaLeuPhePhePheLeu	446 1107
446 1106	2 ProMetAspLysTyrIleHisArgArgTrpValLeuValTrpLe	432 1060
1059	0 ACCCTGTGACTGTGCCCTGCCCAGTAATCTCAAATACCACAGTTCCCAAG	1010
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seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-022-255-1
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                                                                                                                                                                                                                                              NAME/KEY:
LOCATION:
S-09-022-255-1
                                        lign seg 1/1 to: US-09-022-255-1
                                                                           IS-09-899-471-2 x US-09-022-255-1
                                                                                                ignment_block:
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                                                                                                                                ercent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3288 base pairs
TYPE: nucleic acid
224 LysAsnLeuThr.....GlyProGlnAsnIleThrLeuAsn..... 235
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TOPOLOGY: line
MOLECULE TYPE: c
HYPOTHETICAL: NC
ANTI-SENSE: NO
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MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
ORGANISM: Mou
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APPLICATION NUMBER: USSN 08/620,694
FILING DATE: 21 MARCH 1996
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NTTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
RELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 51 Unit CITY: Seattle STATE: WA COUNTRY: USA
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPLICATION NUMBER: USSN 08/410,535
ILING DATE: 23 MARCH 1995
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Ratio:
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51 University Street
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Fanslow, William
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Gaps: 28
Percent Identity: 20.619
                                      from: 1 to: 3288
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431		431
A 95	TGTCACATTCACTCTAAGCAAGTTTCAC	0
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	uGlyGluGluLeuLeuGlnAspPheArg	0
TTG 859	AGGTCCTGCTGGAAAGTTTCTCCGACTCAGAGAAGACACCACAGCTG	810 CC
laAla 401	lyCysThrProLeuProSerMetAlaSerThrArgA	387
CTA		779
38	sThrGlyLeuAsnAsnThrSerValCysAlaLeuGluPr	2
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1 MG 373	 	356 77
sSer 355 ::: CGAG 775	TIPGITILYSVAIGINLEUGINALOCYS	346 726 TTG
CCT	AGCAAGATGAAGATGACTACCTCATGCGTGAGCTCAGG	76
345	Serhhr	343 1S
ACTGT 675	AGATCATCTTTGTGCCTGA	653
lnVa 343	oGlnAspPheGlnLeuValAlaGlyHisProAsnLeuCysValG	327 Pr
TCCA 652	: ::: :::: TGGGGACCCAAACCACA	604 .
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roCy 310	ysvalThrLe	294 Le
582	GCCACTTTGTGGTAGATCCTGGC	560 G
sCys 293	ValLeuSerProGlyValTrpGlnLeuAspAlaProCy	278 eı
TTCA 559		510 GT
ArgL 278	heArgGluAspProGlyAlaHisArgAsnLeuTrpHisIleAla	261 oi
.CA 50	::: GAACACCAATGAGCGGCTGTGTGTCAAGTTC	463 To
ysPr 261	GluArgValGluPheC	254
GCTG 462	GCCAGCATCCTGTACCTCGAGGGTGCAGA	413 G
253	erLeuGluProA	248 r
Valī 248 	TTCCTCTACCCAGCACGAGAATTAGTCCCTGTGTTGCATGTTGAG	236 . 366 Tr
GIGT 365	<u>ACCCCGTCTTCCCCAAAAACATCTATATC</u>	10
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Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1157 CCTGGAGGCTTTCTGGCGCCCGATCAAGAGAAACATGGTGATGACTCCAAA 1206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1060 CCAGTTGCAGACTACATT...CCCCTGTGGGTGTATGGCCTCATCACACT 1106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           556 nThrValGluProGlyProHisAspAlaLeuAlaAlaTrpLeuSerCysV 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   505 AlaValAspLeuTrpSerArgArgGluLeuSerAlaHisGlyAlaLeuAl 521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alLeuProAspPheLeuGlnGlyArgAlaThrGlyArgTyrValGlyVal 589
                                                                                                                                                                          GGCTGTGCTTAGGTTCCAGGAGTGGCAAACCCAGTGCCCCG 1876
                                                                                                                                                                                                                    rgSerAlaLeuAspSerCysThrSerSerSerGluAlaPro
                                                                                                                                                                                                                                                             CTCACAGGGGACAATTACCTGCAGAGCCCTAGTGGCCGGCAGCTCAAGGA 1835
                                                                                                                                                                                                                                                                                                       rSerAlaGlyArgProAlaAspArgValGluArgValThrGlnAlaLeuA 646
                                                                                                                                                                                                                                                                                                                                                                                            CACCTCCAGGTACCCACTCATGGACAGATTTGAGGAGGTTTACTTCCGGA 1735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TyrPheAspGlyLeuLeuHisProAspSerValProSerProPheArgVa 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ......AAGCCTGCT...GGGGACCTTTTCACTGCAGCCATGAACATGA 1585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGCTGAGCCTGTCCAGCTACGGTGTGACCACTGG...... 1545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCATCCTGTGTTCCCGAGGCACCCCAAGCAAAGTGGAAAGCTATCTTGGGT 1506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   leLeuLeuPheSer.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGGGTGAGCCGACAGAAGCAGGAGATGGTGGAGAGCAACTCCAAAATCA 1456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aTrpPheHisHisGlnArgArgIleLeuGlnGluGlyGlyValValI 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGGTCCTAAAGTTCGCCCAGTTCCTGATCACTGCCTGTGGCACTGAAGTA 1356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          euValGlyAlaLeuAlaSerAlaLeu...SerGlnMetProLeuArgVal 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGGAAGGTCTGGATCGTCTACTCGGCCGACCACCCCCTCTATGTGGAGG 1306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATCGCCATTCTGCTGGGGATCTGTCATCGTGCTGATCATCTGTATGA 1156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .........ProAlaAlaValAlaGlnCysGlnGlnTrpLeuGlnLeuGl 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ArgThrAlaLeuLeuHisSerAlaAspGlyAlaGlyTyrGluArgL 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .....LeuLeuLysLysAspArgArgLysAlaAlaArgGlySer... 472
Yao, Zhengbin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                472
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alignment_block

Percent Similarity:

Percent Identity:

20.619

Ratio:

US-09-899-471-2

x US-09-022-696-1

Align seg 1/1

to: US-09-022-696-1

from: 1

to: 3288

ï

316 AAAAACCTGACCCCGTCTTCCCCAAAAAACATCTATATCAATCTTAGTGT 365

.....HisThrAspLeuValProCysLeuCysIleGlnValT 248

224 LysAsnLeuThr.....GlyProGlnAsnIleThrLeuAsn......

366 TTCCTCTACCCAGCACGAGAATTAGTCCCTGTGTTGCATGTTGAG...T

412 253

rpSerLeuGluProAsp

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alignment_scores:
Quality:
                                                                                              ;
US-09-022-696-1
                                                                                                                                                                                                                                                                                                             NAME: Perkins, Patricia Anne REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX; (206)
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                           FEATURE:
                                                                                                                                                                                        ORIGINAL SOURCE:
                                                                                                                                                                                                         HYPOTHETICAL:
ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: Seattle
                                                                                                                                                          STRAIN: | HVS13 receptor
                                                                                                                                                                           ORGANISM:
                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operation
                                                                                                                              NAME/KEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: UZIP: 98101
                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                    ENGTH:
                                                                                                                                                                                                                                                                                   nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SYSTEM: Apple Operating System 7.5.
Microsoft Word for Apple, Version 6
                                                                                                                                                                                                                                                        linear
                                                                                                              121..2715
                                                                                                                                                                          Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunex Corporation
174.50
0.687
43.643
                                                                                                                                                                                                                                       cDNA to mRNA
                                                                                                                                                                                                                                                                     single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 us/09/022,696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08/620,694
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472 1206	460LeuLeuLysLysAspArgArgLysalaAlaArgGlySer
459 1156	446 uAlaCysLeuLeuLleuAlaAlaAlaLeuPhePhePheLeu
446 1106	
1059	1010 ACGCTGTGACTGTGCCCTGCCCAGTAATCTCAAATACCACAGTTCCCAAG
431	431
1009	TTGAGAC
431	•
431 959	418 nLeuTrpAsnAspAspAsnMetG1ySerLeuTrpAlaCys
418 909	402 ATGLEUGIYG.UGIULEULEUGINASPPNEATGSETHISGINCYSMETGI :::::: :::
401 859	SerGlyCysThrProLeuProSerMetAlaSerThrArgAlaAla :::
386 809	LysThrGlyLeuAsnAsnThrSerValCysAlaLeuGluPro
778	166
372	356 TrpAlaAspSerLeuGlyProPheLysAspAspMetLeuLeuValGluMe
355 775	
725	
345	343 lSerThr
343 675	327 ProGlnAspPheGlnLeuValAlaGlyHisProAsnLeuCysValGlnVa ::: :: ::: 653AGATCATCTTTGTGCCTGACTGT
652	.:: ::: ::: ::: ::: :::
3 6	sGinProLeuVaiDroProVaiDroGinLvsasn alamhrVailasnGin
310	294 LeuProGlyLysValThrLeuCysTrpGlnAlaProAspGlnSerProCy ::: ::: 583 CAGGAGTATGAAGTGACTGTT
293 582	278 euArgValLeuSerProGlyValTrpGlnLeuAspAlaProCysCys ::: ::::: 560 GCCACTTTGTGGTAGATCCTGGC
278 559	261 oPheArgGluAspProGlyAlaHisArgAsnLeuTrpHisIleAlaArgL
26 1 509	254ValGluPheCysPr :::
462	13 GGACCCTGCAGACAGATGCCAGCATCCTGTACCTCGAGGGTGCAGAGCTG

7 SEQUENCES: 4 ADDRESS: Immunex Corporati 51 University Street Seattle WA USA	eq_documentation_block: Sequence 1, Application US/08978773 Sequence 1, 6083906 GENERAL INFORMATION: APPLICANT: Troutt, Anthony TITLE OF INVENTION: Method of Regul	646 rgSeralaLeuAspSerCysThrSerSerSerGluAlaPro	1736 TCCAGGACCTGGAGATGTTTGAACCCGGCCGGATGCACCATGTCAGAGAG 629 rSerAlaGlyArgProAlaAspArgValGluArgValThrGlnAlaLeuA :	606 LALAPE 606 LALAPE :::: 686 CACCTO	573 alleuproAspPheLeuGlnGlyArgAlaThrGlyArgTyrValGlyVal :::	543 ProAlaAlaValAlaGlnCysGlnGlnTrpLeuGlnLeuGl	538 leLeuLeuPheSer	521 aTrpPheHisHisGlnArgArgArgIleLeuGlnGluGlyGlyValVal : ::: :::::::::::::::::::::::::::	505 357	489_euValGlyAlaLeuAlaSerAlaLeuSerGlnMetProLeuArgVal 	473 .ArgThralaLeuLeuLeuHlsSeralaAspGlyAlaGlyTyrGluArgL	1207 ATCAATGGCATCTTGCCCGTAGCAGACCTGACTCCCCCACCCCTGAGGCC
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278 euArgValLeuSerProGlyValTrpGlnLeuAspAlaProCysCys 293 :: ::::: 560 GCCACTTTGTGGTAGATCCTGGC	261 oPheArgGluAspProGlyAlaHisArgAsnLeuTrpHisIleAlaArgL 278	254ValGluPheCysPr 261 :::	248 rpSerLeuGluProAsp	236	224 LysAsnLeuThrGlyProGlnAsnIleThrLeuAsn 235	llgn seg 1/1 to: US-08-978-773-1 from: 1 to: 3288	119nment_block: ps-09-899-471-2 x US-08-978-773-1	Quality: 174.50 Length: 582 Ratio: 0.687 Gaps: 28 ercent Similarity: 43.643 Percent Identity: 20.619	<pre>1gnment_scores:</pre>	NAME/KEY: CDS LOCATION: 1212712 -08-978-773-1	ORGANISM: Mouse IMMEDIATE SOURCE:	ANTI-SENSE: NO ORIGINAL SOURCE:	PE	DEDNESS: OGY: line	LENGTH: 3288 base pairs	52	TELECOMMUNICATION INFORMATION: TELEPHONE: (206)587-0430 TELEPHONE: (206)	REFERENCE/DOCKET	FORMATION:	APPLICATION NUMBER: USSN 60/052,525 FILING DATE: 27 NOVEMBER 1996 CLASSIFICATION: 530	ION: 530 FION DATA:	APPLICATION NUMBER: US/08/978,773 FILING DATE:	TER: Apple Power TING SYSTEM: Apple Power	MEDIUM TYPE: Florov disk

504 1356	489 euValGlyAlaLeuAlaSerAlaLeuSerGlnMetProLeuArgVal ::: ::: 1307 TGGTCCTAAAGTTCCTCGAGTCCTGGTCTGGCACTGACTG
489 1306	473 .ArgThrAlaLeuLeuHisSerAlaAspGlyAlaGlyTyrGluArgL
1256	1207 ATCAATGGCATCTTGCCCGTAGCAGACCTGACTCCCCCACCCCTGAGGCC
472	472
472 1206	460LeuLeuLysLysAspArgArgLysAlaAlaAlaArggTyser
1156	CATCGCCATTCTGCTGGTGGGATCTGTCATCGTGCTGATC
459	uAlaCysLeuLeuLeuAlaAlaAlaLeuPho
110	GGC
446	tAspLysTyrIleHisArgArgTrpValLeuVal
1059	1010 ACGCTGTGACTGTGCCCTGCCCAGTAATCTCAAATACCACAGTTCCCAAG
431	431
1009	960 CGTGCAGGTCCAGCCCTTCTTCAGCAGCTGCCTAAATGACTGTTTGAGAC
431	431
959	TGTCACATTCACTCTAAGCAAG
431	ySerLeuTr
909	860 ATGTCGTTAAACAAATATTTGCGCCCAGGCAAGAAGAATTCCATCAGCGA
418	SluLeuLeuGlnAspPheArgSe
859	GCTGGAAAGTTTCTCCGACTCAGAGAACCACAG
401	oSerMetAlaSerThrArgAl
809	779ACTTCACCCTGTGGAATGAATCCACCCCTA
386	rSerValCysAlaLeuGluPr
778	776 TGG
372	356 TrpAlaAspSerLeuGlyProPheLysAspAspMetLeuLeuValGluMe
775	
355	rpGluLysValGlnLeuGlnAlaCysS
725	676 GAGGACAGCAAGATGAAGATGACTACCTCATGCGTGAGCTCAGGCAGCCT
345	343 SerThr
675	653 AGATCATCTTTGTGCCTGACTGT
343	laGlyHisProAsnLeu
652	TGGGGACCCAAA
326	lnProLeuValProProValProGlnLysAsn.AlaThrVal
603	GTGACT
310	ysValThr

505 AlaValAspLeuTrpSerArgArgGluLeuSerAlaHisGlyAlaLeuAl 521

THE TITLE OF THE POWNERS OF THE POWNERS OF THE POWNERS OF SEQUENCES: CORRESPONDENCE ADDRESS ADDRESSE: Immunex STREET: 51 Universi CITY: Seattle STATE: WA COUNTRY: WA COUNTRY: WA COUNTRY: B101 COMPUTER READABLE FORM MEDIUM TYPE: Floppy COMPUTER: APPLE OWNERS MEDIUM TYPE: Ploppy COMPUTER: APPLICATION DARE: FILING DATE: CLASSIFICATION:	seq_name: /cgn2_6/ seq_documentation_	646 rgs 1836 GGC	629 rS : 1786 CT	623 L 1736 T	606 I	590 :	573 1586	556 1546	543 1507	538 1457	521 1407	1357
Application US/09022253 6096305 WT: Yao, Zhengbin WT: Spriggs, Melanie WT: Fanslow, William FINVENTION: No. 6096305el Receptor That Binds ONDENCE ADDRESS: 10 ONDENCE ADDRESS: 12 SEE: Immunex Corporation F: 51 University Street Seattle WA WTYPE: Floppy disk WTYPE: Floppy disk WTYPE: Apple Power Macintosh FER: Apple Power Macintosh FER: Apple Power Macintosh FER: Apple Power Macintosh FER: Apple Power Macintosh SYSTEM: Apple Operating System 7.5.5 APE: Microsoft Word for Apple, Version 6.0.1 APPLICATION DATA: DATION NUMBER: US/09/022,253 SDATE:	ptodata/2/ block:	rgSerAlaLeuAspSerCysThrSerSerSerGluAlaPro 659 :: - ::	rSeralaGlyArgProAlaAspArgValGluArgValThrGlnAlaLeuA 	Leuglnh ::: :::::::::::::::::::::::::::	AALAPTOLeuPheSerLeuPro.ThrGlnLeuProAlaPheLeuAspAla 	TyrPheAspGlyLeuLeuHisProAspSerValProSerProPheArgVa ::: ::: ::: TACTTCAGTGGCATCTGTAGTGAGAGGGATGTCCCCGACCTCTTCAACAT	alLeuProAspPheLeuGlnGlyArgAlaThrGlyArgTyrValGlyVal :: TCCTGCCAGACTTCAAGAGGCCAGCCTGCTTCGGCACCTACGTTGTTTGC	oThrValGluProGlyProHisAspAlaLeuAlaAlaTrpLeuSerCysV ::: :::::::::::::::::::::::::::::::	ProAlaAlaValAlaGlnCysGlnGlnTrpLeuGlnLeuG ::: 	leLeuLeuPheSer	aTrpPheHisHisGlnArgArgArgIleLeuGlnGluGlyGlyValValI: : : CTGGGTGAGCCGACAGAAGCAGGAGATGGTGGAGAGCAACTCCAAAATCA	
IL-17			1835	1785	1735	1685	1635	7 573 1 1585	1 556 . 1545	1506	1456	1406

310 sGlnProLeuValProProValProGlnLysAsn.AlaThrValAsnGlu 326 :::	TCCGTCCTGCAGCTGAACACCAATGAGCGGCTGTGTGTGT	75 rpserieudluProAsp	236HisThrAspLeuValProCysLeuCysIleGlnValT 248	224 LysashLeuThrGlyProGlnasnIleThrLeuAsn	11ign seg 1/1 to: US-09-022-253-1 from: 1 to: 3288	lignment_block: JS-09-899-471-2 x US-09-022-253-1	Lignment_scores: Quality: 174.50 Ratio: 0.687 Percent Similarity: 43.643 Percent Identity: 20.619	09	GINAL SOUR RGANISM: TRAIN: HV	ECULE TYPE: OTHETICAL: N I-SENSE: NO	EDNESS:	HARACTERISTICS: 3288 base pairs	(206) FOR SEQ	NUMBER: 34,69 KET NUMBER: 2 ON INFORMATION 2061587-0430	INFORMATION: s, Patricia An	PRIOR APPLICATION DATA: APPLICATION NUMBER: USSN 08/410,535 FILING DATE: 23 MARCH 1995 CLASSIFICATION:	FILING CLASSI
	278 euArgValLeuSerProGlyValTrpGlnLeuAspAlaProCysCys 293 :::	TCCGTCCTGCAGCTGAACACCAATGAGCGGCTGTGTGTCAAGTTCCA OPheArgGluAspProGlyAlaHisArgAsnLeuTTPHisIleAlaArgL	rpserleuGluProAsp. : : : :	TTCCTCTACCCAGCACGAGAATTAGTCCCTGTACCCAGCACGAGAATTAGTCCCTGTACCCAGCACGAGAATTAGTCCCTGTGTTGCATGTTGAGr rpserLeuGluProAsp	LysashLeuThrGlyProGlnasnIleThrLeuAsn	seg 1/1 to: US-09-022-253-1 from: 1 to: 3288 24 LysasnLeuThrGlyProGlnAsnIleThrLeuAsn	nment_block: 09-899-471-2 x US-09-022-253-1 109-899-471-2 x US-09-022-253-1 from: 1 to: 3288 224 LysasnLeuThrGlyProGlnasnIleThrLeuAsn 214 lysasnLeuThrGlyProGlnasnIleThrLeuAsn 216 lill	nment_scores: Quality: 174.50 Ratio: 0.687 Ratio: 0.687 Ratio: 0.687 Ratio: 0.687 Ratio: 0.687 Ratio: 0.687 Ratio: 0.687 Ratio: 0.687 Ratio: 0.687 Ratio: 0.687 Ratio: 0.687 Ratio: 0.687 Ratio: 0.687 Ratio: 0.687 Ratio: 0.687 Ratio: 0.687 Raps: 28 Raps: 28 Raps: 29 Ratio: 0.687 Raps: 28 Raps: 29 Raps: 1 Raps: 20.619 Ratio: 0.687 Raps: 1 to: 3288	PANAME/REP: CDS LOCATION: 121.2715 9-022-253-1 nnment_scores: Quality: 174.50 Ratio: 0.687 cent Similarity: 43.643 Percent Identity: 20.619 nnment_block: 09-899-471-2 x US-09-022-253-1 gn seg 1/1 to: US-09-022-253-1 from: 1 to: 3288 224 LysAsnLeuThrGlyProGlnAsnIleThrLeuAsn	ORGANISH: MOUSE: ORGANISH: MOUSE STRAIN: HVS13 receptor FEATURE: HVS13 receptor FEATURE: LOCATION: 121.2715 9-022-253-1 nmment_scores: Quality: 174.50 Quality: 174.50 Gaps: 28 cent Similarity: 43.643 Percent Identity: 20.619 nment_block: 09-899-471-2 x US-09-022-253-1 from: 1 to: 3288 gn seg 1/1 to: US-09-022-253-1 from: 1 to: 3288 224 LysasnLeuThrGlyProGlnAsnIleThrLeuAsn	MOLECULE TYPE: CDNA to mRNA HYDOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE: ORGANIAN: MOUSE STRAIN: HVS13 receptor FEATURE: NAME/REF: CDS LOCATION: 1212715 9-022-253-1 nment_scores: Ouality: 174.50 Ratio: 0.687 Gent Similarity: 43.643 Percent Identity: 20.619 nment_block: 09-899-471-2 x US-09-022-253-1 Gop-899-471-2 x US-09-022-253-1 gn seg 1/1 to: US-09-022-253-1 1 316 AAAAACCTGACCCCGTCTTCCCCAAAAAACATCTATATCAATCTTAGTGT 236	STRANDEDNESS: Single TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO ARTI-SENSE: NO ORIGINAL SOURCE: ORGANISM: MOUSE STRAINE SOURCE: ORGANISM: MOUSE STREIT	SEQUENCE CHARACTERISTICS: LENGTH 3288 base pairs TYPE: nucleic acid STRANDEDNESS: single STRANDEDNESS: single MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE: ORGANISM: MOUSE STRAIN: HYS13 receptor FEATURE: HYS13 receptor REATION: 121.2715 9-022-253-1 nument_scores: Quality: 174.50 Length: 582 Gaps: 28 cent Similarity: 43.643 Percent Identity: 20.619 ment_block: 0.687 Gaps: 28 cent Similarity: 43.643 Percent Identity: 20.619 mment_block: 0.687 Gaps: 28 cent Similarity: 43.643 Percent Identity: 20.619 mment_block: 0.687 Gaps: 28 cent Similarity: 43.643 Percent Identity: 20.619 mment_block: 0.687 Gaps: 28 cent Similarity: 43.643 Percent Identity: 20.619 mment_block: 0.687 Gaps: 28 cent Similarity: 43.643 Percent Identity: 20.619 mment_block: 0.687 Gaps: 28 cent Similarity: 43.643 Percent Identity: 20.619 mment_block: 0.687 Gaps: 28 cent Similarity: 43.643 Percent Identity: 20.619 mment_block: 0.687 Gaps: 28 cent Similarity: 43.643 Percent Identity: 20.619 mment_block: 0.687 Gaps: 28 cent Similarity: 43.643 Percent Identity: 20.619 mment_block: 0.687 Gaps: 28 cent Similarity: 43.643 Percent Identity: 20.619 mment_block: 0.687 Gaps: 20.619 cent Similarity: 1.511 Hill::::	TELEPA: (206) NPORMATION FOR SEQ ID NO: 1: SEQUENCE (LARACTERISTICS: LENGTH: 328 base pairs TYPE: nucleic acid STRANDENNESS: single TOPOLOGY: linear MOLECULE TYPE: cDNA to mRNA HYPOTHETICAL: NO ORIGINAL SOURCE: ORGANISM: MOUSE STRAIN: HYS13 receptor FEATURE: NO. ORIGINAL SOURCE: STRAIN: HYS13 receptor NAME/KEY: CDS LOCATION: 121.2715 9-022-253-1 nnment_scores: LOCATION: 121.2715 9-022-253-1 nnment_scores: LOCATION: 121.2715 9-022-253-1 nnment_block: 09-899-471-2 x US-09-022-253-1 from: 1 to: 3288 cent Similarity: 43.643 Percent Identity: 20.619 nnment_block: 09-899-471-1 to: US-09-022-253-1 from: 1 to: 3288 224 LysasnLeuThrGlyProGlnasnIleThrLeuAsn	REFERENCE/DOCKET NUMBER: 2617-B TELECOMMUNICATION INFORMATION: TELEPHAN: (206)587-0430 TELEPHAN: (206) REFERENCE (206) TELEPHAN: (206) TELEPHAN: (206) NFORMATION FOR SEQ ID NO: 1: SEQUENCE (LARACTERISTICS: LENGTH: 3288 base pairs TYPE: nucleic acid STRANDEDESS: single TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO ANTI-SENS: NO ORIGINAL SOURCE: ORGANISM: MOUSE STRAIN: HYS13 receptor FEATURE: NAME/KEY: CDS LOCATION: 1212715 9-022-253-1 174.50 Ratio: 0.687 Cent Similarity: 43.643 Percent Identity: 20.619 nnment_block: 0.687 Cent Similarity: 43.643 Percent Identity: 20.619 nnment_block: 0.687 Cent Similarity: 43.643 Percent Identity: 20.619 nnment_block: 0.687 Cent Similarity: 43.643 Percent Identity: 20.619 nnment_block: 0.687 Cent Similarity: 43.643 Percent Identity: 20.619 nnment_block: 0.687 Cent Similarity: 43.643 Percent Identity: 20.619 nnment_block: 0.687 Cent Similarity: 43.643 Percent Identity: 20.619 nnment_block: 0.687 Cent Similarity: 43.643 Percent Identity: 20.619 nnment_block: 0.687 Cent Similarity: 43.643 Percent Identity: 20.619 nnment_block: 0.687 Cent Similarity: 43.643 Percent Identity: 20.619 nnment_block: 0.687 Cent Similarity: 43.643 Percent Identity: 20.619 nnment_block: 0.687 Cent Similarity: 43.643 Percent Identity: 20.619 nnment_block: 0.687 Cent Similarity: 43.643 Percent Identity: 20.619 nnment_block: 0.687 Cent Similarity: 43.643 Percent Identity: 20.619 nnment_block: 0.687 Cent Similarity: 43.643 Percent Identity: 20.619 nnment_block: 0.687 Cent Similarity: 43.643 Percent Identity: 20.619 nnment_block: 0.687 Cent Similarity: 43.643 Percent Identity: 20.619 nnment_block: 0.687 Cent Similarity: 43.643 Percent Identity: 20.619 nnment_block: 0.687 Cent Similarity: 43.643 Percent Identity: 20.619 nnment_block: 0.687 Cent Similarity: 43.643 Percent Identity: 20.619 Cent Similarity: 43.643 Percent Identity: 20.619 Cent Similarity: 43.643 Percent Identity: 20.619 Cent Similarity: 43.643 Percent Identity: 20.619 Cent Similarity: 43.643 Percent Identity: 20.619 Cent Similarit	NAME: Perkins, Patricia Anne REGISTRATION NUMBER: 34,695 REFERENCE/DOCKET NUMBER: 34,695 REFERENCE/DOCKET NUMBER: 34,695 REFERENCE/DOCKET NUMBER: 34,695 REFERENCE/DOCKET NUMBER: 2617-B REFERENCE/DOCKET NUMBER: 2617-B REFERENCE/DOCKET NUMBER: 2617-B REFERENCE/DOCKET NUMBER: 2617-B REFERENCE/DOCKET NUMBER: 2617-B REFERENCE/DOCKET NUMBER: 2617-B REFERENCE/DOCKET NUMBER: 2018 REFERENCE/DOCKET NUMBER: 2018 REFERENCE/DOCKET NUMBER: 2018 REFERENCE/DOCKET NUMBER: 2018 REFERENCE/DOCKET NUMBER: 2018 REFERENCE/DOCKET NUMBER: 2018 REFERENCE/DOCKET NUMBER: 2018 REFERENCE/DOCKET NUMBER: 2019 REFERENCE/DOCKET NU	PRIOR APPLICATION NUMBER: USSN 08/410,535 FILING DATE: 23 MARCH 1995 CLASSIFICATION NUMBER: 43,695 CLASSIFICATION NUMBER: 34,695 CLASSIFICATION NUMBER: 34,695 REFERENCE/DOCKET NUMBER: 36,695 REFERENCE/DOCKET NUMBER: 2617-B
294 LeuProGlyLysValThrLeuCysTrpGlnAlaProAspGlnSerProCy 310 ::: ::: 583 CAGGAGTATGAAGTGACTGTT		TCCGTCCTGCAGCTGAACACCATGAGCGGCTGTGTGTCAAQTTCCCA oPheArgGluAspProGlyAlaHisArgAsnLeuTpHisIleAlaArgL	rpserieugluproasp	TTCCTCTACCCAGCACGAGAATTAGTCCCTGTAGTGCAAGATTAGTCCTGTACCCTGCAGACGAGAATTAGTCCCTGTGTTGCATGTTGAGT TPSerLeuGluProAsp	LysashLeuThrGlyProGlnasnIleThrLeuAsn	gn seg 1/1 to: US-09-022-253-1 from: 1 to: 3288 224 LysasnLeuThrGlyProGlnAsnIleThrLeuAsn	nment_block: 09-899-471-2 x US-09-022-253-1 from: 1 to: 3288 gn seg 1/1 to: US-09-022-253-1 from: 1 to: 3288 224 LysasnLeuThrGlyProGlnasnIleThrLeuAsn	nment_scores: Quality: 174.50 Ratio: 0.687 Retio: 0.687 R	NAME/KEY: CDS LOCATION: 121.2715 9-022-253-1 nment_scores: Quality: 174.50 Ratio: 0.687 Cent Similarity: 43.643 Percent Identity: 20.619 nment_block: 09-899-471-2 x US-09-022-253-1 11	ORGANISH: MOUSE ORGANISH: MOUSE STRAIN: HVS13 receptor FEATURE: HVS13 receptor FEATURE: HVS13 receptor FEATURE: HVS13 receptor FEATURE: HVS13 receptor FEATURE: HVS13 receptor FEATURE: HVS13 receptor Gaps: 28 Cent Similarity: 174.50 Cent Similarity: 43.643 Percent Identity: 20.619 nment_block: 09-899-471-2 x US-09-022-253-1 09-899-471-2 x US-09-022-253-1 1	MOLECULE TYPE: CDNA to mRNA HYDOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE: ORGANISH: Mouse STRAIN: HVS13 receptor FEATURE: LCCATION: 121.2715 9-022-253-1 nmment_scoxes: LCCATION: 121.2715 9-022-253-1 cent Similarity: 43.643 Percent Identity: 20.619 nmment_block: 09-899-471-2 x US-09-022-253-1 gn seg 1/1 to: US-09-022-253-1 1	STRANDENESS: Single TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA HYDOTHETICAL: NO ORIGINAL SOURCE: STRAIN: HVS13 receptor FEATURE: HVS13 receptor FEATURE: HVS13 receptor FEATURE: NO ORIGINAL SOURCE: ORGANISM: MOUSE STRAIN: HVS13 receptor FEATURE: CDS LOCATION: 1212715 9-022-253-1 10-022-22-253-1 10-022-22-253-1 10-022-22-253-1 10-022-22-253-1 10-022-22-253-1 10-022-22-253-1 10-022-22-253-1 10-022-22-253-1 10-022-22-253-1 10-022-22-253	SEQUENCE CHARACTERISTICS: LENGTH: 3388 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO ANTI-SENSE: NO ANTI-SENSE: NO ANTI-SENSE: NO ANTI-SENSE: HVS13 receptor FEATURE: QUality: 174.50 QUality: 174.50 QUality: 174.50 QUALITY: 174.50 QUALI	TELEFAX: (206) NFORMATION FOR SEQ ID NO: 1: SEQUENCE (LEMARCTERISTICS: LENGTH: 3288 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: CDN to mRNA HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE: CDS LOCATION: 121.2715 9-022-253-1 9-022-253-1 19-022-253-1 109-899-471-2 x US-09-022-253-1 Imment_block: GlyproglnasnileThrLeuasn	REFERENCE/DOCKET NUMBER: 2617-B TELEPHONE: (206)587-0430 TELEPHONE: (206)587-0430 TELEPHONE: (206)587-0430 TELEPHONE: (206) TELEPHONE: (206) TELEPHONE: (206) TELEPHONE: (206) TELEPHONE: (206) TELEPHONE: (206) TELEPHONE: (206) TELEPHONE: (206) TELEPHONE: (206) TELEPHONE: (206) TELEPHONE: (206) TELEPHONESS: single TYPE: characteristics: LENGTH: 3288 base pairs TYPE: characteristics: LENGTH: 3288 base pairs TYPE: characteristics: LENGTH: 3288 base pairs TYPE: characteristics: TYPE	APTORNEY/AGENT INFORMATION: ANHE: Perkins, Fatricia Anne REGISTRATION NUMBER: 34,695 REFERENCE/DOCKET NUMBER: 2617-B TELECOMMUNICATION INFORMATION: TELEPHONE: (206)587-0430 TELEPHONE: (206)587-0430 TELEPHONE: (206)587-0430 TELEPHONE: (206)587-0430 TELEPHONE: (206)587-0430 TELEPHONE: (206)587-0430 TELEPHONE: (206)587-0430 TELEPHONE: (206)587-0430 TELEPHONE: (206)587-0430 TELEPHONE: (206)587-0430 TELEPHONE: (206)587-0430 TELEPHONE: (206)587-0430 TELEPHONE: (206)587-0430 TELEPHONE: (206)587-0430 TELEPHONE: (206)587-0430 TELEPHONE: (208)587-0430 PRIOR APPLICATION NUMBER: USSN 08/410,535 FILING DATE: 23 MARCH 1995 CLASSIFICATION: ATTORNEY/AGENT INFORMATION: NAME: Perkins, Patricia Anne REGISTRATION NUMBER: 34,695 REFERENCE/DOCKET NUMBER: 2617-B REFERENCE/DOCKET REFERENCE/DOCKET NUMBER: 2617-B REF	

327	ProGlnAspPheGlnLeuValAlaGlyHisProAsnLeuCysValGlnVa	343
653	AGATCATCTTGTGCCTGACTGT	75
343	lSerThr	45
676	GAGGACAGCAAGATGAAGATGACTACCTCATGCGTGAGCTCAGGCAGCCT 7	25
346	5 ······TrpGluLysValGlnLeuGlnAlaCysSer 35	55
726	TTGGGAT	75
356	TrpAlaAspSerLeuGlyProPheLysAspAspMetLeuLeuValGluMe 	372
776	TGG	78
372	tLysThrGlyLeuAsnAsnThrSerValCysAlaLeuGluPro 3	98
779	ACTTCACCCTGTGGAATGAATCCACCCCTA 8	09
387	SerGlyCysThrProLeuProSerMetAlaSerThrArgAlaAla 4	01
810	CCAGGTCCTGGAAAGTTTCTCCGACTCAGAGAACCACAGCTGCTTTG 8	59
402	ArgLeuGlyGluGluLeuLeuGlnAspPheArgSerHisGlnCysMetGl	418
860	ATGTCGTTAAACAAATATTTGCGCCCAGGCAAGAAGAATTCCATCAGCGA	09
418	nLeuTrpAsnAspAsnMetGlySerLeuTrpAlaCys 4	31
	4	31
960	CGTGCAGGTCCAGCCCTTCTTCAGCAGCTGCCTAAATGACTGTTTGAGAC	1009
431		31
1010	ACGCTGTGACTGTGCCCTGCCCAGTAATCTCAAATACCACAGT	059
432 1060	PrometAspLysTyrIleHisArgArgTrpValLeuValTrpLe 446	46 106
446	uAlaCysLeuLeuLeuAlaAlaLeuPhePhePheLeu	59
1107	CATCGCCATTCTGCTGGTGGGATCTGTCATCGTGCTGATCATCTGTAT	156
460	LeuLeuLysLysAspArgArgLysAlaAlaArgGlySe	72
1157	CCTGGAGGCTTTCTGGCGCCCGATCAAGAGAAACATGGTGATGACTC	206
472		72
1207	ATCAATGGCATCTTGCCCGTAGCAGACCTG1	256
473	.ArgThrAlaLeuLeuHisSerAlaAspGlyAlaGlyTyrGluArgL 4	89
1257	CAGGAAGGTCTGGATCGTCTACTCGGCCGAC	306
489	euValGlyAlaLeuAlaSerAlaLeuSerGlnMetProLeuArgVal 5 :: ::: :::	04
9	TGGTCCTAAAGTTCGCCCAGTTCCTGATCAC	356
505 1357	AlaValAspLeuTrpSerArgArgGluLeuSerAlaH1sGlyAlaLeuAl 5 ::: ::::::::::::::::::::::::	21
521	aTrpPheHisHisGlnArgArgArgIleLeuGlnGluGlyGlyValValI 53	38
1407	CTGGGTGAGCCGACAGAAGCAGGAGGAGGGAGGAGCAACTCCAAAAATC	אא

PONDENCE ADDRES ESSEE: Immunex ETS: 51 Univers ETRY: USA 98101 ER READABLE PON UTTYPE: Flopp UTER: APPLIC PON WARE: MICTOSOF T APPLICATION UMBER: NG DATE: NG DATE: NG DATE: NG DATE: NG DATE: SIFICATION UMBER: APPLICATION DAT ICATION UMBER: APPLICATION DAT ICATION UMBER: SIFICATION UMBER: APPLICATION UMBER: SIFICATION UMBER: SIFICATION UMBER: APPLICATION UMBER: SIFICATION UMBER: APPLICATION UMBER: SIFICATION UMBER: SIFICATION UMBER: APPLICATION UMBER: SIFICATION UMBER: APPLICATION UMBER: APPLICATION UMBER: SIFICATION UMBER: APPLICATION UMBER:	on_block: pplication US/09022260 00235 RMATION: RTO, Zhengbin Spriggs, Melanie Fanslow, William NVENTION: NO. 6100235el Receptor That Binds	646 rgSerAlaLeuAspSerCysThrSerSerSluAlaPro 659	623 LeuGin		ArgTyrValGlyVal 5	1507 TGGGCTGACCTGCTT	
	IL-17		629 1785 646 1835	7 2 6	589 1635	1545 1545 573 1585	542 1506

REFERENCE/DOCKET NUMBER: 2617-B	
TELEPHONE: (206)587-0430	
ORMATION FOR SEQ ID	
SEQUENCE CHARACTERISTICS: LENGTH: 3288 base pairs	
nucleic acion	
MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO ANTI-SENCE: NO	
SOUR	
FEATURE:	
ment sco	
S	
.ignment_block: 15-09-899-471-2 x US-09-022-260-1	
llign seg 1/1 to: US-09-022-260-1 from: 1 to: 3288	
224 LysasnLeuThrGlyProGlnAsnIleThrLeuAsn 235	J. 01
236HisThrAspLeuValProCysLeuCysIleGlnValT 248	w
248 rpSerLeuGluProAsp	~
:	•
GTGT	_
261 oPheArgGluAspProGlyAlaHisArgAsnLeuTrpHisIleAlaArgL 278	
278 euArgValLeuSerProGlyValTrpGlnLeuAspAlaProCysCys 293 ::: :::: 560 GCCATTTGTGCTAGATCCTGGC	- •
CysTrpGlnAlaProAspGlnS	7
583 CAGGAGTATGAAGTGACTGTT603	
310 sGlnProLeuValProProValProGlnLysAsn.AlaThrValAsnGlu 326 ::: ::: ::: :: ::: 604 .CACCACCTGCCGAAGCCCATCCCTGATGGGGACCCAAACCACAAATCCA 652	-
327 ProGlnAspPheGlnLeuValAlaGlyHisProAsnLeuCysValGlnVa 343	
53	-
43 SerThr	•
6/6 GAGGACAGCAAGATGAAGATGACTACCTCATGCGTGAGCTCAGGCAGCCT 725	

556 1545	543 ProAlaAlaValAlaGlnCysGlnGlnTrpLeuGlnLeuGl !
542 1506	538 leLeuLeuPheSer
538 1456	aTrpPheHisHisGlnArgArgI1eLeuGlnGluGluGluGluGluGluGluGluGluGluGluGluGluG
521 1406	505 AlavajaspLeuTrpSerArgArgGluLeuSerAlaHisGlyATaLeuAl :
504 1356	489 euValGlyAlaLeuAlaSerAlaLeuSerGlnMetProLeuArgVal
489 1306	473 .ArgThrAlaLeuLeuLeuHisSerAlaAspGlyAlaGlyTyrGluArgL
1256	CAATGGCATCTTGCCCGTAGCAGACCTGACTCCCCCACCCCTGAGGCC
472	472
472 1206	460LeuLeuLysLysAspArgArgLysAlaAlaArgGlySer
459 1156	446 uAlaCysLeuLeuLeuAlaAlaAlaLeuPhePhePheLeu
446 1106	432 ProMétAspLysTyrIleHisArgArgTrpValLeuValTrpLe
1059	CTCAAATACCACAGTTCCCAAG
431	431
1009	GGTCCAGCCCTTCTTCAGCAGCTGCCTAAATGACTGTTTGAGAC
431	431
431 959	418 nLeuTrpAsnAspAspAsnMetGlySerLeuTrpAlaCys
0	ATGTCGTTAAACAAATATTTGCGCCCAGGCAAGAAGAATTCCATCAGCGA
ب ر	ArqLeuGlvGluGluLeuLeuGlnAspPheArqSerHisGlnCvsW
401	387SerGlyCysThrProLeuProSerMetAlaSerThrArgAlaAla
386 809	372 tLysThrGlyLeuAsnAsnThrSerValCysAlaLeuGluPro
778	76 TGG
372	356 TrpÅlaAspSerLeuGlyProPheLysAspAspMetLeuLeuValGluMe
355 775	346
	-

556 nThrValGluProGlyProHisAspAlaLeuAlaAlaTrpLeuSerCysV 573

1546

Length:

20.619

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#q_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-022-259-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09022259 Patent No. 6191104
                                                                      INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1786 CTCACAGGGGACAATTACCTGCAGAGCCCTAGTGGCCGGCAGCTCAAGGA 1835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1736 TCCAGGACCTGGAGATGTTTGAACCCGGCCGGATGCACCATGTCAGAGAG 1785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1586 TCCTGCCAGACTTCAAGAGGCCAGCCTGCTTCGGCACCTACGTTGTTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1686 CACCTCCAGGTACCCACTCATGGACAGATTTGAGGAGGTTTACTTCCGGA 1735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1636 TACTTCAGTGGCATCTGTAGTGAGAGGGATGTCCCCGACCTCTTCAACAT 1685
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION MINISTER STATEMENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 0
FILING DATE: 23 MARCH 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     629 rSerAlaGlyArgProAlaAspArgValGluArgValThrGlnAlaLeuA 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      606 lAlaProLeuPheSerLeuPro.ThrGlnLeuProAlaPheLeuAspAla 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              590 TyrPheAspGlyLeuLeuHisProAspSerValProSerProPheArgVa 606
                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: NO. 6191104e1
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         573 alLeuProAspPheLeuGlnGlyArgAlaThrGlyArgTyrValGlyVal 589 ::(|||||||||
                                                                                                                                                   NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operatin
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/022,259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCCTGTGCTTAGGTTCCAGGAGTGGCAAACCCAGTGCCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rgSerAlaLeuAspSerCysThrSerSerSerGluAlaPro 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .....AAGCCTGCT...GGGGACCTTTTCACTGCAGCCATGAACATGA 1585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Immunex Corporation
51 University Street
                                                                                                                                                                                                                                                                                      USSN 08/410,535
                                                                                                                                                                                                                                                                                                                                                                        08/620,694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Receptor That Binds IL-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1876
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US-09-899-471-2 x US-09-022-259-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1
                                                                                                                               726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        463 TCCGTCCTGCAGCTGAACACCAATGAGCGGCTGTGTGTCAAGTTC...CA 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   224 LysAsnLeuThr.....GlyProGlnAsnIleThrLeuAsn.....
372 tLysThrGlyLeuAsnAsnThrSerValCysAlaLeuGluPro...
                                                                               356 TrpAlaAspSerLeuGlyProPheLysAspAspMetLeuLeuValGluMe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                     ProGlnAspPheGlnLeuValAlaGlyHisProAsnLeuCyeValGlnVa
                                                                                                                                                                                                                                                                                                                                                                                                                      sGlnProLeuValProProValProGlnLysAsn.AlaThrValAsnGlu 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGGAGTATGAAGTGACTGTT..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LeuProGlyLysValThrLeuCysTrpGlnAlaProAspGlnSerProCy 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCACTTTGTGGTAGATCCTGGC.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              oPheArgGluAspProGlyAlaHisArgAsnLeuTrpHisIleAlaArgL 278
                                                                                                                          TTGGGATCCCAACATCACTGTGGAGACCTTGGACACACAGCATCTGCGAG
                                                                                                                                                                                                              GAGGACAGCAAGATGAAGATGACTACCTCATGCGTGAGCTCAGGCAGCCT 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               euArg...ValLeuSerProGlyValTrpGlnLeuAspAlaProCysCys 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTTTCTGTCCATGCTGCAGCATCACCGTAAGCGGTGGCGGTTTTCCTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGACCCTGCAGACAGATGCCAGCATCCTGTACCTCGAGGGTGCAGAGCTG 462
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                                                                                                                                                                                                                                                                                                                                                                                .CACCACCTGCCGAAGCCCATCCCTGATGGGGACCCAÄACCACAATCCA 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio:
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121..2715
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                                                                                                                                                                                                                                                                                               ....AGATCATCTTTGTGCCTGACTGT
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q_documentation_block:

1836

GENERAL INFORMATION:

APPLICANT:

Zhengbin

CORRESPONDENCE ADDRESS:

STREET:

ADDRESSEE:

COUNTRY:

USA

98101 Seattle : WA

SEQUENCE CHARACTERISTICS:

3288 base pairs

TELEPHONE:

(206)587-0430

775

372

386 778 675 343

345

582

603

559

253

(206)

APPLICATION NUMBER:

CLASSIFICATION: FILING DATE:

CLASSIFICATION: FILING DATE:

CLASSIFICATION:

	909	<pre>70 TyrPheAspGlyLeuLeuHisProAspSerValProSerProPheArgVa 111111:::: </pre>	590
	589 1635	3 alLeuProAspPheLeuGlnGlyArgAlaThrGlyArgTyrValGlyVa :: 6 TCCTGCCAGACTTCAAGAGGCCAGCCTGCTTCGGCACCTACGTTGTTTG	57: 158(
	573 1585	6 nThrValGluProGlyProHisAspAlaLeuAlaAlaTrpLeuSerC ::: ::: ::::: 6AAGCCTGCTGGGGACCTTTTCACTGCAGCCATGAACA	55 154
	556 1545	3ProAlaAlaValAlaGlnCysGlnGlnTrpI :::::: 7 TGGGCTGAGCCTGCTGCCAGCTACGGTGTGACCACTGG	54: 150:
	542 1506	8 leLeuLeuPheSer	538 145
	538 1456	21 aTrpPheHisHisGlnArgArgArgIleLeuGlnGluGlyGlyValValI 	0 0
	521 1406	5 AlaValAspLeuTrpSerArgArgGluLeuSer/ ::: GCCCTTGACCTCCTGGAAGAGCAGGTTATCTCTC	50 <u>5</u>
	504 1356	9 euValGlyAlaLeuA :: ::: 7 TGGTCCTAAAGTTCG	489 1307
•	489 1306	3 .ArgThrAlaLeuLeuHisSerAlaAspGlyAla ::: :::::: 7 CAGGAAGGTCTGGATCGTCTACTCGGCCGACCACCCC	5 7
•	N,	7 ATCAATGGCATCTTGCCCGTAGCAGACCTGACTCCCCCACCCCTGAGGC	0
•	72	22	7
•	472	00LeuLeuLysLysAspArgArgLysAlaAlaArgGlySer	46 115
.	459 1156	uAlaCysLeuLeuLeuAlaAlaAlaLeuPhePhePheLeu. ::::: :::::::::::: CATCGCCATTCTGCTGGTGGGATCTGTTCATCGTGCTGATCA	446 1107
.	446 1106	2 ProMetAspLysTyrII ::: CCAGTTGCAGACTACAT	43: 106
•	1059	0 ACGCTGTGACTGTGCCCTGCCCAGTAATCTCAAATACCACAGTT	101
	431	1	43
•	1009	O CGTGCAGGTCCAGCCCTTCTTCAGCAGCTGCCTAAATGACTGTTTGAGA	96
	431		43
	431 959	18 nLeuTrpAsnAspAspAsnMetGlySerLeuTrpAlaCys 	41 91
	418 909	2 ArgLeuG 0 ATGTCGT	86
	401 859	7SerGlyCysThrProLeuProSerMeta	38 81
		9ACTTCACCTGTGGAATGAATCCACCCCC	7

	402 ArgLeuGlyGluLeuLeuGlnAspPheArgSerHisGlnCysMetGl 418
	810 CCAGGTCCTGCAAAGTTTCTCCGACTCAGAGAACCACAGCTGCTTTG 859
	387SerGlyCysThrProLeuProSerMetAlaSerThrArgAlaAla 401
	372 tlysThrGlyLeuAsnAsnThrSerValCysAlaLeuGluPro 386
•	356 TrpAlaAspSerLeuGlyProPheLysAspAspMetLeuLeuValGluMe 372
	346
-	676 GAGGACAGCAAGATGAAGATGACCTACCTCATGCGTGAGCTCAGGCAGCCT 725
	343 1SerThr
	327 ProGlnAspPheGlnLeuValAlaGlyHisProAsnLeuCysValGlnVa 343 ::: ::: ::: 653AGATCATCTTTGTGCCTGACTGT 675
	310 SG1nProLeuValProProValProG1nLySAsn.AlaThrValAsnG1u 326 :::
	CIGI
	294 LeuProGlyLysValThrLeuCysTrpGlnAlaProAspGlnSerProCy 310
	278 euArgValLeuSerProGlyValTrpGlnLeuAspAlaProCysCys 293 :: ::::: 560 GCCACTTTGTGGGAGATCCTGGC
	261 oPheArgGluAspProGlyAlaHisArgAsnLeuTrpHisTleAlaArgL 278
U F	254ValGluPheCysPr 261 :::
	248 rpSerLeuGluProAsp
	236HisthraspLeuvalProCysLeuCysIleGlnValT 248
0.	224 LysasnLeuThrGlyProGlnAsnIleThrLeuAsn 235
	Align seg 1/1 to: US-09-022-257-1 from: 1 to: 3288
	alignment_block: US-09-899-471-2 x US-09-022-257-1
	#lignment_scores: Quality: 174.50 Length: 582 Ratio: 0.687 Gaps: 28 Percent Similarity: 43.643 Percent Identity: 20.619
	NAME/KEY: CDS LOCATION: 1212715 US-09-022-257-1

629 1785	TCCAGGACCTGGAGATGTTTGAACCCGGCCGGATGCACCATGTCAGAGAG	623 1736
622 1735	lalaProLeuPheSerLeuPro.ThrGlnLeuProAlaPheLeuAspAla ::::	606 1686
606 1685	TyrPheAspGlyLeuLeuHisProAspSerValProSerProPheArgVa ::: ::: :::: TACTTC AGTGGCATCTGTAGTGAGAGGGATGTCCCCGACCTCTTCAACAT	590 1636
589 1635	alLeuProAspPheLeuGlnGlyArgAlaThrGlyArgTyrValGlyVal :: TCCTGCCAGACTTCAAGAGGCCAGCCTGCTTCGGCACCTACGTTGTTTGC	573 1586
573 1585	6 nThrValGluProGlyProHisAspAlaLeuAlaAlaTrpLeuSerCysV ::: :::::::::::::::::::::::::::::	154
556 1545	TGGGCTGAGCCTGCCAGCTACGGTGTGACCACTGG	543 1507
542 1506	18 leLeuleuPheSer	53 145
538 1456	11 aTrpPheHisHisGlnArgArgArgIleLeuGlnGluGlyGlyValValI 	521 1407
521 1406	5	505 1357
504 1356	89 euValĠlyAlaLeuAlaSerAlaLeuSerGlnMetProLeuArgVal 	489 1307
489 1306	3 .ArgThralaLeuLeuLeuHisSerAlaAspGlyAlaGlyTyrGluArgL	473 1257
io .	7 ATCAATGGCATCTTGCCCGTAGCAGACCTGACTCCCCCACCCCTGAGGC	120
472	2	47
472 1206	00LeuLeuLysLysAspArgArgLysAlaAlaArgGlySer	46 115
459 1156	16 uAlaCysLeuLeuAlaAlaAlaLeuPhePhePheLeu	446 1107
446 1106	32 ProMetAspLysTyrIleHisArgArgTrpValLeuValTrpLe	432 1060
1059	ACGCTGTGACTGTGCCC	1010
431		431
	CGTGCAGGTCCAGCCCTTCTTCAGCAGCTGCCTAAATGAC	960
431		43
431 959	18 nLeutrpAsnAspAspAsnMetGlySerLeuTrpAlaCys	418 910
909	50 ATGTCGTTAAACAAATÁTTTGCGCCCAGGCAAGAAGAATTCCATCAGCGA	860

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alignment_scores:
Quality:
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     Percent Similarity:
                                                                                                          NAME/KEY:
LOCATION:
-08-620-694A-9
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                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1786 CTCACAGGGGACAATTACCTGCAGAGCCCTAGTGGCCGGCAGCTCAAGGA 1835
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                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                               ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  629 rSerAlaGlyArgProAlaAspArgValGluArgValThrGlnAlaLeuA 646
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                    HYPOTHETICAL:
                                                                                                                                                                                                                                                                   OLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                              STRAIN: IL-17 R (hCTLA8 receptor)
                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Perkins, Patricia Anne REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 2
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0
                                                                                                                                                                                                   ORGANISM: Human
                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 98101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: USSN 00
FILING DATE: 23 MARCH 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                        nucleic acid
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                      Ratio:
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VENTION: No. 5869286el Receptor That Binds IL-17

EQUENCES: 10
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                                                                                                                             CDS
93..2693
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                                                                                                                                                                                                                                                                                                                                                                                                               (206)587-0430
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21 MARCH 1996
                                                                                                                                                                                                                                                                     cDNA to mRNA
                                                                                                                                                                                                                                                                                                      single
 154.00
0.552
38.115
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 Gaps:
Percent Identity:
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: 732
: 33
: 19.399
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alignment_block:
US-09-899-471-2 x US-08-620-694A-9
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                                252 oAspSerGluArgValGluPheCys.....
                                                                             717
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                                                                                                                                                                                                                                                                                                     609
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                                                                                                                                                                                                                                                                                                                                                                                                                 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                     530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       480 GAGTTTCTGTCCAAACTGAGGCATCACCACAGGCGGTGGCGTTTTACCTT 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 153 rAlaValPheAspCysPheGluAlaSerLeu..........GlyAlaG 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 uValPro.....ThrArgLeuGlnThrGluLeuValLeuArgC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 ysProGlnLysThrAspCysAlaLeuArgValArgValValValHisLeu
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                                                                                                                                                                                                                                                                                               snLeuThrGlnGlnLeuProAspGlyAspAsnValLeuLeuThrLeuAsp 198
CCACCAGCTGTGAGCTTCACCCTGTGGAACGAATCTACCCATTACC 783
                                                                                                           HisThrAspLeuValProCysLeuCysIleGlnValTrpSerLeuGluPr 252
                                                                                                                                                    GCAGCCTGTGGGACCCCAACATCACC.
                                                                                                                                                                                                                                                                                                                                                                                                                                               CAGCCACTTTGTGGTTGACCCTGACCAGGAATATGAGGTGACCGTTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGTTATCTGTCCTGCAGCTGAACACCAATGAACGTTTGTGCGTCAGGTTT 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAATGGACACTGCAGACAGAC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rGluLeuGlnGluSerArgAsnAlaSerLeuGlnAlaGlnValValLeuS 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCTCCCAGCCG......GGGCTAAACTGCACGGTCAAGAATAGTACC 260
                                                                                                                                                                                   ysSerLeuTrpTyrLysAsnLeuThrGlyProGlnAsnIleThrLeuAsn 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AACCTGACCCCCTCCCCAAAGGACCTGCAGATCCAGCTGCACTTTG
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                                                                         GTGGAGACCCTGGAGGC 733
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	522 1374	505 aValAspLeuTrpSerArgArgGluLeuSerAlaHisGlyAlaLeuAlaT -:: :::::::::::::::::::: ::::
	505 1324	490 ValGlyAlaLeuAlaSerAlaLeuSerGlnMetProLeuArgValAl
	489 1274	473 rgThrAlaLeuLeuLeuHisSerAlaAspGlyAlaGlyTyrGluArgLeu
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,	431	415 GlnCysMetGlnLeuTrpAsnAspAspAsnMetGlySerLeuTrpAlaCy
	414 1040	398 hrargalaalaargLeuGlyGluGluLeuLeuGlnaspPheargSerHis
	398 1017	381 lCysAlaLeuGluProSerGlyCysThrProLeuProSerMetAlaSerT::: ::: ::: ::: ::: ::: :::
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	364 950	348 ysValGlnLeuGlnAlaCysSerTrpAlaAspSerLeuGlyProPheLys :: ::: 931 AAGTGCAGATCCAG
	348 930	332 .LeuValAlaGlÿHisProAsnLeuCysValGlnValSerThrTrpGluL :::::::::::::::::::::::::::::::::
	331 892	321 AsnAlaThrValAsnGluProGlnAspPheGln
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	848	
	304	287 nLeuAspAlaProCysCysLeuProGlyLysValThrLeuCysTrpGlnA
	848	834 CACATGCACCACATA
	287	271 AsnLeuTrpHisIleAlaArgLeuArgValLeuSerProGlyValTrpGl
	270 833	261ProPheArgGluAspProGlyAlaHisArg

COUNTRY; USA COUNTRY; USA ZIP: 98101 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: Apple Power Macintosh OPERATING SYSTEM: Apple Operating System 7.5.5 SOFTWARE: MICROSOft Word for Apple, Version 6.0.1 CURRENT APPLICATION DATA: APPLICATION UNMBER: US/09/022,255 FILING DATE: CLASSIFICATION UNBER: USN 08/620,694 FILING DATE: 21 MARCH 1996 APPLICATION UNBER: USSN 08/538,765 FILING DATE: 7 AUGUST 1995 PRIOR APPLICATION UNBER: USSN 08/538,765 FILING DATE: 7 AUGUST 1995 PRIOR APPLICATION UNBER: USSN 08/538,765 FILING DATE: 23 MARCH 1995 PRIOR APPLICATION UNBER: USSN 08/410,535 FILING DATE: 23 MARCH 1995 ATTORNEY/AGENT INFORMATION: NAME: DATA: DATA: DATA: DATA: APPLICATION UNBER: USSN 08/410,535	seq_documentation_block: Sequence 9, Application US/09022255 Patent No. 6072033 GENERAL INFORMATION: APPLICANT: Yao, Zhengbin APPLICANT: Spriggs, Melanie APPLICANT: Fanslow, William TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17 NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS: ADDRESSEE: Immunex Corporation STREET: 51 University Street CITTY. Seattle	648 laLeuAspSerCysThrSerSerGluAlaProGlyCysCys 662	615 lnLeuProAlaPheLeuAspAlaLeuGlnGlyGlyCysSerThrSerAla 631 1667 1667 632 GlyArgProAlaAspArgValGlu.ArgValThrGlnAlaLeuArgSerA 648	82 AlaThr ::: 75 TGCTTC 98 pSerVa ::: 25 CGACGT	554	522 rpPh@HisHisGlnArgArgArgIleLeuGlnGluGlyGlyValValIle 538

	80 GAGTTTCTGTCCAAACTGAGGCATCACCACAGGCGG
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yAlaG 166 TGCAG 429	153 rAlaValPheAspCysPheGluAlaSerLeuGlyAlaG
Glyse 153	137 GluValGlnValProAlaAspLeuValGlnProGlyGlnSerValG
euLeu 136 ::: ATC 380	124 erPheGlnAlaTyrProIleAlaArgCysAlaLeuLeu :: :: :: ::: ::: 340 CCCACACCCAACAAGGAGACCTGTTCCCCGTGGCTCACATC
lLeus 124 :::: CTTTG 339	107 rGluLeuGlnGluSerArgAsnAlaSerLeuGlnAlaGlnValValLeuS :::
AspSe 107	91 AlavalHisGlyHisTrpAlaGluProGluGluAlaGlyLysSerAspSe :::::: ::: ::: 261 TGCCTGGATGACAGCTGGATTCACCCTCGA
isLeu 90 GTACC 260	74 ysProGlnLysThrAspCysAlaLeuArgValArgValValValHisLeu
uArgC 74	61 uValProThrArgLeuGlnThrGluLeuValLeuArgC :::
ValLe 61 GTGCT 169	laProGlyPro
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ΦωΝ	alignment_scores: Ouality: 154.00 Length: 732 Ratio: 0.552 Gaps: 33 Percent Similarity: 38.115 Percent Identity: 19.399
	NAME LOCA 022-2
	7 E 8 8
	TOPOLOGY: INDEX MOLECULE TYPE: cDNA to mRNA HYPOTHETICAL: NO
	ES ES
	FOR SEQ ID
	0 H C
	ION NUMBER: 34,69

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ATCCAG	GATC	931
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GAGACCCTGC		717
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GAGCACGCCAGGATGAAGGTAACCACGCCATGCATGAGCTCAG 69	TGACTGTGAGCACG	641
:: ≱	oAsp	215
	ccaaacc	609
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IGANGLINLEUPTOASPÓLJAASPÁSNVAILPEULEUThrLeuAsp	ACCTGCCCAA	085 781
TGTGGTTGACCCTGACCAGGAATATGAGGTGACCGTTCACC 5		
u	} -:-	174

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seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-022-696-9
                                                                                                                            Sequence 9, Application US/09022696 Patent No. 6072037
                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                      _documentation_block:
                                                       APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1081 TCCTGCTGGTGGGCTCCGTCATC.....CTGCTCATCGTCTGCATGACC 1124
    APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6072037el Receptor That Binds IL-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 465 ArgArgLysAlaAlaArgGlySer......472
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                                                                                                                                                                                                                                                      GGAGATGTTCCAGCCGGGCCGCATGCACCGCGTAGGGGAGCTGT 1752
                                                                                                                                                                                                                                                                                                  laLeuAspSerCysThrSerSerSerGluAlaProGlyCysCys
                                                                                                                                                                                                                                                                                                                                                                          GlyArgProAlaAspArgValGlu.ArgValThrGlnAlaLeuArgSerA 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGACGTCCCCGACCTGTTCGGCGCGCGCGCGCCGCGTACCCGCTC..... 1667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGCTTCGGCACCTACGTAGTCTGCTACTTCAGCGAGGTCAGCTGTGACGG 1624
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGTTCACTGCAGCCATGAACATGATCCTCCCGGACTTCAAGAGGCCAGCC 1574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             laLeuAlaAlaTrpLeuSerCysValLeuProAspPheLeuGlnGlyArg 581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGTGGGCCGTCAGAAGCAGGAGATGGTGGAGAGCAACTCTAAGATCATC 1424
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                                                                              Yao, Zhengbin
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US-09-899-471-2 x US-09-022-696-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
LOCATION:
US-09-022-696-9
                                                                                                                                                                                                                                                                                                                                                                                                                               Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                     Align seg 1/1
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                        120 GCTGTCCCGGGGCCCCTGCTGGGCTGCTCCTGCTCCTGGGCGTGCT
                                                220
                                                                                                                                        170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 3223 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL | SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 23 MARCI
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ADDRESSEE: Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                  55 SerAlaProGlyPro......ValLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                   74 ysProGlnLysThrAspCysAlaLeuArgValArgValValValHisLeu
                                                                                                                                                                                 61 uValPro.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 51 Uni
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
AlaValHisGlyHisTrpAlaGluProGluGluAlaGlyLysSerAspSe 107
                                              GCTCCCAGCCG.
                                                                                                                                 GGCCCCGGGTGGCGTCCCTGCGACTCCTGGACCACCGGGCGCTGGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98101
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                                                                                                                                                                                                                                                                                                                     to: US-09-022-696-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 MARCH 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                                                                                                                                                                                             154.00
0.552
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                                                                                                                                                                             ..ThrArgLeuGlnThrGluLeuValLeuArgC
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                                              GGGCTAAACTGCACGGTCAAGAATAGTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anne
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90 219 74 169 61 1668

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 21 AsnAlaThrValAsnGluProGlnAspPheGln
 laProAspGlnSerProCysGlnProLeuValProProValProGlnLys
48 848
.87 nLeuAspAlaProCysCysLeuProGlyLysValThxLeuCysTrpGlnA 304
P11 AsnLeuTrpHisIleAlaArgLeuArgValLeuSerProGlyValTrpGl 287 :::::
 10 10 10 10 10 10 10 10
 34 CCACCAGCTGCGTGAGCTTCACCCTGTGGAACGAATCTACCCATTACC 783
IleGlnValTrpSerLeuGluPr :: GTGGAGACCCTGGAGGC
 19 ysSerLeuTrpTyrLysAsnLeuThrGlyProGlnAsnIleThrLeuAsn 235
115 oAspAlaLeuL 219
 99 ValSerGluGlnAspPheSerPheLeuLeuTyrLeuArgProValPr 215
82 snLeuThrGlnGlnLeuProAspGlyAspAsnValLeuLeuThrLeuAsp 198 :: :: ::
 74
70TrpSerTyrThr. 173
66 luValGlnIle
153 rAlavalPheAspCysPheGluAlaSerLeu
 137 GluValGlnValProAlaAspLeuValGlnProGlyGlnSerValGlySe 153
 24 erPheGlnAlaTyrProIleAlaArgCysAlaLeuLeu 136
 107 rGluLeuGlnGluSerArgAsnAlaSerLeuGlnAlaGlnValValLeuS 124 :::
 :::::: ::: ::: 261 TGCCTGGATGACAGCTGGATTCACCCTCGA

GAACATGATCCTCCCGG		582 A
uSerCysValLeuProAspPheLeuGlnGlyArg 581 :::: ::: :::	laLeuAlaAlaTrpLe ::::: :: TGTTCACTGCAGCCAT	565 1525
GlnLeuGlnThrValGluProGlyProHisAspA 565	GGGGGCGCCTGT	554 1475
erProAlaAlaValAlaGlnC: ::::: ::: CCCGCGGCACGCGCGCCAAGT	LeuLeuPheSer ::: GTCCTGTGCTCC	539 1425
HisHisGlnArgArgArgIleLeuG ::: ::::::::::::::: GGCCGTCAGAAGCAGGAGATGGTGGT	rpPheHisHisG	522 1375
oLeuTrps	aValAspLeuTr ::: CCTGGACCTGCT	505 1325
lyAlaLeuAlaSerAlaLeuSerGlnMetProLeuArgValAl 505 ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::	ValGlyAlaLeu	490 1275
GThrhlaLeuLeuHisSerAlaAspGlyAlaGlyTyrGluArgLeu 489	rgThrAlaLeuL ::: :: GGAAGGTCTGGA	473 1225
GATGGCCTGCCTGACCTGATCCCCCCACCGCTGAAGCCCA 1224	CACCGATGGCCT	473 1175
GLYSAlaAlaArgGlySer 	SAla - AGC:	N O
uLeuLeuAlaAlaAlaLeuPhePhePheLeuLeuLeuLysLysAsp 464 ::::::::::::::::::::::::::::::::	LeuA ::::	448 1081
MetAspLysTyrIleHisArgArgTrpValLeuValTrpLeuAlaC 448	: tAs	431 1053
ATGCCCCTGTGG		1041
VSMotGlnTeuTrpasnAspAspAspAspAspAspAspAspAspAspAspAspAspA	CT	1018
 gAlaAlaArgLeuGlyGluGluLeuLeuGlnAspPheArqSerHi	Argalaala	398
aLeuGluProSerGlyCysThrProLeuProSerMetAlaSerT 398 - ::: ::: ;:: CTTCAGACACTCCCCACTTCTTTTCCCCCCCACAAATCCCACACA	ysAlaLeuG	381 972
spMetLeuValGluMetLysThrGlyLeuAsnAsnThrSerVa 381 ::::::::: :::	MetLe	365 951
GInLeuGlnAlaCysSerTrpAlaAspSerLeuGlyProPheLys 364 :: GCAGATCCAG950	alGlnLeud	348 931
ValAlaGlyHisProAsnLeuCysValGlnValSerThrTrpGluL 348	alalagi	332

alignment_scores:

Ty: 38.115 Percent Identity: 19.39 x US-08-978-773-3 c: US-08-978-773-3 c: US-08-978-773-3 dGlyPro	Quality: 154.00 Length: 73 Ratio: 0.552 Gaps: 3
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522	05 aValAspLeuTrpSerArgArgGluLeuSerAlaHisGlyAlaLeuAlaT	505
505 1324	0 ValGlyAlaLeuAlaSerAlaLeuSerGlnMetProLeuArgValAl ::: ::	490 1275
489 1274	73 rgThrAlaLeuLeuLeuHisSerAlaAspGlyAlaGlyTyrGluArgLeu 	473 1225
1224	CACCGATGGCCTGCCTGCGGCTGACCTGATCCCCCCCACCGCTGAAG	1175
473		473
472 1174	55 ArgArgLysalaalaArgGlySer	465 1125
464 1124	48 ysLeuLeuLeuAlaAlaAlaLeuPhePhePheLeuLeuLysLysAsp ::::::::::::::::::::::::::::::	1081
448 1080		1053
1052	ATGCCCCTGTGG	1041
431	GlnCy	415
414 1040	nrArgAlaAlaArgLeuGlyGluGluLeuLeuGlnAspPheArgSer	1018
1017	::: ::: TGCCTCAGACACTCC	97:
971	1TTCAGCAGCTGCCTCAATGAC 1 1CysAlaLeuGluProSerGlyCysThrProLeuProSerMe+al	38.
381	5 AspAspMetLeuLeuValGluMetLysThrGlyLeuAsnAsn	்
364 950	48 ysValGlnLeuGlnAlaCysSerTrpAlaAspSerLeuGlyProPheLys :: :: 11 AAGTGCAGATCCAG	93
348 930 ·	32 .LeuValAlaGlyHisProAsnLeuCysValGlnValSerThrTrpGluL	89 3
892		86
331	GluProGlı	32
098		849
320	laProAspGlnSerProCvsGlnProLeuValProProValProClnLw	304
304	nLeuAspAlaProCysCysL	28
848	CACATGCACCACATA	834
K)	1 AsnLeuTrpHisIleAlaArgLeuArgValLeuSe	27
270 833	bi ProPheArgGluAspProGlyAlaHisArg ProPheArgaNagNProGlyAlaHisArg ProPheArgNProGlyAlaHisArg ProPheArgNProGlyAlaHisArg ProPheArgNProGlyAlaHisArg ProPheArgNProGlyAlaHisArg ProPheArgNProGlyAlaHisArg ProPheArgNProGlyAlaHisArg ProPheArgNProGlyAlaHisArg	78
	4 CCACCAGCTGCGTGTGAGCTTCACCCTGTGGAACG	73
260	OAspSerGluArgValGluPheCys	25

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	ING DATE: / AUGUST 199 SSIFICATION:	
	PPLICATION NUMBER: USSN	
	; APPLICATION NUMBER: US/08/620,694 ; FILING DATE: 21-MARCH-1996	
	R APPLICATION DATA:	
	; FILING DATE:	
	APPLICA	
	SOFTWARE: Microsoft Word for Apple, Version	
	G SYSTEM: Apple Operat	
	MEDIUM TYPE: Floppy disk	
	COMPUTER READABLE FORM:	
	OUNTRY:	
	STATE: WA	
	TREET: 51 Universi	
	S:	
1	R OF SEQUENCES: 10	
11	William	
	; APPLICANT: Spriggs, Melanie	
	INFORMATION:	
	<pre>seq_documentation_block: sequence 9, Application US/09022253 Patent No. 6096305</pre>	
	me: /cgn2_6/F	
	CCAGCCGGCCATGCACCGCGTAGGGGAGCTG	
	648 laLeuAspSerCysThrSerSerSerGluAlaProGlyCysCys 662	
1708	BACAGGTTCGAGGAG	
648	ArgValGlu.ArgValThrGlnAlaLeuArgSe	
1667	1667	
631	615 lnLeuproAlaPheLeuAspAlaLeuGlnGlyGlyCysSerThrSerAla	
1667		
615	erValProSerProPheArgValAlaProLeuPheSer	
1624	CTACGTAGTCTGCTAC	
598	hrGlyArgTyrValGlyValTyrPheAspGlyL	
1574	TCACTGCAGCCATGAACATGATCCTCCCGG	
581	AlaAlaTrpLeuSerCysValLeuProAspPheLeuG	
1524	1475 GGGGCCCTGTGCGGCTGCGACCACGGAAAGCCCGTGGGGGACC	
565	nThrValGluProGlyProHisA	
1474	1425 GTCCTGTGCTCCCGCGCGCACGCGCCCAAGTGGCAGGCGCTCCTGGGCCG	
553	539 LeuLeuPheSerProAlaAlaValAlaGlnCysGlnGlnTrpLeu	
538 1424	522 rpPheHisHisGlnArgArgArgIleLeuGlnGluGlyGlyValValIle	
1374	1325 CCTGGACCTGGAAGAGCAGGCCATCTCGGAGGCAGGAGTCATGACCT	

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	166 luValGlnIle	153 rAlaValPheAspCysPheGluAlaSerLeuGlyAlaG 166	137 GluValGlnValProAlaAspLeuValGlnProGlyGlnSerValGlySe 153 ::: ::: 381 GAATGGACACTGCAGACACACAC	124 erPheGlnAlaTyrProIleAlaArgCysAlaLeuLeu 136 :: :: :: :: :: :: :: :: :: :: :: :: ::	107 rGluLeuGlnGluSerArgAsnAlaSerLeuGlnAlaGlnValValLeuS 124 ::: :::	91 AlaValHisGlyHisTrpAlaGluProGluGluAlaGlyLysSerAspSe 107 :::::: ::: ::: ::: 261 TGCCTGGATGACAGCTGGATTCACCCTCGA	74 ysProGlnLysThrAspCysAlaLeuArgValArgValValValHisLeu 90 ::: ::: 220 GCTCCCAGCCGGGGCTAAACTGCACGGTCAAGAATAGTACC 260	61 uValProThrArgLeuGlnThrGluLeuValLeuArgC 74 ::: 1 170 GGCCCGGGTGGCGCCTCCCTGCGACTCCTGGACCACCGGGCGTTGTT 219	55 SerAlaProGlyProValle 61 :::::: 120 GCTGTCCCGGGGCCCCTGCTGGGGCTGCTGCTGCTGCTGC	:o: US-09-022-253-9 f	allgnment_block: US-09-899-471-2 x US-09-022-253-9		ignm	; RAME/KEY: CDS ; LOCATION: 932693 US-09-022-253-9		HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:		INFORMATION FO SEQUENCE CHA LENGTH: 3	RECISTRATION NUMBER: 34,695 REFERENCE/DOCKET NUMBER: 2617-B TELECOMMUNICATION INFORMATION: TELEPHONE: (206)587-0430	CLASSIFICATION: ATTORNEY/AGENT INFORMATION: NAME: Perkins, Patricia Anne	APPLICATION NUMBER: USSN 08/410,535 FILING DATE: 23 MARCH 1995
	398 hrArgAlaAlaArgLeuGlyGluGluLeuLeuGlaAspPheArgSerHis 414		365 AspasphetLeuLeuValGlumetLysThrGlyLeuAsnAsnThrSerVa 381 ::::::::	ysValGlnLeuGlnAlaCysSerTrpAlaAspSerWeuGlyProPheLys :: ::: AAGTGCAGATCCAG		. >			271 AsnLeuTrpHisIleAlaArgLeuArgValLeuSerProGlyValTrpG1 287 :::::	AGATCCTGCTGACCAGTTTTCCGCACATGGAGAACCACAGTTGCTTTGAG	261 ProPheArgGluAspProGlyAlaHisArg 270	252 oAspSerGluArgValGluPheCys	717GTGGAGACCCTGGAGGC 733		219 ysSerLeuTrpTyrLysAsnLeuThrGlyProGlnAsnIleThrLeuAsn 235		199 ValSerGluGluGlnAspPheSerPheLeuLeuTyrLeuArgProValPr 215 :::::: ::: 609CCAAACCACCAGTCCAAGAATTTCCTT	182 snLeuThrGlnGlnLeuProAspGlyAspAsnValLeuLeuThrLeuAsp 198 :: ::: :::	174LysProArgTyrGlnLysGluLeuA 182	GAGTTTCTGTCCAAACTGAGGCATCACCACAGGCGGTGGCGTTTTACCTT	170 TrpSerTvrThr 173

415 GL	GlnCysMetGlnLeuTrpAsnAspAspAsnMetGlySerLeuTrpAlaCy 4	431
1041		1052
431 sp	pLysTyrIleHisArgArgTrpValLeuValTrpLeuAlaC	448
	hePhePheLeuLeuLysLysAsp ::: :::::	464
465 Ar		472
473	AAATA	473
75 c	CGATGGCCTGCCTGCGGCTGACCTGATCCCCCCACCGCTGAAGCCCA	1224
473 rg:	rgThrAlaLeuLeuLeuHisSerAlaAspGlyAlaGlyTyrGluArgLeu 4 	489 1274
490 Val 1275 GTC	ValGlyAlaLeuAlaSerAlaLeuSerGlnMetProLeuArgValAl 5 ::: ::: ::: 5	505 1324
505 ava :: 1325 CCT	aValAspLeuTrpSerArgArgGluLeuSerAlaHisGlyAlaLeuAlaT 5 	522 1374
522 rps 1375 GGC	rpPheHisHisGlnArgArgArgIleLeuGlnGluGlyGlyValValIle 5 	538 1424
539 Leu ::: 1425 GTC	LeuLeuPheSerProAlaAlaValAlaGlnCysGlnGlnTrpLeu5 ::: :::::: ::: GTCCTGTGCTCCCGCGGCACGCGCGCCAAGTGGCAGGCGCTCCTGGGCCG 1	553 1474
554 1475 GGG	GlnLeuGlnThrValGluProGlyProHisAspA ::: :::	565 1524
565 laLeu ::: 1525 TGTTC	AlaAlaTrpLeuSerCysValLeuProAspPheLeuGlnGlyArg ::: ::::: ###	581 1574
582 Ala ::: 1575 TGC	AlaThrGlyArgTyrValGlyValTyrPheAspGlyLeuLeuHisProAs 5:::	598 1624
598 pser ::: 1625 cgac	ValProSerProPheArgValAlaProLeuPheSerLeuProThrG :::	615 1667
15	lnLeuProAlaPheLeuAspAlaLeuGlnGlyGlyCysSerThrSerAla 631	}1
632 G1y	ArgProAlaAspArgValGlu.ArgValThrGlnAlaLeuArgSerA	1667 648 1708
	spSerCysThrSerSerSerGluAlaProGlyCys	
documentation luence 9, App luence 9, App	tation_block: 9, Application US/09022260 , 6100235	

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alignment_block:
US-09-899-471-2 x US-09-022-260-9
                                                                                                                                                                                                                                                                                 alignment_scores:
                                                                                                                                             Align seg 1/1
                                                                                                                                                                                                                                Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Yao, Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NFORMATION FOR SEQ ID NO:
                                                                   120 GCTGTCCCGGGGCCCCTGCTGCGGGCTGCTTGCTGCTCCTGGGCGTGCT 169
170 GGCCCCGGGTGGCGCCTCCCTGCGACTCCTGGACCACCGGGCGCTGGTCT 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 3223 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION DATA:
                                       61 uValPro
                                                                                                 55 SerAlaProGlyPro......Valle 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operation
OPERATING SYSTEM: Apple Operation
OPERATING SYSTEM: Apple Operation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 26
ELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DLECULE TYPE: cDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Perkins, Patricia REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                           GINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               I-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INVENTION:
                                                                                                                                           to: US-09-022-260-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : Yao, Zhengbin
                                                                                                                                                                                                                                                                                                                                                                                                     : Human IL-17 R (hCTLA8 receptor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Immunex Corporation
51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spriggs, Melanie
Fanslow, William
VENTION: No. 6100235el Receptor That Binds IL-17
                                                                                                                                                                                                                                                                                                                                                      CDS
93..2693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (206)
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                                                                                                                                                                                                                              154.00
0.552
38.115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                                  .ThrArgLeuGlnThrGluLeuValLeuArgC 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34,695
ER:
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                                                                                                                                                                                                                                Percent Identit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2617-в
                                                                                                                                         from: 1 to: 3223
                                                                                                                                                                                                                                : 19.399
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8		848
	oGlyLysValThrL	287
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7	AsnLeuTrpHisIleAlaArgLeuArgValLeuSerProGlyValTrpGl 287 ::::	271
3		261 784
3	CCACCAGCTGCGTGTGAGCTTCACCCTGTGGAACGAATCTACCCATTACC 783	734
0	oAspSerGluArgValGluPheCys	252
ω έλ	uGluPr 25 GGAGGC 73	236 717
6	GCAGCCTGTGGGACCCCAACATCACC716	-
U	ysSerLeuTrpTyrLysAsnLeuThrGlyProGlnAsnIleThrLeuAsn 235	
	oAspAlaLeuL 219 	215 641
O VI	ValSerGluGluGlnAspPheSerPheLeuLeuTyrLeuArgProValPr 215 ::::: ::::	199
	snLeuThrGlnGlnLeuProAspGlyAspAsnValLeuLeuThrLeuAsp 198 :: :: :: ACCTGCCCAAGCCCATCCCTGATGGGGAC	580
6 N		17 <u>4</u> 530
vo w	TrpSerTyrThr. 173 GAGTTTCTGTCCAAACTGAGGCATCACCACAGGCGGTGGCGTTTTACCTT 529	
vo v		430
ف م	luvalGlnileGCCAGCATCCTGTACCTCGAGGGTGCAG 429	166
, a	AlaValPheAspCysPheGluAlaSerLeuGlyAlaG 1	153
μ ω	GluvalGlnValProAlaAspLeuValGlnProGlyGlnSerValGlySe 153 :: :: GAATGGACACTGCAGACACAC	137 381
O 01	erPheGlnAlaTyrProIleAlaArgCysAlaLeuLeu 136 :: ::	4 2
خة ب	rGluLeuGlnGluSerArgAsnAlaSerLeuGlnAlaGlnValValLeuS 124 :::	107 291
	AlaValHisGlyHisTrpAlaGluProGluGluAlaGlyLysSerAspSe 107 ::::: TGCCTGGATGACAGCTGGATTCACCCTCGA	91 261
	ysProGlnLysThrAspCysAlaLeuArgValArgValValValHisLeu 90 	74 220

581	5 laLeuAlaAlaTrpLeuSerCysValLeuProAspPheLeuGlnGlyArg	56
565 1524	5 GGGGGCCTGTGCGGCTGCGCGCACCACGGAAAGCCCGTGGGGGACC	147
` 4a (n	9 LeuLeuPheSerProAlaAlaValAlaGlnCysGlnGlnTrpLeu 1	
538 1424	22 rpPheHisHisGlnArgArgArgIleLeuGlnGluGlyGlyValValIle	52 137
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505 1324	0 ValGiyAlaLeuAlaSerAlaLeuSerGlnMetProLeuArgVe	49 127
489 1274	73 rgThrAlaLeuLeuLisSerAlaAspGlyAlaGlyTyrGluArgLeu	122
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1080	SI SPTOMECASPLYSTYTITEHISATGATGTTPVALLEUVALTTPLEUALIAC	105
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398 1017	1 lCysAlaLeuGluProSerGlyCysThrProLeuProSerMetAlaSer	38 97
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-DB-EST -QFMT=fastap -SUFFIX=rst -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -QGAPOP=4.500
-GAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
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-DELEXT=7.000 -START=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_NX=100 -THR_MIN=0
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-MINLEN=0 -MAXLEN=200000000 -USER=US0989471_@CGN1_1_7278
-NCDU=3 -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30
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                     /organism="Mus musculus"
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Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y., Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
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Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, I., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kout, M., KOya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, H., Sakai, C., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasal, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.

RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
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AV010326 Mus musculus 18-day embryo
clone 1110025H02, mRNA sequence.
                                                       CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                   Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
                                                                                                                                                                                                                                                                                                                             RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 |(11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y., and Hayashizaki,Y.
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Tel: 81-298-36-9145
Fax: 81-298-36-9098
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on May 11, 1999 this sequence version replaced gi:4787313
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Computational Analysis of Full singth Mouse cDNAs Compared with Juman Genome Sequences Mamm. Genome. 12, 673-677 (2001)
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                                                                                             GlyGlyValValIleLeuLeuPheSerProAlaAlaValAlaGlnCysGl 550
                                                                                                                                                      isGlyAlaLeuAlaTrpPheHisHisGlnArgArgArgIleLeuGlnGlu 533
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.laAlaTrpLeuSerCysValLeuProAspPheLeuGlnGlyArgAlaThr 583
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                                                                               GGTGGCGTGGTAATCCTTCTCTCTCGCCCGCGGCCGTGGCGCAGTGTCA
                                                                                                                                      ACGGAGCCCTAGCCTG. TTCCACCACCAGCGACGCCGTATCCTGCAGGAG
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Ratio: 4.489
milarity: 92.128
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/dev_stage="18-day embryo"
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AUTHORS
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               BASE COUNT
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                                                                                                                                                                                                                                                   DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1133 row: k column: 20
High quality sequence stop: 697.
                                                                                                                                                                                                                  High quality sequence stop: (Location/Qualifiers 1..697
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

1 | (bases 1 to 697)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
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                  141
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/clone="IMAGE:5135755"
/clone="IMAGE:5135755"
/clone="IMAGE:5135755"
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Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 212 c 205 g 139 t
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IMAGE:5135755 5',
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alignment_scores:

Quality: 1226.00

Length:

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                                     DEFINITION
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                                                                                                                            AlaAlaLeuPhePhePheLeuLeuLysLysAspArgArgLysAlaAl 469
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                                 BG968034 784 k
602832412F1 NCI_CGAP_Co24 Mus
                          mRNA sequence.
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IMAGE:4987035 5',
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Quality: 1187.00
Ratio: 5.051
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TITLE
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
                                                                                                                                                                                                                                                                                                                                                                                                                                            found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov plate: LLAM10997 row: 9 column: 04
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian (1999)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                    quality sequence stop: 646.
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Site_2: Sall; Cloned unidirectionally. Primer: C
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 231 c 229 g 151 t
                                                                                                                                                                                                                            /db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/strain="FVB/N"
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Percent Identity: Length: Gaps: 89.370

to: BG968034 from: 1 ç t

uGluProAspSerGluArgValGluPheCysProPheArgGluAspProG AGAGCCAGACTCTGAGAGGGTCGAATTCTGCCCCTTCCGGGAAGATCCCG 52 102 267

lyAlaHisArgAsnLeuTrpHisIleAlaArgLeuAggValLeuSerPro GTGCACACAGGAACCTCTGGCACATAGCCAGGCTGCGGGTACTGTCCCCA 152

GlyValTrpGlnLeuAspAlaProCysCysLeuP GGGGTATGGCAGCTAGATGCGCCTTGCTGTCTGCCGGCCAAGGTAACACT 317 300

252

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                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1006)

Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Koud, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasak, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.

RIKEN Mouse ESTs (Arakawa, T., et al. 2001)

Unpublished (2001)
Email: genome-res@gc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
                                                                                                                                                                                               Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jar
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BB609618 RIKEN full-length enriched, 18 days cDNA clone 1110025H02 5', mRNA sequence.
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                                                                                                                                                                                                                Kanagawa 230-0045, Japan
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ThrLysProArgTyrGlnLysGluLeuAsnLeuThrGlnGlnLeuPro.. ACGAAGCCCAGGTACCAGAAAGAGCTCAACCTCACACAGCAGCTGCCTGA

188

162

112

63

188

139

nValProAlaAspLeuValGlnProGlyGlnSerValGlySerAlaValP 156

heAspCysPheGluAlaSerLeuGlyAlaGluValGlnIleTrpSerTyr 172 GGTGCCCGCTGACCTGGTGCA.CCTGGTCAGTCCGTGGGTTCTGCGGTAT

TGTTTCGAGGCTAGTCTTGGGGCTGAGGTACAGATCTGGTCCTAC

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alignment_block:
US-09-899-471-2 x BB609618
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequencing pipeline with 384 multicapillary 10 (11), 1757-1771 (2000)
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4.227
76.989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="18 days embryo
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DEFINITION ua81f02.rl Soares_mammary_gland_NbMMG M.
IMAGE:1363899 5', mRNA sequence.
                                   seq_documentation_block:
LOCUS AI007139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                          373 LysThrGlyLeuAsnAsnThrSerValCysAlaLeuGluProSerGlyCy
406 luLeufeuGlnAspPheArgSerHisGlnCysMetGlnLeuTrpAsnAsp
                                                    389 sThrProLeuProSerMetAlaSerThrArgAlaAlaArgLeuGlyGluG 406
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                                                                                            3 AAAACCGGCCTCAACAACACATCAGTCTGTGCCTTGGAACCCAGTGGCTG
                                         TACACCACTGCCCAGCATGGCCTCCACGAGAGCTGCTCGCCTGGGAGAGG
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1 (bases 1 to 775)
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/lab_host="DH10B"
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52 389 86:822

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Seq primer: -28m13 rev2 ET from High quality sequence stop: 495. Location/Qualifiers 1. .775
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Marra M/Mouse EST Project
Washu-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. LA
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mouseest@watson.wustl.edu
                                               adaptors (Pharmacia), digeste
the Not I and Eco RI sites of
RNA provided by Dr. Minoru Ko,
constructed and normalized by
                                                                                                                                                               T 3']; double-stranded cDNA was ligated to Eco
                                                                                                                                                                                                                                               /note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia
) with a modified polylinker; Site_1: Not I; Site_2: Eco
RI; it strand cDNA was primed with a Not I - oligo(dT)
                                                                                                                                                                                          /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1363899"
                                                                                                                                                                                                                                                                                                                                                                                             tissue_type="mammary gland"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Soares_mammary_gland_NbMMG"
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163 t
                                                                            digested with Not I and cloned into ites of the modified pT7T3 vector noru Ko, Wayne State Univ. Library
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                                                     Soares and M.Fatima
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REFERENCE
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KEYWORDS
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                                                                                                                                                                                         ACCESSION
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                                                                                                                                                                                                                                                                                                           CTTAAGGGAAGGTGATCAATTTCG
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        NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                          Mus musculus
                                                                                                                                                                                       mRNA sequence.
BF237179
                                                                                                                                                                                                                  602028133F1 NCI_CGAP_L19
Email: cgapbs-r@mail.nih.gov
                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus (bases 1 to 722)
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COMMENT

SOURCE

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alignment_block:
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                                                                                                                                                       AlaPhéLeuAspAlaLeuGlnGlyGlyCysSerThrSerAlaGlyArgPr
                                         YARGTYrValGlyValTyrPheAspGlyLeuLeuHisProAspSerValP
                                                                                                                                                                                                                                                                  aGlyTyrGluArgLeuValGlyAlaLeuAlaSerAlaLeuSerGlnMetp
                                                                                                  CCGCTACGTCGGGGTCTACTTCGACGGGCTGCTGCACCCAGACTCTGTGC
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4163217"
/clone_lib="NGI_CGAP_Li9"
/clone_lib="NGI_CGAP_Li9"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: Not
Site_2: SalI; Cloned unidirectionally. Primer: Oligo
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
28 a 238 c 255 g 101 t
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Percent Identity:
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ocus BB625706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNa libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

Wagi, Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BB625706 RIKEN full-length enriched, adult male demusculus cDNA clone 9330110N14 5', mRNA sequence.
                                                                                                                                                                                                                          Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, J., Alzawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: genome res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci.p., Shibata.Y., Hayatsu,N.,
M., Konno.H., Okazaki,Y., Muramatsu,
                                                                                     Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Yoshihide Hayashizaki
                                                                                                                                                                                          Hayashizaki,Y
                                                                                                                                                                                                                                                                                                                                                    sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                       do,S., Shinagawa,A.,
Fukuda,S., Hara,A.,
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                                                              tissues.
            Location/Qualifiers
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                                                                                                                                                                                                             Itoh, M., Kawai, J., Shibata, K.
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d, adult male diencephalon
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US-09-899-471-2 x BB625706/rev
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                                                     rProalaAlaValAlaGlnCysGlnGlnTrpLeuGlnLeuGlnThrValG
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              AspPheLeuGlnGlyArgAlaThrGlyArgTyrValGlyValTyrPheAs
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5.247
99.497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diencephalon"
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/dev_stage="adult"
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AUTHORS
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SOURCE
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Arakawa,T.; Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
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Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTS (Arakawa,T., et al. 2001)
Contact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jaj
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Please visit our web site (http://genome. 12, further details.
                                                                                                                                encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) KONDO, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Alzawa, K., Fukuda, S., Hara, A., Itoh, M., Kawal, J., Shibata, K. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                   sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
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Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: genome-res@gsc.riken.go.jp,
URL:http://genome-gsc.riken.go.jp/
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                               Computational Analysis of Full-Length Mouse cDNAs Compared with Juman Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                          Computer-based methods for the mouse full-length cDNA

    Y. and Hayashizaki, Y.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-*Site_1: Sal1; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGAGCCCAAGAGCCTCTTTTTTTTTTTTTYN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. CDNA went through one round of normalization
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/dev_stage="adult"
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/db_xref="taxon:10090"
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Gaps: 0
Percent Identity: 99.476
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a lignment_scores:
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US-09-899-471-2
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                                                                                              Quality:
                                                                                                                                                                                                                                                                                                                                                                                  DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM8516 row: f column: 07
High quality sequence stop: 562.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humph
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; 1 cbases 1 to 562)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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5.342
100.000
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Site_2: NotI; Cloned unidirectionally. Primer: Oligo do
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
                                                                                                                                                                                                                                                         /tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                   /clone="IMAGE:3484038"
/clone_lib="NCI_CGAP_Mam5"
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                                                                                                                                                                                                                                                                                                                             gb_est2:BF160122
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies,
cDNA Library Arrayed by: The I.M.A.G.E. Conso
DNA Sequencing by: Incyte Genomics, Inc.
                                                                                                                                 Mus musculus
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
1 (bases 1 to 635)
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National Institutes of Health, Mammalian
                                                                                         Unpublished (1999)
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                             LeuAspAlaLeuGlnGlyGlyCysSerThrSerAlaGlyArgPro.AlaA 636
                                                                                                                                               rValGlyValTyrPheAspGlyLeuLeuHisProAspSerValProSerP 603
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95.652
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229 c 204 g 110 t
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Stem cell origin."
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/strain="CZECH II (feral)"
/db_xref="taxon:10090"
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/clone_lib="NCI_CGAP_Lu29"
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                                                                                                                                                                                        Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphre
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM.1371 row: m column: 03
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Eukaryota; Metazoa; Chordata; Cra
Mammalia; Eutheria; Rodentia; Sci
1 (bases 1 to 839)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
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mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 836.
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                                                                                                                                                                                                                                                                                         /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sa
Site_2: NotI; Cloned unidirectionally. Primer: Oligo
Library constructed by Life Technologies. Investigator
providing samples: Lothar Hennighausen/Robin Humnhrown
NIH"
                                                                                                                                                       967.50
5.013
91.469
                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:5150378"
/clone_lib="NCI_CGAP_Mam5"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/strain="C57/B6"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                     gb_est2:BG761977
                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                       1 (bases 1 to 935)
Nati-NGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                     Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                 mRNA sequence.
BG761977
BG761977.1 GI:14072630
                                                                                                                                                                                                                                    602718928F1 NIH_MGC_49
                                                                                                                                                                            human.
cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
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Homo s
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                                                                                                                                   Craniata; Vertebrata; Catarrhini; Hominidae;
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http://image.llnl.gov
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/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9606"
/clone="IMAGE:4858806"
/clone_lib="NIH_MGC_49"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence contained an oligo-dT track that was present in the oligonuclectide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the non-normalized rat aorta pool library cDNA Library Preparation: M.B. Scares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com)
                                                                                                                                                              Program for Rat Gene Discovery and Mapping University of Iowa 451 Eckstein Medical Research Building Iowa City, Tel: 319 335 8250 Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BI282622
619 bp mRNA linear EST 19-JUL-20: UI-R-CW0s-ccd-b-11-0-UI.sl UI-R-CW0s Rattus norvegicus cDNA clone UI-R-CW0s-ccd-b-11-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                      Contact: Soares, MB
                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                          97044477
                                                                                                                                                                                                                                                                                       Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                             discovery
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                                                                                                                                                                                                                                                                                                                                            Bonaldo, M.F.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BI282622
                                                                                                                                             Email: msoares@blue.weeg.uiowa.edu
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                        approaches
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Ratio:
Percent Similarity:
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erAlaHisGlyAlaLeuAlaTrpPheHisHisGlnArgArgArgIleLeu 531
                                                                                                                                                                                                                           AlaThrGlyArgTyrValGlyValTyrPheAspGlyLeuLeuHisProAs
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                                                                                                                                                                                                                                                                                                                                                   GCGACCGGCCCTACGTCGGGGTCTACTTTGACGGGCTGCTGCACCCAGA
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POLYA=Yes.
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/note="vector: py773D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-CW0s
library is a non-normalized library constructed from the
following rat aorta tissues: embryonic day 19, embryonic
day 21, adult day 1, adult day 12, adult day 75, adult day
200. For a detailed description of the library from which
this clone was derived, please visit our web site at
ratest.eng.uiowa.edu. The subtraction has been previously
described in (Bonaldo, Lennon and Soares, Genome Research
6:791-806, 1996)
TAG_ILB=UI-R-CW0S
TAG_ILB=UI-R-CW0S
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TAG_SEQ=CTGTAGGATC"
a 197 c 211 g 106
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/db_xref="taxon:10116"
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eq_name: gb_est2:BM210218
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BM210218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Piao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Lim,M.K., Luo,A., Tanaka,T., Kunath,T., Rossant,J. and Ko,M.S.H.
Systematic Analyses of NIA Mouse Trophoblast Stem Cell cDNA Library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cdna@lgsun.grc.nia.nih.gov
Plate: C0660 row: H column: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Dawood B. Dudekula
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BM210218.1 GI:17766987
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4 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-L. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with Sal1 and NotI enzymes and cloned into Sal1/NotI site of pSPORT1 plasmid vector.
                                                                                                                                                                                                                                                                          /note-*Vector: pSPORT1 (Invitrogen); Site_1: SalI; Site_2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a short-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were obtained from Dr. Janet Rossant and Tilo Kunath (Samuel Lunenfeld Research Institute, Canada). Double-stranded CDNAs were synthesized with an Oligo(dT) primer
                                                                                                                                                                                                                                    /tissue_type="Trophoblast stem cell"
/dev_stage="3.5-dpc"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="B5/EGFP transgenic
/db_xref="niaEST:C0660H10-3"
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                                                                                                                                                                                                                                                                  Invitrogen
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Homo sapiens
                                                     BM009552.1 GI:16523906
EST.
                                                                                                       BM00955
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ATURES

source

AUTHORS FERENCE

MMENT JOURNAL TITLE ORGANISM YWORDS RSION CESSION FINITION

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alignment_block:
US-09-899-471-2 x BM210218/rev
                                           seq_documentation_block:
            DEFINITION · 603630118F1 NIH_MGC_41 Homo sapiens
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                                                                                                                                                              561 yProHisAspAlaLeuAlaAlaTrpLeuSerCysValLeuProAspPheL 578
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                                                                                                                                                                                                                                                                                                                                                                                                                                      euGlnGlyArgAlaThrGlyArgTyrValGlyValTyrPheAspGlyLeu
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                                                                                                                                                                                                                                  CCACATT.CCGGGGCGACCCGCGACCGGGTGGAACGAGTGACCCAGGCG
                                                                                                                                                                                                                                                              erThrSerAlaGlyArgProAlaAspArgValGluArgValThrGlnAla
                                                                                                                                                                                                                                                                                              rLeuProThrGlnLeuProAlaPheLeuAspAlaLeuGlnGlyGlyCysS
                                                                                                                                                                                                                                                                                                                                                          CTGCACCCAGACTCTGTGCCCTCCCCGTTCCGCGTCGCCCCCCCTCTTCTC
                                                                                                                                                                                                                                                                                                                                                                         LeuH1sProAspSerValProSerProPheArgValAlaProLeuPheSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCCGCATGACGCCCTCGCCGCCTGGCTCAGCTGCGTGCTACCCGATTTCC
                                                                                                       CTGCGAGGAATGGGACCTGGGACCCTGCACTACACTAGAA 23
                                                                                                                                                                                                                                                                                                                                                                                                                         TGCAAGGCCGGGCGACCGGCCGCTACGTCGGGGTCTACTTCGACGGGCTG
                                                                          gb_est2:BM009552
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mRNA sequence.
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TITLE
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JS-09-899-471-2 x BM009552
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AspAsnMetGlySerLeuTrpAlaCysProMetAspLysTyrIleHisAr 439
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CAAGGCCCCCAGGACAACAGATCCCTCTGTGCCTTGGAACCCAGTGGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTGTGGACAAGGTTCTCGAGTTCCCATTGCTGAAAGGCCCACCCTAACCT
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1 (bases 1 to 702)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://image.llnl.gov
Plate: LLCM1922 row: c column:
High quality sequence stop: 697.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       into EcoRI/XhoI sites using the following 5 adaptor: GCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    872.50
4.256
88.362
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/db_xref="taxon:9606"
/clone="IMAGE:5443900"
/clone_lib="NIH_MGC_41"
/tlssue_type="amelanotic melanoma, cell line"
/tlssue_type="amelanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2: ECORI; cDNA made by oligo-dT priming. Directionally clon
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Percent Identity: 71.983
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uLeuPheSerProAlaAlaValAlaGlnCysGlnGlnTrpLeuGln 554
                                                                                                                                                                                                                                  ArgThrAlaLeuLeuHisSerAlaAspGlyAlaGlyTyrGluArgLe 489
                                                                                                                                                                                                                                                                                                           gArgTrpValLeuValTrpLeuAlaCysLeuLeuLeuAlaAlaAlaLeuP 456
                                                                          PheHisHisGlnArgArgArgIleLeuGlnGluGlyGlyValValIleLe 539
                                                                                                                  TAGACCTGTGGAGCCGTCGTGAACTGAGCGCGCAGGGGCCCCGTGGCTTGG
                                                                                                                                alAspLeuTrpSerArgArgGluLeuSerAlaHisGlyAlaLeuAlaTrp 522
                                                                                                                                                                           uValGlyAlaLeuAlaSerAlaLeuSerGlnMetProLeuArgValAlaV 506
                                                                                                                                                                                                                                                                                            CCCTCATCCTCCTCCTCAAAAAGGATCACGCGAAAGCGGCCGCCAGGGGC
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b_htg:AC026685
b_htg:AC024612
b_htg:AC068099
b_htg:AC096599
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b_htg:AC026685
b_htg:AC026196
b_pat:AX350982
b_ro:AF456232
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b_htg:AC099658
b_om:AF130972
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b_pat:AX350973
b_pat:AX136341
b_pat:AX073996
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Natabase length: 1873333701
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-Q-/G9D2_1/USPTO_Spool/US09899471/runat_27092002_142439_17908/app_query.fasta_1.2519
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-DB=GenEmb1 -QFMT-fastap -SUFFIX=rge -GAPOP=12.000 -GAPEXT=4.000
-MINLATCH=0.100 -LOOPELAP -0.000 -COOPEXT=0.000 -GAPOP=4.500
-QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
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-DELEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.7500 -THR_MIN-0
-LIST=45 -DOCALIGN=200 -THR_SCORE=PCT -THR_MX=100 -THR_MIN-0
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-MINLEN=0 -MAXLEN=2000000000 -USER=US09899471_@CGN1_111274
-NCPU=6 -ICPU=3 -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30
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b_pat:AX350978
b_pat:AX073993
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b_pr:AC007783
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_pat:AX180776
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3.8e-14

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                         i ACO05258 Homo sapiens chromos
i ACO93640 Homo sapiens chromo
l ACO93646 Homo sapiens chromo
l ACO92466 Homo sapiens chromo
i ACO904973 Homo sapiens BAC cl
i ACO10973 Homo sapiens BAC cl
i ACO10973 Homo sapiens BAC cl
i A79049 Sequence 1 from Patent
i X60469 R. rattus FE65 mRNA for
AF333983 Rattus norvegicus FE6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AX350976 Sequence 10 from Patel AX350978 Sequence 12 from Patel AX073993 Sequence 1 from Patel AX073993 Sequence 161 from Patel AX073993 Sequence 13 from Patel AX180776 Sequence 13 from Patel BC006411 Homo sapiens, clone AX350973 Sequence 7 from Patel AX350973 Sequence 263 from Patel AX073996 Sequence 3 from Patel AX073996 Sequence 6 from Patel AX073998 Sequence 6 from Patel AX073998 Sequence 6 from Patel AX073998 Sequence 6 from Patel AX073998 Sequence 6 from Patel AX073998 Sequence 6 from Patel AX073998 Sequence 6 from Patel AX073998 Sequence 6 from Patel AX073998 Sequence 6 from Patel AX073998 Sequence 6 from Patel AX073998 Sequence 6 from Patel AX073998 Sequence 6 from Patel AX073998 Sequence 6 from Patel AX073998 Sequence 6 from Patel AX073998 Sequence 6 from Patel AX073998 Sequence 6 from Patel AX073998 Sequence 6 from Patel AX073998 Sequence 6 from Patel AX073998 Sequence 6 from Patel AX073998 Sequence 6 from Patel AX073998 Sequence 9 from Patel AX073998 Sequence 9 from Patel AX073998 Sequence 9 from Patel AX073998 Sequence 9 from Patel AX073998 Sequence 9 from Patel AX073998 Sequence 9 from Patel AX073998 Sequence 9 from Patel AX073998 Sequence 9 from Patel AX073998 Sequence 9 from Patel AX073998 Sequence 9 from Patel AX073998 Sequence 9 from Patel AX073998 Sequence 9 from Patel AX073998 Sequence 9 from Patel AX073998 Sequence 9 from Patel AX073998 Sequence 9 from Patel AX073998 Sequence 9 from Patel AX073998 Sequence 9 from Patel AX073998 Sequence 9 from Patel AX073998 Sequence 9 from Patel AX073998 Sequence 9 from Patel AX073998 Sequence 9 from Patel AX073998 Sequence 9 from Patel AX073998 Sequence 9 from Patel AX073998 Sequence 9 from Patel AX073998 Sequence 9 from Patel AX073998 Sequence 9 from Patel AX073998 Sequence 9 from Patel AX073998 Sequence 9 from Patel AX073998 Sequence 9 from Patel AX073998 Sequence 9 from Patel AX073998 Sequence 9 from Patel AX073998 Sequence 9 from Patel AX073998 Sequence 9 from Patel AX073998 Sequence 9 from Patel AX073998 Sequence 9 from Patel AX073998 Sequence 9 from 
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gb_htg:AC103308
gb_htg:AC060230
gb_htg:AC073808
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LOCUS BC004759
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Center code: BCM-HGSC
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117.57
110.57
116.98
114.56
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Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 6 Row: c Column: 3.
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Der
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., I
AlM., Holloway, M., Telford, B, Hodgson, A., Bouck,
Muzny,D.M., Gibbs,R.A.
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Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Direct Submission
Direct Submission
Direct Submission
Submitted (21-MAR-2001) National Institutes of Health, Mammalian
Submitted (21-MAR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Gene Collection (MGC), Cancer Genomics Office, National Cancer
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Mus musculus, clone MGC:6973 INJ
                                                    /product="Unknown (protein for MGC:6973)"
/product="Unknown (protein for MGC:6973)"
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177. .1880
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IMAGE:3154616, mRNA, complete cds.
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0 Homo sapiens chr
8 Mus musculus clc
7 Homo sapiens BAC
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alignment_scores:
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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                   unidentified
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                           PAT 06-FEB-2002
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SOURCE ORGANISM

unidentified. unidentified unclassified.

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Patent: WO 0190358-A 12 29-NOV-2001;
SCHERING CORPORATION (US)
Location/Qualifiers
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    AUTHORS
                                                         ORGANISM
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AX073993
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1 (bases 1 to 2255)
  Presnell, S.R.,
                                                      Homo sapiens
                                                                                                   AX073993.1 GI:12710225
 Burkhead, S.K.
and Pownder, S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KRWALVWLACLLFAAALSLILLLKKDHAKAAARGRAALLLYSADDSGFERLVGALASA
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200720	7h	
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gb_pat:AX092430

seq_documentation_block:

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DEFINITION
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Ratio: 4.281
Percent Similarity: 83.834
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147 ValGlnIleTrpSerTyrThrLysProArgTyrGlnLysGluLeuAsnLe 163
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Sequence 161 from Patent W00116318.
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AX092430.1 GI:13444529
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1 (Dases 1 to 2380)
Eaton,D.L., Filvaroff,E., Gerritsen,M.E., Goddard,A., Goddowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Secreted and transmembrane polypeptides and nucleic acids encoding
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776	TrpAl	rgser :: AGTCA	tAlas AGCCT	hrs GAI	7-0	rTrp6	AspPl ::: GAGT1	roLet CACTO	oGlyI ::::	lArgValLet :::: CGACTGCTO	heArg TCAGG	eGln\ CAG	ProGI CCGCI	rgPro :: ATCA	uThrLe ::: GGTTCT	€3 ·	CCTA
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	LYSTY NAATA	InLet	aArgI	A Lur	S E	uGln <i>i</i> GCAGG	G1yH1 GGCC7	roGli	sTrp(CTGG(YValTrpG. SAGCTGGCT	laHis CACAC	uPro/ ACCT(AsnH: AACC/	aLeuLysSe CCCAAAACC	3luGluGln/ 3AGGAGCAG	AACG	ACGA
	TILE	TGG.	TIGG	roserg CCAGTG	uValG ::: GTTGG	llaCy AGTG	SPro	ıLysa ::: GAGA	31nA1 ::: :GGGC	rpGln GCTG	5 ° 6	AspSe ACTC	isThr \CACA	S I	31nAs CAGCA	TGTCA	3AAGG
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ACCESSION VERSION

2380 bp Sequence 13 from Patent W00146420. AX180776 .1 GI:15132622

DNA

linear

PAT 06-AUG-2001

DEFINITION

seq_documentation_block: LOCUS AX180776

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alignment_scores:
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GTGCTGAGGTGCCAGAAGGAGACCGACTGTGACCTCTGTCGCGTGTGGC 49
  uThrGlnGlnLeuPro.
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Ratio: 4.281
nilarity: 83.834
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1. (bases 1 to 2380)
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Il-17 and il-17r homologous polypeptides and therapeutic uses
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ACCESSION VERSION

KEYWORDS ORGANISM

Homo MGC BC006411.1

sapiens

DEFINITION

6411 2507 k sapiens, clone MGC:10763

bp mRNA linear
3 IMAGE:3606276, mRNA,

complete PRI 12-JUL-2001 complete cds.

GI:13623590

seq_documentation_block: LOCUS BC006411

seq_name:

gb_pr|:BC006411

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                                                                                                                                                                                                                                                                                                                             Quality: 1554.00
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Susanna Chan, Readman Chiu, C
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
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Tissue Procurement: ATCC
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Contact: MGC help desk
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info@bcgsc.bc.ca
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83.834
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Chris Fjell, Erin Garland, Ran Guin,
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LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLe 17

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SerProCysGlnProLeuValProProValProGlnLysAsnAlaThrVa 304
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757 c 731 g
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LeuCysIleGlnValTrpSerLeuGluProAspSerGluArgValGluPh

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SOURCE
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                                                                                                                                                           JOURNAL
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                                                                                                                                                                           TITLE
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1 (bases 1 to 2499)
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AX073995
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                                                                                                                                                        MGNATHTGGWSNTAYACNCARCCNMGNTAYGARAARGARYTNAAYCAYAC
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1. .2076
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SOURCE
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                                                                                                                                                                        Sequence 9 from Patent W00190358
        Gorman, D.M.

Mammalian receptor proteins; related reagents and methods Patent: WO 0190358-A 9 29-NOV-2001; SCHERING CORPORATION (US)
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                                                                                                                 SNTGYTGGGCNYTNCCNTGGYTNAAYGTNWSNGCNGAYGGNGAYAAYGTN
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/db_xxef="taxon:32644"
/note="primate; surmised Homo sapiens"
/note="grimate; surmised Homo sapiens"
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          Presnell,S.R., Burkhead,S.K. and Pownder,S.
Human cytokine receptor
Patent: WO 0104304-A 6 18-JAN-2001;
2ymoGenetics, Inc. (US)
Location/Qualifiers
1. .1725
                                                                                                                                                                                                        1725 bp
AX073998
                                                                                                                                         synthetic construct.
synthetic construct
                                                                                                           artificial sequence.
1 (bases 1 to 1725)
                                                                                                                                                                                            AX073998.1 GI:12710230
/organism="synthetic construct"
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US-09-899-471-2_COPY_21_440 x AX073998
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                                     CysTrpGlnAlaProAspGlnSerProCysGlnProLeuValProProVa
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        TGYTGGMGNGCNCCNGGNGGNGAYCCNTGYCARCCNYTNGTNCCNCCNYT 650
                                                                    ARWSNTGGYTNYTNGAYGCNCCNTGYWSNYTNCCNGCNGARGCNGCNYTN 600
                                                                                                   lyValTrpGlnLeuAspAlaProCysCysLeuProGlyLysValThrLeu
                                                                                                                                                                                                 GluProAspSerGluArgValGluPheCysProPheArgGfuAspProGl 247
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                                                                                                                                   NGCNCAYCARAAYYTNTGGCARGCNGCNMGNYTNMGNYTNYTNACNYTNC 550
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/note="This degenerate sequence
sequence of SEQ ID NO:5."
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226 c 332 g 216 t
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Gaps:
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  17 uSerCysHisLeuTrpAspGlyAspValLeuCysLeuProGlySerLeuG
                                                                              LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLe 17
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                                            CTGGAGAGGCTTGTGGGGCCTCAGGACGCTACCCACTGCTCTCCGGGCCCT 317
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Ratio:
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3.803
85.915
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/db_xref="taxon:9606"
214 c 219 g 14
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AUTHORS
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Ma,Q., Rong,L., Shen,Y., Tan,X., Wang,H., X1,Y., Xu,Y., Yao,Z.,
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Yang,X., Yu,B., Zeng,Y., Zhang,H., Zhang,H., Zhang,L.,
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Yu,J., and Yang,Y., Zhang,X., Zhang,Y., Zhang,Z., Zhu,B.,
Yu,J., and Yang,Y., Zhang,X., Zhang,Y., Zhang,Z., Zhu,B.,
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                 Submitted (21-MAR-2000) Human Genomic Center, Institute of Genetics, Chinese Academy of Sciences, Datun Road, Beijing, 100101, P.R.China
On May 29, 2000 this sequence version replaced q1:8050894
                                                                                                                                    Wang, R., Hu, S., Dong, W., Wang, J., Zhang, Y., Zhang, H., Liu, B., Bao, W., Sun, Y., Wu, Q., Wang, H., Yang, X., Cheng, C., Wang, Y., Niu, Y., Qi, X., Li, T., Zhang, H., Liu, N., Wu, D., Yan, H., Zhang, H., Liu, Y., Li, G., Li, C., Bao, Q., Bao, J., Wang, X., Song, L., Zhang, L., Guo, D., Hang, F., Zhang, G., Li, J., Bian, X., Zhang, M., Li, L., Feng, X., Yu, J., Li, B., Zhang, G., Li, J., Bian, X., Zhang, M., Li, L., Feng, X., Yu, J.
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                                                                                                      Direct Submission
                                                                                                                                                                                                                                            Unpublished 2 (bases 1 to 191834)
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1 (bases 1 to 191834)
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Sequencing vector: pUC18; 100% of reads chemistry: Dye-terminator: ET 55% of reads Chemistry: Dye-terminator Big Dye; 45% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 185328 bases at least Q40 Consensus quality: 192037 bases at least Q30 Consensus quality: 192037 bases at least Q30 Consensus quality: 196045 bases at least Q20 Insert size: 179116; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center project name:1% project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact:hgc@igtp.ac.cn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Website:http://hgc.igtp.ac.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center:Beijing Center
Center code:Beijing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 22 contigs. The true order of the pieces is not known and their order in this sequence record is
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             23 AspGlyAspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyPr 39
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145072. .191834
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/chromosome="3"
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                                                                                                                                                                    AC026196 from: 1, %o: 191834
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2152 others

307

EATURES

source

3869

	181 uGluGlnAspPheSerPhe 187 ::: ::: 37979 GAGGTGGGACTATTCTTTT 37961
181 37980	166GlnLeuProAspGlyAspAsnValLeuLeuThrLeuAspValSerGl
165 38030	156 rgTyrGlnLysGluLeuAsnLeuThrGln
156 38080	139 eGluAlaSerLeuGlyAlaGluValGlnIleTrpSerTyrThrLysProA :
139 38091	136PheAspCysPh
135 38141	119 InValProAlaAspLeuValGInProGlyGInSerValGIySerAlaVal
119 38191	102 ILeuSerPheGlnAlaTyrProIleAlaArgCysAlaLeuLeuGluValG
102 38241	95AlaSerLeuGlnAlaGlnValVa
38291	38340 TGGCTGGCCCAACTGCCCATGCCAAGGCCTGGCCTGCCGCTCCTGGGCC
94	94
94 38341	82 aGlyLysSerAspSerGluLeuGlnGluSerArgAsn
82 38391	74
38441	38490 GCCAAAGCCAGCCCAGAGCAGGGGGCCTCACCCAGGGCCTTGCTCT
73	73
38491	38540 TCTCCCCAGCCCCTGCTTCCCAGCACTGGGCTTTCCAGAAGGAAG
73	73
38541	38590 TCAGTGTTCTCCTGGAGGACACCAGCAGAAGGACCCCCCAGGCCAGTGTGG
73	73
38591	38640 CTGGGGTGGGCATGAGGGCCAGGGGGATCTCTCAAGCAGTGCTAGGCATCC
73	73
38641	CAT
73.	73 His

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Database lenyun. ...
Search time (sec):
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Database length: 858457221
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Database: N_Genes
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-NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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alignment_block:
US-09-899-471-2_COPY_21_440 x AAS18132
                                                                                                                                                                                                                                                                                                                           alignment_scores:
                                                                                                                                                                     Percent Similarity:
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Quality: 2240.00 Ratio: 5.359 milarity: 94.144

Percent Identity:

94.144

2314 BP; 411 A;

725 C;

705 G; 473 T; 0 other;

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/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AALD6868
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AALF8106
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAF71674
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH66653
                                                   subunit (DCRS) polypeptides and the polynucleotides encoding them. The receptors, or their portions may be useful as phosphate labelling enzymes to label general or specific substrates. The subunits may also be functional immunogens to elicit recognising antibodies, or antigens capable of binding antibodies. A combination, e.g., including a DCRS can be used as an immunogen for the production of antisera or antibodies capable of distinguishing between other cytoking receptor family members. A purified DCRS can also be used as a reagent to detect antibodies generated in response to the presence of elevated levels of expression, or immunological disorders which lead to antibody production to the endogenous receptor. This sequence represents cDNA encoding the mouse DCRS7 polypeptide.
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AAS18132 standard; cDNA; 2314 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to primate and rodent DNAX cytokine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 17-20; 148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated antigenic human or mouse DNAX receptor subunit-like polypeptide useful for detecting antibodies generated in respective of increased protein levels or immunological disordures.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNAX cytokine receptor subunit 7; DCRS7; phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             increased protein levels or immunological disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein therapy; immunological disorder
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199..2295
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                                                                                   Isolated antigenic human or mouse DNAX receptor subunit-like polypeptide useful for detecting antibodies generated in response to presence of increased protein levels or immunological disorders -
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Disclosure; Page 20-21; 148pp; English

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                                            NGAYTGYMGNGGNYTNGARGTNMGNGAYWSNATHCARWSNTGYTGGGTNY
                                                                                                                                                                                                                                                                                                                                                                                                                 lHisLeuAlaValHisGlyHisTrpAlaGluProGluGluAlaGlyLysS
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77.551
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Identity:
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XX AX XX DE

08-MAY-2001

(first entry)

Human cytokine receptor Zcytor14 encoding

CDNA

seq_name: /SID\$1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAC85027

_documentation_block: AAC85027 standard;

cDNA;

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1314
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ysProMetAspLysTyrIleHis 418
                                                                                                                                                                                     TNTGYGCNYTNGARCCNWSNGGNTGYACNCCNYTNCCNWSNATGGCNWSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lProProValProGlnLysAsnAlaThrValAsnGluProGlnAspPheG
                                            YCARTGYATGCARYTNTGGAAYGAYGAYAAYATGGGNWSNYTNTGGGCNT
                                                                 sGlnCysMetGlnLeuTrpAsnAspAspAsnMetGTYSerLeuTrpAlaC
                                                                                                                                                                                                                     alCysAlaLeuGluProSerGlyCysThrProLeuProSerMetAlaSer
                                                                                                                                                                                                                                                      LysValGlnLeuGlnAlaCysSerTrpAlaAspSerLeuGlyProPheLy
                                                                                                                                                                                                                                                                                                                                                                                                               lnLeuValAlaGlyHisProAsnLeuCysValGlnValSerThrTrpGlu
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                                                                                                                 ACUMGUGCUGCUMGUYTUGGUGARGARYTUYTUCARGAYTTYMGUWSUCA
                                                                                                                                                                                                                                                                                     sAspAspMetLeuLeuValGluMetLysThrGlyLeuAsnAsnThrSerV
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|ignment_block:
|s-09-899-471-2_COPY_21_440 x AAC85027
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214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2255 BP; 369 A; 748 C; 703 G; 435 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arthritis. In contrast, Zcytor14 antagonists (e.g. anti-Zcytor14 antibodies) can be used to treat a subject who produces an excess of Zcytor14. Zcytor14 nucleotide sequences can also be used to provide Zcytor14 to a subject. The present sequence represents a cDNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 8; Page 87-91; 112pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polypeptide encoding a human cytokine receptor Zcytor14, for treating inflammation e.g. rheumatoid arthritis - {\sf rec}
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                                                                                                                                                                                                                       17 uSerCysHisLeuTrpAspGlyAspValLeuCysLeuProGlySerLeuG
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3..2232
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Percent Identity: 67.667
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CCATCTGGATCTGAATGTCCTGAAGACC TLEUARIGPTOVALPTOASPALALEULY CTGGAATCAAGGTCCAAGGCCCCCCAAA THGLYPTOGLASTLLETTLEUASTL CTGGACCACCACACCCCCAAA THGLYPTOGLASTLLETTLCTTGAACC CCYSILEGLAVALTTPSETLEUGTTAACCT CCYSILEGLAVALTTPSETLEUGTAACCCT SPTOPPHEATGGGTGTGGCCTCTGGAACCT TGTATTCAGGTGTGTGCCTCTGCAACCCT SPTOPHEATGAGTCTGCACCCCCGCCACACCCT CCCCTTCAGGGAGGACCCCCCGCCAGACCT TGLEUARIGVALLEUSETPTOGLYVALT CCCCTTCCGAACCTGCTGCAGACCT TGLIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	
	TGTCTTGAGGAGCACCACTTCGGCCTTGGCCTTGAGGAGCACCACTTCGGCCTTAGGAGCACCACTTCGGCCTTGAGGAGCACCACTTCGGCCTTAGGACCCCCCAAAACCCCCGGTGGCACAAACCCCCGGTGGCACAAACCCCCGGTGGAACCTTGAACCTTGAACCACAAACCCCGGTAGGACCTTGAACCTTGAACCACAAACCCTGAACCTTGAGAACCTTGGAACCTTGAACCCTGGAACCTTGAACCACCAGAACCTTGGAACCTCTGGAACCTTGGAACCTCTGGAACCTTGGAACCTTGGAACCTTGGAACCTTGGAACCTTGGAACCTTGGAACCTTGGAACCTTGGAACCTTGGAACCTTGGAACCTTGAACCTTGAAACCTCTGGAACCTTGAAACCTCTGGAACCTTGAAACATTAGAAAAATATATAT

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eq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAS46223
                                                                     18-APR-2000;
25-APR-2000;
25-APR-2000;
25-APR-2000;
03-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dog; cat; p1g; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;
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04-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss; dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNP-alpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human DNA encoding PRO polypeptide sequence #299
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|||||||||:::::||| |||||:::||||||||| |||||::
CTACAAGACCTGCAGTCAGGCCAGTGTCTGCAGCTATGG...GACGATGA 1460
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                                          2000WO-US14042
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US-09-899-471-2_COPY_21_440 x AAS46223
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Percent Similarity:
                                                                                                                                                                                                                                                                                                           Align seg 1/1
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22-AUG-2000;
24-AUG-2000;
08-NOV-2000;
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20-DEC-2000;
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            82
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Ratio: 4.281
milarity: 83.834
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AlaGlyLysSerAspSerGluLeuGlnGluSerArgAsnAlaSer
                                                                                                                                                                                                                                                                                                           to: AAS46223
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2000US-0644848.
2000WO-US23328.
2000WO-US30952.
2000WO-US30952.
2000WO-US32678.
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CC primers for PRO polypeptides of the invention. The sequences of the CC invention can be used to detect the presence of a tumour in a mammal by CC comparing the level of expression of a PRO polypeptide in a test sample CC of cells from the animal and a control sample of normal cells, whereby a CC higher level of expression in the test sample indicates the presence of a CC tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep, CC gigs, goats and rabbits but are preferably human. The polypeptides can be CC used to stimulate tumour necrosis factor (TMF) alpha release from human CC stimulate the proliferation or differentiation of chondrocyte cells. The CC Stimulate the proliferation or differentiation of chondrocyte cells. The CC susceptibility to tumour development, particularly adrenal, lung, colon, CC susceptibility to tumour development, particularly adrenal, lung, colon, CC susceptibility to tumour development, particularly adrenal, lung, colon, CC susceptibility colon cervical, or liver tumours, in mammalian CC subjects. The oligonucleotide probes specific for the PRO nucleic acids CC can be used for genetic analysis of individuals with genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel nucleic acids encoding PRO polypeptides, used to diagnose the presence of tumours, such as prostate and breast tumours, in mammals to screen for modulators of the compounds -
Sequence 2380 BP; 411 A; 776 C; 743 G; 450 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAS45925-AAS46231 represent DNA molecules encoding and PCR or PRO polypeptides of the invention. The sequences of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Goddard A, Godowski PJ,
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293 CTGGAGAGGCTTGTGGGGGCCTCAGGACGCTACCCACTGCTCTCCGGGCCT
                                                                                                                                                                              17 uSerCysHisLeuTrpAspGlyAspValLeuCysLeuPToGlySerLeuG
                                                                                                                                                                                                                                  1 LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLe
                                                                                                         lValHisLeualaValHisGlyHisTrpAlaGluProGluGlu.....
                                                                   ValLeuArgCysProGlnLysThrAspCysAlaLeuArgValArgValVa
                                                     CTCCTGCCGCCTCTGGGACAGTGACATACTCTGCGGGCCTGGGGACATCG
TGTCCACTTGGCCGTGCATGGGCACTGGGAAGAGCCTGAAGATGAGGAAA
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Gaps:
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67.667
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CACTACCCAGCAAAGCCTCCACGAGGGCAGCTCGCCTTGGAGAGTACTTA 1492
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30-DEC-1999;
11-JAN-2000;
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02-MAR-2000;
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                                                                             CK,
                                                                           Filvaroff E, Fong S, Goddard A, Godowski PJ,
J, Li H, Hillan KJ, Tumas D, Van Lookeren M,
CK, Williams PM, Wood WI, Yansura DG;
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                                                                                                                                       2000US-0253646
2000WO-US32678
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2000WO-US23328.
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2000US-0213087.
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                                                                                     Grimaldi
Vandlen F
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                                                                                     RL;
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diagnosis arthritis

polypeptides homologous to interleukin-17, useful for the and treatment of immune related disease e.g. rheumatoid and diabetes -

Novel PRO

WPI; 2001-451708/48. P-PSDB; AAU04956.

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alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC The sequence (DNA 164625-2890) encodes a PRO polypeptide (PRO20040)
CC which is the human Interleukin 17 receptor, II-17RH2. A composition
CC containing ant/agonists to the PRO polypeptides or individual components
CC are useful for treating a mammal with an immune related disease, e.g.
CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
CC diopathic inflammatory myopathy, Sjogren's syndrome, systemic
CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
CC thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal
CC disease, a demyelinating disease, an autoimmune or immune-mediated skin
CC disease, contact dermatitis, an allergic disease e.g. food
CI hypersensitivity, asthma, a transplantation associated disease, or a
CC chronic inflammatory demyelinating polypeuropathy. Treating a PRO1031 or
CR CRO1122 polypeptide agonist, or antagonist to the mammal. Numerous
CC examples of the diseases and disorders are given in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: AAS09515
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                                                           ValGlnIleTrpSerTyrThrLysProArgTyrGlnLysGluLeuAsnLe 163
                                                                                                              sAlaLeuLeuGluValGlnValProAlaAspLeuValGlnProGlyGlnS
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    uThrGlnGlnLeuPro.
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                                                                                                 LeuGlnAspPheArgSerHisGlnCysMetGlnLeuTrpAsnAspAspAs 404
                                                                                                                                                                                         roLeuProSerMetAlaSerThrArgAlaAlaArgLeuGlyGluGluLeu 387
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seq_documentation_block:
ID AAF92138 standard; cI
XX
AC AAF92138;
XX
DT 15-MAY-2001 (first e
XX
DE Human PRO20040 cDNA.

(first entry)

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lignment_block:
US-09-899-471-2_COPY_21_440 x AAF92138
                                                                                                                                                                                             Quality: 1554.00
Ratio: 4.281
Percent Similarity: 83.834
                                                                                                                                       Align seg 1/1
                                                                                                                                                                                                                                lignment_scores:
                                                                                                                                                                                                                                                                                           The present sequence is the coding sequence for a human PRO polypeptide (secreted and transmembrane). The PRO protein, and PRO agonists, PRO antagonists or anti-PRO antibodies are useful for preparation of a medicament useful in the treatment of a condition which is responsive to the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO protein may also be employed as molecular weight markers for protein electrophoresis. The PRO coding sequence has applications in molecular biology, including use as hybridisation probes, and in chromosome and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-SEP-1999;
15-SEP-1999;
07-DEC-1999;
    393
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                                                                                      Sequence 2380 BP; 411 A;
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                                                                                                                                                                                                                                                                                                                                                                                                                         Eighty four nucleic acids encoding PRO polypeptides, useful in molecular biology, including use as hybridization probes, and in chromosome and gene mapping. -
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22-FEB-2000;
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18-FEB-2000;
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                                          InSerAlaProGlyProValLeuValProThrArgLeuGlnThrGluLeu 50
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J, Gurney AL,
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Watanabe CK,
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                                                                                                                                                                                                                                                                 743 G;
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              alGlnValSerThrTrpGluLysValGlnLeuGlnAlaCysSerTrpAla 337
TTCAGGTGAACAGCTCGGAGAAGCTGCAGCTGCAGGAGTGCTTGTGGGCT
                                                                                                                                                                                                                                                                                                                                                                                                 roCysLeuCysIleGlnValTrpSerLeuGluProAspSerGluArgVal 237
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                                                             GGACAAGGTTCTCGAGTTCCCATTGCTGAAAGGCCACCCTAACCTCTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                Human; secreted protein; cancer; tumour; developmental abnormality; foetal deficiency; blood disorder; immune system disorder; inflammation; autoimmune disease; allergy; Alzheimer's disease; cognitive disorder; schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder; atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;
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                                                                                                                                                                                                                                                                                                                                                                                              therapy; chromosome
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12-MAY-1998
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                                                                                                                                                                                                                                                                                                                                                                                                         disorder;
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98US-0085928.
98US-0085925.
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98US-0085922.
98US-0085923.
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980S-0085920
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Ruben SM, Olsen HS,

Florence K, Shi Y, Your

Ni J, Rosen CA, Can ng PE, Wei F, Brewer Ebner R;

Carter KC, Moore PA;
wer LA, Soppet DR;

Young

₽W,

Endress

AAY76143

(HUMA-) HUMAN GENOME SCI INC.

New isolated human genes and the secreted polypeptides they encode, useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders -

ValGlnIleTrpSerTyrThrLysProArgTyrGlnLysGluLeuAsnLe

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alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CC AAZ65250 to AAZ65350 represent 97 isolated human secreted protein genes.

CC This sequence was found to be present on human chromosome 3.

CC AAY76124 to AAY76223 represent the secreted proteins encoded by the 97 cc AAY76124 to AAY76223 represent the secreted proteins encoded by the 97 cc e.g. by protein or genes and their corresponding secreted polypeptides are certified by protein or gene therapy. Also pathological conditions, can be compared by determining the amount of the new polypeptides in a sample cor by determining the presence of mutations in the new genes. Specific cuses are described for each of the 97 genes, based on which tissues they care most highly expressed in, and include developing products for the care diagnosis or treatment of cancer, tumours, developmental abnormalities and foetal deficiencies, blood disorders, diseases of the immune system, cu autoimmune diseases, inflammation, allergies, Alzheimer's and cognitive condisorders, atherosclerosis, diabetes, cardiovascular disorders, kidney consument of digestive/endocrine disorders, infections and AIDS. The sequences shown in AAY76224 to AAY76424 represent fragments of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
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XX 25-MAY-2001; 2001WO-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         functional immunogens to elicit recognising antibodies, or antigens capable of binding antibodies. A combination, e.g., including a DCRS can be used as an immunogen for the production of antisera or antibodies capable of distinguishing between other cytokine receptor family members. A purified DCRS can also be used as a reagent to detect antibodies generated in response to the presence of elevated levels of expression, or immunological disorders which lead to antibody production to the endogenous receptor. This sequence represents cDNA encoding the human DCRS7 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    subunit (PCRS) polypeptides and the polynucleotides encoding them. The receptors, or their portions may be useful as phosphate labelling enzymes to label general or specific substrates. The subunits may also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated antigenic human or mouse DNAX receptor subunit-like polypeptide useful for detecting antibodies generated in response presence of increased protein levels or immunological disorders -
17 uSerCyśHisLeuTrpAspGlyAspValLeuCysLeuProGlySerLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to primate and rodent DNAX cytokine receptor
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| CTGCCAGCCACTGGTCCCACCGCTTTCCTGGGAGAATGTCACTGTGGAC. 1239
                                         TCGCTGCCCGCAGAAGCGGCACTGTGCTGGCGGGCTCCGGGTGGGGACCC
                                                    CysLeuProGlyLysValThrLeuCysTrpGlnAlaProAspGlnSerPr
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02-MAY-2000;
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                                                                                                                      Nucleic acids encoding secretory proteins/membrane proteins, useful gene therapy or as candidate target molecules in drug development -
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rheumatoid arthritis; diabetes; ss.
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DB; AAB88448.
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; 2000JP-0118775.
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which encode human secretory or membrane proteins represented by AAB88317 - AAB88419. Included in the invention are primers AAF93917 - AAF94295 and AAF96233 - AAF62235 which are used to isolate the cDNA sequences of the invention. The invention also includes methods for the production of antibodies directed against the proteins, and cDNA

This invention relates to nucleic acid sequences AAF93744 -

SEQ ID 263; 609pp + CD ROM; English.

Claim 1;

alignment_scores:
Quality: 1397.00
Ratio: 4.061 alignment_block: US-09-899-471-2_COPY_21_440 x AAF93875 Align seg 1/1 to: AAF93875 from: 1 to: 2499 procein/membrane protein expression. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples. They may also be used to study the expression and function of secretory proteins/membrane polypeptides and their role in metabolism. The polypeptides may be used as antigens in the production of antibodies against them and in assays to identify modulators (agonists and antagonists) of expression and activity. The antibodies and antagonists be used as therapeutic agents to down regulate expression and activity. The antibodies and antagonists be used as diagnostic agents for detecting the presence of the polypeptides in samples (e.g. by enzyme linked immunosorbant assay (ELISA). Examples of diseases which may be treated include rheumatoid 718 147 899 130 618 113 sAlaLeuLeuGluValGlnValProAlaAspLeuValGlnProGlyGlnS 130 568 518 418 318 163 uThrGlnGlnLeuPro.. 268 CTGGAGAGGCTTGTGGGGCCTCAGGACGCTACCCACTGCTCTCCGGGCCT 317 Sequence 2499 BP; 418 A; 821 C; 764 G; 496 T; 0 other; sequences, which can be used in vaccines. The polynucleotide sequences can be used in gene therapy. The polynucleotide sequences and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate secretory 97 82 51 17 arthritis and 1 LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLe 17 LeuGlnAlaGlnValValLeuSerPheGlnAlaTyrProIleAlaArgCy 113 ValLeuArgCysProGlnLysThrAspCysAlaLeuArgValArgValVa 67 uSerCysHisLeuTrpAspGlyAspValLeuCysLeuProGlySerLeuG 34 CGTCCTGCTGGAGGTGCAAGTGCCTGCTGCCCTTGTGCAGTTTGGTCAGTAlaGlyLysSerAspSerGluLeuGlnGluSerArgAsnAlaSer 96 AGTTTGGAGGAGCAGCTGACTCAGGGGTGGAGGAGCCTAGGAATGCCTCT diabetes. Percent Identity: 54.960 Length: ..AspGlyA 171 504 6 667 617 567 417

100	84 lyGluCluLeuLeuGlnAspPheArgSerHisGlnCysMetGlnLeuTr	ω
6	18 TGGCTGTACTTCACTACCCAGCAAAGCCTCCACG	16
84	67 rGlyCysThrProLeuProSerMetAlaSerThrArgAlaAlaArgLeuG	w
367 1617	351 GluMétLysThrGlyLeuAsnAsnThrSerValCysAlaLeuGluProSe 3 	15
350 1567	34 ysSerTrpAlaAspSerLeuGlyProPheLysAspAspMetLeuLeuVal 	15
334 1517	17 OASNLEUCYSVAIGINVAISETThrTrpGluLySVAIGINLEUGINAIAC	3 14
317 1467	01 AsnalaThrValAsnGluProGlnAspPheGlnLeuValAlaGlyHisPr 	11 3 44 3
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187 867	171 spasnvalLeuLeuThrLeuAspValSerGluGluGlnAspPheSerPhe	
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AAC85029 standard; cDNA; 1753
                                                                                                                                                                     The invention provides a new human cytokine receptor desinated Zcytor14. Ecytor14 can be expressed by standard recombinant methodology. The encoding nucleic acid is useful for detecting the expression of a Zcytor14 gene in a biological sample. Anti-Zcytor14 antibodies can be used to screen biological samples in vitro for the presence of Zcytor14. Proteins, polypeptides and peptides having Zcytor14 activity can be administered to a subject who lacks an adequate amount of this polypeptide, for treating inflammation and conditions such as rheumatoid arthritis. In contrast, Zcytor14 antagonists (e.g. anti-Zcytor14 antibodies) can be used to treat a subject who produces an excess of Zcytor14. Zcytor14 nucleotide sequences can also be used to provide Zcytor14 to a subject. The present sequence represents a cDNA encoding a variant of the human cytokine receptor Zcytor14, designated Zcytor14-1. The variant is a truncated form of the receptor polypeptide and lacks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polypeptide encoding a human cytokine receptor Zcytor14, treating inflammation e.g. rheumatoid arthritis -
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                                                                                                                Sequence 1753 BP; 287 A; 584 C;
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52 GGCCTACCCTACTGCCCGCTGCTGCTGCTGGAGGTGCAAGTGCCTGCTG 101
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          tLeuLeuValGluMetLysThrGlyLeuAsnAsnThrSerValCysAlaL:|||||||:::||||||||
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                                                                    CTGCAGGAGTGCTTGTGGGGCTGACTCCCTGGGGCCTCTCAAAGACGATGT
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                                                                                                                                                     The invention provides a new human cytokine receptor desinated Zcytor14. Zcytor14 can be expressed by standard recombinant methodology. The encoding nucleic acid is useful for detecting the expression of a Zcytor14 gene in a biological sample. Anti-Zcytor14 antibodies can be used to screen biological samples in vitro for the presence of Zcytor14.
                          Proteins, polypeptides and peptides having 2cytor14 activity can be administered to a subject who lacks an adequate amount of this polypeptide, for treating inflammation and conditions such as rheumatoid arthritis. In contrast, Zcytor14 antagonists (e.g. anti-Zcytor14 antibodies) can be used to treat a subject who produces an excess of Zcytor14. Ccytor14 nucleotide sequences can also be used to provide zcytor14 to a subject. The present sequence represents the human cytokine receptor Zcytor14 degenerate nucleotide sequence.
                                                                                                                                                                                                                                                       Claim 8; Page 94-95; 112pp; English
                                                                                                                                                                                                                                                                                     New polypeptide encoding a human cytokine receptor Zcytor14, treating inflammation e.g. rheumatoid arthritis -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human cytokine receptor Zcytorl4 degenerate nucleotide sequence
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 Sequence 2076
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                                                                                                                                                                                                                                                                                                                                                                                        Burkhead SK,
 B₽;
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 232 A;
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273 C;
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 399 G;
265 T; 907 other;
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ignment_scores

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alignment_block:
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eAlaArgLeuArgValLeuSerProGlyValTrpGlnLeuAspAlaProC
                                                 YTNTAYTGGAAYCARGTNCARGGNCCNCCNAARCGNIGNTGGCAYAARAA
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                                                                                               GYYTNTGYATHCARGTNTGGCCNYTNGARCCNGAYWSNGTNMGNACNAAY
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<u>EZZERDZERDZERDZERZERZZERZZERZERZ</u>

Isolated antigenic human or mouse DNAX receptor subunit-like polypeptide useful for detecting antibodies generated in response presence of increased protein levels or immunological disorders -

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NCARCARYTNCCNGAYTGYMGNGGNYTNGARGTNTGGAAYWSNATHCCNW

613

WPI;

2002-106198/14.

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alignment_block:
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                                                                                                                                                         NYTNYTNGARGTNCARGTNCCNGCNGCNYTNGTNCARTTYGGNCARWSNG
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                                 CNGCNCCNGGNCCNGTNYTNGCNCCNACNCAYYTNCARACNGARYTNGTN
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                                                      seq_documentation_block:
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08-MAY-2001

(first entry)

gTyrGlnLysGluLeuAsnLeuThrGlnGlnLeuPro....

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                                                                                                            123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  arthritis. In contrast, Zcytor14 antagonists (e.g. anti-Zcytor14 antibodies) can be used to treat a subject who produces an excess of Zcytor14. Zcytor14 nucleotide sequences can also be used to provide Zcytor14 to a subject. The present sequence represents a degenerate nucleotide sequence of a variant of the human cytokine receptor Zcytor14. The variant is a truncated form of the receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention provides a new human cytokine receptor desinated Zcytor14. Zcytor14 can be expressed by standard recombinant methodology. The encoding nucleic acid is useful for detecting the expression of a Zcytor14 gene in a biological sample. Anti-Zcytor14 antibodies can be used to screen biological samples in vitro for the presence of Zcytor14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1725 BP; 192 A; 226 C; 332 G; 216 T; 759 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proteins, polypeptides and peptides having Zcytor14 activity can be administered to a subject who lacks an adequate amount of this polypeptide, for treating inflammation and conditions such as rheumatoid arthritis. In contrast, Zcytor14 antagonists (e.g. anti-Zcytor14
                                                                                                                                               51
                                                                                                                                                                                                             polypeptide and lacks amino acid residues 1-113 of Zcytor14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 101; 112pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polypeptide encoding a human cytokine receptor Zcytor14, treating inflammation e.g: rheumatoid arthritis -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytokine receptor; Zcytor14; human; antiinflammatory; gene therapy; vac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human Zcytor14 variant Zcytor14-1 degenerate nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ZYMO ) ZYMOGENETICS INC.
GARGCNGCNYTNGGNWSNGARGTNMGNATHTGGWSNTAYACNCARCCNMG 200
                                                                                      spLeuValGlnProGlyGlnSerValGlySerAlaValPheAspCysPhe
                                                                                                                                                               nAlaTyrProIleAlaArgCysAlaLeuLeuGluValGlnV&1ProAlaA 123
                               GluAlaSerLeuGlyAlaGluValGlnIleTrpSerTyrThrLysProAr 156
                                                                       CNYTNGTNCARTTYGGNCARWSNGTNGGNWSNGTNGTNTAYGAYTGYTTY
                                                                                                                                       RGCNTAYCCNACNGCNMGNTGYGTNYTNYTNGARGTNCARGTNCCNGCNG
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DB; AAB61881.
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Ratio:
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3.947
63.717
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vaccine;
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cine; variant;
                                                                                                                                                                                                                                                                                                                                                                               48.968
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Zcytor14-1; ss.
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antibacterial; endocrine; cardiant; central nervous system; virucide; anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema; dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;

antiinflammatory; antirheumatic; antiarthritic;

cancer; ulcer; HIV infection; human immunodeficiency virus;

immunosuppressive;

anaemia;

16-OCT-2001

(first entry)

Human protein

encoding cDNA sequence

SEQ ID NO:640

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seq_name:
_documentation_block:
AAH99805 standard;
                                                                           947
                                                                                                       414
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                                                                                                                                                                                                              AlaArgLeuGlyGluGluLeuLeuGlnAspPheArgSerHisGlnCysMe
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                                                                                                                                                  tGlnLeuTrpAsnAspAspAsnMetGlySerLeuTrpAlaCysProMetA 414
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                                                                                                                                    NCARYTNTGG...GAYGAYGAYYTNGGNGCNYTNTGGGCNTGYCCNATGG
                                                                                                                                                                                          GCNMGNYTNGGNGARTAYYTNYTNCARGAYYTNCARWSNGGNCARTGYYT
                                                                                                                                                                                                                                                                                                             NYTNYTNYARACNMGNGGNCCNCARGAYAAYMGNWSNYTNTGYGCNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lProGlnLysAsnAlaThrValAsnGluProGlnAspPheGlnLeuValA
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                                            /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH99805
 CDNA; 1210
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дан99805;

alignment_scores:
 Quality:
 Ratio:

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3d
                                                             antiparkinsonian; and immunostimulant. The proteins and polynucleotides encoding them can be used in gene therapy, antisense therapy and vaccine production, The proteins and polynucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, rheumatidid arthritis, septic shock, pandcreatitis, cardiac dysfunction, neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, Taematopoietic disorders, anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers, osteoporosis, severe combined immunodeficiency, eczema, allergic rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-DEC-1999;
21-JAN-2000;
25-APR-2000;
                                                                                                                                                                                                                                                         central hervous system; virucide; anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; dermatological; antialtergic; antiasthatic; antidiabètic; cytostatic; neuroprotective; antidepressant; nootropic;
                                                                                                                                                                                                                                                                                                                      AAH99166 to AAH99904 encode the human proteins given in AAM25225 to AAM25963. The proteins can have activities based on the tissues and cells they are expressed in, such as: antiinflammatory; antirheumatic; antiarthritic; immunosuppressive; antierrial; endocrine; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neuroprotective; antidapressant; nootropic; antiparkinsonian; infection; immunostimulant; gene therapy; antisense therapy; vaccine; inflammation; antianaphylactic; rheumatoid arthritis; septic shock; panoreatitis; cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity; genetic disease; haematopoietic disorder; platelet disorder; asthma; thrombocytopaenia; osteoporosis; severe combined immunodeficiency; allergic rhinitis; diabetes; multiple sclerosis; depression;
Sequence
                                                rhinitis, asthma, diabetes, cancer, multi
Alzheimer's disease, Parkinson's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      treatment
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1210
                                                                                                                                                                                                                                                                                                                                                                                                                Page 659-660; 1217pp; English
                                  cal disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 human polynucleotides encoding and diagnosis of e.g. cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liu C, Drmanac
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2000US-0488725.
2000US-0552317.
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BP;
227
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352
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254 T; 0 other
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ulcers and HIV
                                                neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  useful for
V infection
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alignment_block:
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234 erGluArgValGluPheCysProPheArgGluAspProGlyAlaHisArg
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                                                                                                                                                                                                                                                                                                                  uThrGlnGlnLeuPro.....
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                                                            sLeuCys.....
                                                                                                             euThrGlyProGlnAsnIleThrLeuAsnHisThrAspLeuValPro.Cy
                                                                                                                                                               uTyrLeuArgProValProAspAlaLeuLysSerLeuTrpTyrLysAsnL
                                                                                                                                                                                          ValLeuLeuThrLeuAspValSerGluGluGlnAspPheSerPheLeuLe 189
                                                                                                                                                                                                                                                                                            CACACAGCAGCTGCCTGACTGCAGGGGGCTCGAAGTCTGGAACAGCATCC 808
                                                                                                                                                                                                                                                                                                                                                               ValGlnIleTrpSerTyrThrLysProArgTyrGlnLysGluLeuAsnLe 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SAlaLeuLeuGluValGlnValProAlaAspLeuValGlnProGlyGlnS 130
                                     CCTGTGCAAAGGACGCAGTGCCATATCAGAGGAGGATCCTTGAAGAGGACT
                                                                                      TGGTGAGGCCTCCCCTTCCCAAGTC...CATTCCCACTGTAGGCCGATG
                                                                                                                                        GTACTGGAATCAGGTCCAGGGCCCCCCAAAACCCCGGTGGCACAAAAACC
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                                                           .....IleGlnValTrpSerLeuGluProAspS
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                                     1055
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, complymerase chain reaction (PCR) primers, oligomers, and for chromosome complymerase chain reaction (PCR) primers, oligomers, and for chromosome complymerase chain reaction (PCR) primers, oligomers, and for chromosome complymerase chain reaction of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques complyment (II) is useful for generating antipodies magnist it, detecting or companies and a citivity of (II) or to treat disease states involving companies. (II) is useful for generating antipodies magnist it, detecting or companies of the superessing of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating companies involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in codisorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in codisorations for ensuring in the primers of data and products dependent on DNA and companies. AAS64197-AAS94564 represent novel human codisoration sequences of the invention.

Content the sequence and for this patent did not appear in the printed content for the vine in the printed at formal companies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DR XX PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /STDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:AAS78822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAS78822 standard;
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                              at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID No 14626; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB;
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding novel human diagnostic protein #14626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   food supplement;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chromosome mapping; gene mapping; gene therapy; forensic upplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG14635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ... GGGAACTTCTGCCTTCCTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YT;
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Sequence 980 BP; 182 A; 313 C; 315 G; 170 T; 0 other;

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alignment_block:
    US-09-899-471-2_COPY_21_440 x AAS78822/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to reverse of: AAS78822 from: 1 to: 980
                                                                                                                             162 nLeuThrGlnGlnLeuPro 168
| |||||||||||||||
| 100 CACACACAGCAGCTGCCT 202
                                                    146 GluValGlnIleTrpSerTyrThrLysProArgTyrGlnLysGluLeuAs 162
                                                                                   470 AAAAGTTTGGAGGAGCAGCTGACTTAGGGGTGGAGGAGCCTAGGAATGCC
                                                                                                                                                                                                                                                            620 GTGCCTGCTTCGGGCCCCCGGCTTGTGGCCTAACCACCTTGAGAACAGAG
                                                                                                                                                                                                                                                                                                                                                                                                670
                                                                                                                                                                                                                                                                                                                                                                                                                                          720
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                                                                                                                                                                                                                                                                                                                                                                                            GAGGTACGAATCTGGTCCTATACTCAGCCCAGGTACGAGAAGGAACTCAA 221
                                                                                                                                                                                                                             .....AlaGlyLysSerAspSerGluLeuGlnGluSerArgAsnAla 95
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4.000
85.143
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Gaps: 4
Percent Identity: 69.714
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earch information block:
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OB-ISSUEd_Patents_NA -OFMT-fastap -SUFFIX=rni -GAPOP=12.000
GAPEXT=4.000 -MINNATCH=0.100 -LOOPECL-0.000 -LOOPEXT=0.000
OGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-TRANS-human40.cdi -LIST=45 -ALIGN-15 -MODE=LOCAL -OUTFMT=pfs
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cout: Results were produced by the GenCore software, version
Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ery length: 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  te: Sep 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mand line parameters:
'Ptodata/2/ina/PCTUS_COMB.seq:PCT-US94-10166-6
'Ptodata/2/ina/6B_COMB.seq:US-09-150-460B-3 +
'Ptodata/2/ina/5B_COMB.seq:US-08-540-406-18 +
                                                                     /ptodata/2/ina/5B_COMB.seq:US-08-800-825A-
/ptodata/2/ina/6B_COMB.seq:US-09-158-657-6
                                                                                                                      /ptodata/2/ina/5A_COMB.seq:US-08-348-006B-6
                                                                                                                                                                   /ptodata/2/ina/6B_COMB.seq:US-09-150-460B-5
                                                                                                                                                                                      /ptodata/2/ina/PCTUS_COMB.seq:PCT-C/ptodata/2/ina/5A_COMB.seq:US-08-37
                                                                                                                                                                                                                                             /ptodata/2/ina/PCTUS
                                                                                                                                                                                                                                                                     /ptodata/2
                                                                                                                                                                                                                                                                                       /ptodata/2/ina/6A_COMB
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sequences: 383533
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                                                                                                                                                                                                                                                                                                                                                                           S_COMB.seq:PCT-US94-
OMB.seq:US-09-062-41
OMB.seq:US-09-167-68
OMB.seq:US-08-442-13
OMB.seq:US-08-444-5
OMB.seq:US-08-446-5
                                                                                                                                                                                                                                     _COMB.seq:PCT-US92-05374A-I
                                                                                                                                                                                                                                                                .seq:US-08-254-353A-1
                                                                                                                                                                                                                                                                                       :US-08-750-:
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96.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LENGTH: 2165
; TYPE: DNA
; ORGANISM: Mouse
US-09-188-930-226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
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Percent Similarity:
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GENERAL INFORMATION:
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                                                                                    300
                                                                                                                                                                                                                                                                                                                              766
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alignment_block:
US-09-899-471-2_COPY_21_440 x US-09-188-930-226
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/188,930A CURRENT FILING DATE: 1998-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
                                                                                                                                                                                                                                                             266 pGlnLeuAspAlaProCysCysLeuProGlyLyswannhrLeuCysTrpG
                                                                                                                                                                                                                                                                                                                                                                                                                                      237 alGluPheCysProPheArgGluAspProGlyAlaHis...ArgAsnLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         220 lProCysLeuCysIleGlnValTrpSerLeuGluProAspSerGluArgV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           616 AAAATTGTGTCTGGAGGCCACACTGTAGACCTGCCTTATGAATTCCTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   204 LysasnLeuThrGlyProGlnAsnIleThrLeuAsnHisThrAspLeuVa
                                        CCCAACGCCACAGCACAGGAGTCAGAAGGATGGTATATCCTGGAGAATGT
                                                                                                                                                                                                            TrpHisIleAlaArgLeuArgValLeuSerProGly,......ValTr
                                                                                   LysAsnAlaThrValAsnGluProGlnAspPheGlnLeuValAlaGly..
                                                                                                                                                                        lnAlaProAspGlnSerProCysGlnProLeuValProProValProGln
                                                                                                                                                                                                                                                                                                                                                                                              GCAAAAAGTGTCCCTTCCAGAGCTGGCCTGAAGCTTATGGCTCAGACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCCCTGCATGTGCATAGAGGCCTCCTACCTGCAAGAGGACACTGTGAGGC
                                                                                                                                                                                                                                                                                                    TGGCAGTCAATACGCTTCACTGACTACAGCCAGCACAATÇAGATGGTCAT
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HisProAsnLeuCysValGlnValSerThrTrpGluLysValG
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1.340
52.743
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Percent Identity:
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11
25.316
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128.33
126.33
126.33
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18.49
23.90
24.11
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	237 alGluPheCysProPheArgGluAspProGlyAlaHisArgAsnLeu 252 ::: ::::::::::::::::::::::::::
	220 lProCysLeuCysIleGlnValTrpSerLeuGluProAspSerGluArgV 237
	204 LysasnLeuThrGlyProGlnAsnIleThrLeuAsnHisThrAspLeuVa 220 ::::: :::::: ::: ::::: 616 AAAATTGTGTCTGGAGGCCACACTGTAGACCTGCCTTATGAATTCCTTCT 665
	Align seg 1/1 to: US-09-188-930-6 from: 1 to: 1059
	lignment_block: JS-09-899-471-2_COPY_21_440 x US-09-188-930-6
	lignment_scores: Quality: 149.00 Length: 152 Ratio: 1.795 Gaps: 6 Percent Similarity: 54.605 Percent Identity: 28.289
	ENGTH: YPE: DN RGANISM -188-93
	FastSEQ for
	CURRENT APPLICATION NUMBER: US/09/188,930A CURRENT FILING DATE: 1998-11-09 NUMBER OF SEO ID NOS: 348
	TITLE OF INVENTION: Compositions Isolated From Skin Cells TITLE OF INVENTION: and Methods For Their Use FILE REFERENCE: 11000 101161
	Watson, 3 Strachan, Sleeman, Onrust, F
	aq_documentation_block: Sequence 6, Application US/09188930A Patent No. 6150502 GENERAL INFORMATION:
	eq_name: /cgn2_6/ptodata/2/1na/6A_COMB.seq:US-09-188-930-6
	411 ysProMetAsp 414 1289 GTCCTGATGAC 1299
•	397 tGlnLeuTrpAsnAspAspAsnMetGlySerLeuTrpAlaC 411 :::: :::: ::: 1242 CCTGGTGTGGAGGTCAGATGTCCATTTTGCCTGGAAGCACGTCTTGT 1288
	386 GluLeuLeuGlnAspPheArgSerHisGlnCysMe 397 ::: :::: :::::: ::: 1192 CCAGTGACGCTAGACCTCATCATCCCCTTCCTGAGGCAGAAATTGCAT 1241
	370ThrProLeuProSerMetAlaSerThrArgAlaAlaArgLeuGlyGlu 385 ::: ::: ::: 1142 ATACCCCCATGCCTCCTGTGTACAGCAGCCAGAGCCCAGGGCTCAGTC 1191
	355 yLeuAsnAsnThrSerValCysAlaLeuGluProSerGlyCys 369
	339 SerLeuGlyProPheLysAspAspMetLeuLeuValGluMetLysThrGl 355
	330 lnLeuGlnAlaCysSerTrpAlaAsp 338 :

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seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-342-930-1
                                                relex: | 706141
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: | 5455 harm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    equence 1, atent No. 5
                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: KONSKI, ANTOINETTE F.
REGISTRATION NUMBER: 34,202
REFERENCE DOCKET NUMBER: 20344-20975.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1045 AGCATG 1050
                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     339 SerLeu 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            995 GCCACGTTGAATGTCCCCACCAGAGTGGCTCTCCCCATCCTGGACTGTG 1044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         330 lnLeuGlnAlaCys.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        898 CCCAACGCCACAGCACAGGAGTCAGAAGGATGGTATATCCTGGAGAATGT 947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               300 LysasnAlaThrValAsnGluProGlnAspPheGlnLeuValAlaGly.. 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               866 GGCAGGACCCACTCACACCCTGCGAAACCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   283 lnAlaProAspGlnSerProCysGlnProLeuValProProValProGln 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   266 pGlnIeuAspAlaProCysCysLeuProGlyLysValThrLeuCysTrpG 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        766 TGGCAGTCAATACGCTTCACTGACTACAGCCAGCACAATCAGATGGTCAT 815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    253 TrpHisIleAlaArgLeuArgValLeuSerProGly.....ValTr 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               716 GCAAAAAGTGTCCCTTCCAGAGCTGGCCTGAAGCTTATGGCTCAGACTTC 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                              FILING DATE: 2: CLASSIFICATION:
STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/342,930 FILING DATE: 21-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGACTTGCACCCCCAGCTCTGCTTTAAGTTCTCA...TTTGAAAACAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/08342930
5821084
                                      5455 base pairs
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .HisProAsnLeuCysValGlnValSerThrTrpGluLysValG 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: MORRISON & FOERSTER 755 Page Mill Road
                                                                                                                                                     (415) 813-5600
(415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DAVIS, ALAN R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAURO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OLMSTED, ELIZABETH A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAURA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHOSPHATASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OSTEOBLAST-TESTICULAR PROTEIN TYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .....SerTrpAlaAsp 338
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187 PheLeuLeuTyrLeuArgProValProAspAlaLeuLysSe 200	1648ATCAGCAGGAGCAGCCCATCTGAC 1671	AAGTCCCCTGCCACCGCAGTCACTGGAGGTC	158 GACATCTCTCAGAGCATCTCAGGCTATAC 1616		:	TPTOIleAlaArgCysAlaLeuLeuGluValGlnValProAlaAs 	98 InAlaGInValValLeuSerPheGln 106 ::: 1388 CCAGGGAGGTCCCTGGTGCCAGACTGTGGCTAGATGGACTGGAAGCTTCC 1437	85 rAspSerGluLeuGlnGluSerArgAsnAlaSerLeuG 98 ::: ::::	69 isLeuAlaValHisGlyHisTrpAlaGluProGluGlu.AlaGlyLysSe 85 ::: :::: 1306 ACTTTGCAGCTGAAGGTTCTAGCTGGACCTTA 1337	55 oGlnLysThrAspCysAlaLeuArgValArgValValValH 69 ::::::: ::: 1256 CGGAAGAGTGCAATGCAGTCTTCCCAGGGCCCCTGCCTCCGGGACACTAC 1305	46 LeuGloThrGluLeu	32SerLeuGlnSerAlaProGlyProValLeuValProThrArg 45 ::: ::: :::	20 sLeuTrpAspGlyAspValLeuCysLeuProGly	8 GlnAspThrAlaArgCysSerLeuGlyLeuSerCysHi 20 ::: ::: ::: ::: :::	Align seg 1/1 to: US-08-342-930-1 from: 1 to: 5455	alignment_block: US-09-899-471-2_COPY_21_440 x US-08-342-930-1	alignment_scores: Quality: 108.50	; FEATURE: ; NAME/KEY: CDS ; LOCATION: 2055337 US-08-342-930-1

	MetAlaSerThrArgAlaAlaArgLeuGlyGluGluLeu 387	375
374 2553	ysThrProLeuProSer	369 2509
369 2508	tLysThrG1yLeuAsnAsnThrSerValCysAlaLeuGluProSerG1yC ::::::	352 2466
352 2465	GlyProPheLysAspAspMetLeuLeuValGluMe	341 2416
340 2415	InLeuGlnAlaCysSerTrpAlaAspSerLeu	330 2366
330 2365	CAAGGAAGATGGCACGAGCTTTTTGGGTTTGACTCGTGGCACTAAGTACA	328 2316
327 2315	ValSerThrTrpGlu	323 2266
322 2265	spPheGlnLeuValAlaGlyHisProAsnLeuCysValGln::::: ::: :::	309 2216
309 2215	OLeuValProProValProGlnLysAsnAlaThrValAsnGluProGlnA	292 2172
292 2171	TrpGlnAlaProAspGlnSerProCysGln	282 2122
281 2121	rpGlnLeuAspAlaProCysCysLeuProGlyLysValThrLeuCys	266 2072
266 2071	uSerProGlyValT	261 2022
261 2021	CCGGGTGGCAGGGATGCCTTTCACTTACGGCTTTACAGGCTGAGGCCTCT	255 1972
254 1971	TGGGCTTTGCCCACCAGCCTGCGGCACTGAAGGCTTCCTGGTATCACCCA	242 1922
241 1921	rGluargValGluPheCysPro	234 1872
234 1871	CysLeuCysIleGlnValTrpSerLeuGluProAspSe	222 1822
221 1821	GlyProGlnAsnIleThrLeuAsnHisThrAspLeuValPro 	208 1772
207 1771	rLeuTrpTyrLysAsnLeuThr	200 1722
1721	:::	1672

169 .AspGlyAspAsnValLeuLeuThrLeuAspValSerGluGluGlnAspP 185 ::: ::: ::: :::	157 TyrGlnLysGluLeuAsnLeuThrGlnGlnLeuPro	140 luAlaSerLeuGlyAlaGluValGlnIleTrpSerTyrThrLysProArg 156 ::: 4054	123 pLeuValGlnProGlyGlnSerValGlySerAlaValPheAspCysPheG 140 :::::: - 4036TTGTTAATTGCTTGTTTT 4053	107 AlaTyrProIleAlaArgCysAlaLeuLeuGluValGlnValProAlaAs 123	Align seg 1/1 to: US-08-676-169-1 from: 1 to: 12687	alignment_block: US-09-899-471-2_COPY_21_440 x US-08-676-169-1	alignment_scores: Quality: 104.50 Ratio: 0.688 Gaps: 22 Percent Similarity: 36.538 Percent Identity: 21.635	; MOLECULE TYPE: cDNA US-08-676-169-1	Ď.:	; LENGTH: 12687 base pairs ; TYPE: nucleic acid	; INFORMATION FOR SEQ ID NO: 1: ; SEQUENCE CHARACTERISTICS:	; TELEPHONE: (703) 816-4006 ; TELEPAX: (703) 816-4100	DOCKET NUMBI ATION INFOR	; NAME: Crawford, Arthur R.; REGISTRATION NUMBER: 25,327	교육	APPLICATION NUMBER: US/08/676,169 FILING DATE: 31-UL-96	, H	COMPUTER: IBM PC COMPATIBLE COPERATING SYSTEM: DC-DOC MC-DOC	ER READABI	; STATE: VITGINIA ; COUNTRY: U.S.A : ZIP: 22201-4714	Arlington	; CORRESPONDENCE ADDRESS: ADDRESSEE: NIXON & VANDERHYE P.C.	FION: AND THEIR USE IN ENCES: 7	ide, Ewan Douglas : EOUINE ARTERITIS VIRUS PEPTINI	Sequence 1, Application US/08676169 Patent No. 5773235 CENERAL TRIBUTES	Seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-676-169-1	2554 CACCTCTCATGGGAGCAACCCCTGAAACTAGGCCAAGAGCTC 2595	
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o o	GAAGCCAATGACACCCCAGTTAAGCCAA	4908
375	LeuGluProSerGlyCysThrProLeuProSerM	363
363 490	MetheuLeuYalGluMetLysThrGlyLeuAsnAsnThrSerValCysAl :::: :::: TTGGTGCTGGTTCCTTTGACCACCAAAGTAGTAGGCGGTTCTAGGTGCAC	4858
485	TGTTGTGGTTATCGACGGTCTGGACCGCATGGCTCACTTCAAAGACGAT	4808
346	rpAlaAspSerLeuGlyProPheLysAspAsp	334
480	TTTGCGGTTGAACAAGAAGTAACAGCTGGAGACC	4758
333	GlnLeuGlnAla	330
475	AATGCATCCTTGCAAGTCGATCGTGACGCTGC	4708
3 6	*	329
329 470	GINVALSeThrTrp61ULysVal	4658
465	ATTCCTCTGATGTGCTTGACTGTCGGGCCGTCCGAT	4608
321	су	320
460	CAGGAGAGTCTCACTGCAACATTAGCTGCCCTCACTGATGATGACTTCCA	4558
319	ProAsnLe	317
455	AAGAGAGTGTCACCGCCTC	4508
316	ValAsnGluProGlnAspPheGlnLeuValAlaGlyH	304
450	TCGCTTTGACAGGACTTTCATGATGAAATACTTCCTGGAGGGAG	4458
303	ysAsnAlaThr	300
445	GCTGCCCTCGGTCACACCCTGTTACTGGATGTGTTCTCCGCCTCA	4411
300	nAlaProAspGlnSerProCysGlnProLeuValProProValProC	283
283	GLYGLY.GCTATTGGCACAGTA	4361
436	CTATCCCACCATGTTGTTGTGCCACGGTTCCTAGTGTACCAGTTCCCC	4311
275	euAspAlaProCysCysLeu	268
431	CTGG	4274
268	nLeuTrpHisIleAlaArgLeuArgValLeuSerProGlyValTrpGl	. 251
427	GAAAACGTGATATCTTTGTGGTTCTACATCACTGCCG	4238
42	TTGTGCTTGTTCCATCTGGTC	, 0
234	pLeuValProCysLeuCysIle.GlnValTrpSerLeuGl 	N
420	TG	4165
218	TrpTyrLysAsnLeuThrGlyProGlnAsn	202
416	heber rheheuryrhenArgricval FroAspalaheurysSerLeu 	4141
414	CTTTGCCGCTAACTTCTTCCTGCCAAAAAGTGTTGGC	102

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luAlaSerLeuGlyAlaGluValGlnIleTrpSerTyrThrLysProArg 156	140 luAlaSerLeuGlyAl
preuvateinrioglyeinservalelyseralavalpheaspcyspheG 140 ::::::	40364036
	OD.
: 2_COPY_21_440 x US-08-981-459-1	111gnment_block: US-09-899-471-2_COPY_21_
y: 104.50 Length: 416 o: 0.688 Gaps: 22 y: 36.538 Percent Identity: 21.635	ilignment_scores: Quality: 104 Ratio: 0.6 Percent Similarity: 36.
ACYLON NUMBER: 22,769 WCE/DOCKET NUMBER: P61784USO NICATION INFORMATION: NE: 202-638-6666 K: 202-393-5350 FOR SEQ ID NO: 1: CHARACTERISTICS: 12687 base pairs nucleic acid EDNESS: single 3Y: linear TYPE: cDNA	REFERENCE/DOCKET NUMBER: 22,/69 REFERENCE/DOCKET NUMBER: P6 TELECOMMUNICATION INFORMATION: TELEPHONE: 202-638-6666 TELEPAX: 202-393-3950 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 12687 base pairs TEMPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: CDNA
NUMBER: US/08/ 19-FEB-1998 ON: INFORMATION: N, John C.	CATION N G DATE: IFICATIO Y/AGENT HOLMAN
ABLE FORM: ABLE FORM: Floppy disk IBM PC compatible YSTEM: PC-DOS/MS-DOS Patentin RC-DOS/MS-DOS CATION DATA:	STATE: D.C. COUNTRY: U.S.A. ZIP: 20004 COMPUTER READABLE FO MEDDIM TYPE: Flop COMPUTER: IBM PC COMPUTER: IBM PC COPERATING SYSTEM: SOFTMARE: PAtentl CURRENT APPLICATION
DANCES: 4 JACOBSON, PRICE, HOLMAN & STERN, PLLC O Seventh Street, N.W.	Washin
_block: lication US/08981459 1390 ATION: CHIRNSIDE, Ewan Douglas ENTION: Diagnostic Test For Equine Arteritis Virus	seq_documentation_block: Sequence 1, Application Patent No. 6090390 GENERAL INFORMATION: APPLICANT: CHIRNSID: TITLE OF INVENTION: TITLE OF INVENTION:
/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-981-459-1	seq_name: /cgn2_6/ptodata
etAlaSerThrArgAlaAlaArgLeuGlyGluGluLeuLeu 388	375 etAlaSerThrArgAlaAlaArg.

346 4857	CysserTrpAlaAspSerLeuGlyProPheLysAspAsp 	334 4808
333 4807	GGCAAAACTGGCTGATTTTGCGGTTGAACAAGAAGTAACAGCTGGAGACC	330 4758
4757	AATGCATCCTTGCAAGTCGATCGTGACGCTGCTCGTAGTCGCAGACTAAT	4708
329		329
4707	TCGGTGCCGCTCTCACAAGTTTTCAAGTGGCGCAGTATCGTAACATCCTT	4658
4657	ATTCCTCTCTGATGTGCTTGACTGTCGGGCCGTCCG	4608
321	Cysval	320
4607	: :	4558
319	ProAs	317
316 4557	ValasnGluProGlnAspPheGlnLeuValAlaGlyHis	304 4508
4507	TCGCTTTGACAGGACTTTCATGATGAAATACTTCCTGGAGGGAG	4458
303	ysāsnāla	300
300 4457	nAlaProAspGlnSerProCysGlnProLeuValProProValProGlnL	283 4411
283 4410	GIy	276 4361
275 4360	euAspAlaProCysCysLeuPro	268 4311
268 4310	nLeuTrpHisIleAlaArgLeuArgValLeuSerProGlyValTrpGlnL :::	251 4274
251 4273	GluArgValGluPhec	235 4238
234 4237	pLeuValProCysIeuCysIle.GlnValTrpSex	218 4201
	TGGTTGTGCTGCCTCTTCACACCGCTTTCCATGCGC	4165
, ,, ,		4141
4140	CTTTGCCGCTAACTTCTTCCTGCCAAAAAGTGTTGGC	4104
4103	A SECTIVATION OF THE PROPERTY	4066
168	TyrGlnLysGluLeuAsnLeuThrGlnGlnLeuPro	157

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107 AlaTyrProIleAlaArgCysAlaLeuLeuGluValGlnValProAlaAs 123	lign seg 1/1 to: US-09-063-431A-1 from: 1 to: 12687	ignment_block: s-09-899-471-2_COPY_21_440 x US-09-063-431A-1	ignment_scores: Quality: 104.50 Ratio: 0.688 Gaps: 22 ercent Similarity: 36.538 Percent Identity: 21.635	PACENT C. 1, Application US/0905431A Patent No. 634222 APPLICANT: Chirnside, Ewan Douglas TITLE OF INVENTION: EQUINE ARTERITIS VIRUS PEPTIDES; ANTIBODIES TITLE OF INVENTION: AND THEIR USE IN A DIAGNOSTIC TEST CORRESPONDENCE ADDRESS: ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 No. 6342222th Glebe Road, 8th Floor CITY: Arlington STATE: Virginia COUNTRY: U.S.A LIP: 22201-4714 COMPUTER READABLE FORM: MEDIUM TYPE: Ploppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PACENTION INDREER: US/09/063,431A FILING DATE: APPLICATION NUMBER: US/09/063,431A FILING DATE: APPLICATION NUMBER: US/09/063,431A FILING DATE: APPLICATION NUMBER: US/09/063,431A FILING DATE: 31-UIL-96 ATTORNEY/AGENT INFORMATION: NAME: CTANFORD, Arthur R. RESERBELDOCKET NUMBER: 1498-85 TELEPHONE: (703) 816-4006 TELEPHONE: (703) 816-4006 TELEPHONE: (703) 816-4006 INFORMATION FOR SEG ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 12687 base pairs TYPE: nucleic acid STRANDEDRESS: single TOPOLOGY: unknown HOLECULE TYPE: CDNA -09-063-431A-1	prodata/ block:	GlnAspPheArgSerHisGlnCysMetGlnLeuTrpAsnAspAsp 403	375 etAlaSerThrArgAlaAlaArgLeuGlyGluGluLeuLeu 388 	347 MetLeuLeuValGluMetLysThrGlyLeuAsnAsnThrSerValCysAl 363 :::::: ::: ::: :: 4858 TTGGTGCTGGTTCCTTTGACCACCAAAGTAGTAGGCGGTTCTAGGTGCAC 4907 363 ALeuGluProSerGlyCysThrProLeuProSerM 375 :::: ::::: :::: 4908 CATTTGTGACGTCGTTAAGGAAGAAGCCAATGACACCCCAGTTAAGCCAA 4957

3		2
:::: TATCGTAACATCCTT 4707	TCGGTGCCGCTCTCACAAGTTTTCAAGTGGCGCAGTA	58]
sVal 329	lnValSerThrTrpGluLysV	22
GATCGGCAATGAATC 4657	CTTGACTGTCGGGCCGTCCG	80
321	۰ م	20
TGATGACTTCCA 4	CCTCACTO	
	O.A.	17
AÄCCAATTACC 45	: :::	
Glv#is 31	ValAsnGluProGlnAsnpheGlnIeuva	4
TGGAGGGAGGAGTGA 4507	GCTTTGACAGGACTTTCATGATGAAATACTTCC	
CICCECCICAGE 4	SASUATATION OF THE SASUATE OF THE SA	_
roProValProGlnL 3	Vale	283
ATCACCATGCTGGCT 4	GGCTATTGGCACAGTACTAGCGGTATGCAGC	۰ ۲
lThrLeuCysTrpGl 2	LysVa	, 0
 TGTACCAGTTCCCCG 4360	CTATCCCACCATGTTGTTGTGCCACGGTTCCTAGTGT	311
Pro 275	rocyscy	892
ProGLyValTrpGlnL 268 ::: GTGGTTCGGAGG 4310	CTGGCACGTCTTACCTTTCTGAGATGT	274
G 42	CGTGATATCTTTGTGGTTCTACATCACTGC	3 8
^y roGlyAlaHisArgAs 251 	GluArgValGluPheCysProPheArgGluAspPro(35
GTGCTACCGTC	TGTGCTTGTTCCATCTGGTCTG	201
LeuGluProA	ysile.GlnValTrpSeı	218
3C 4200		165
nrLeuAsnHisThrAs 218	yrLysAsnLeuThrGlyProGlnAsnIleThr	202
3-	CGCCCTGTGGTCACTGGG	141
LeuLysSerI	rgProValPro	185
3GC4140		104
	lyAspAsnValLeuLeuThrLeuAspValSe	169
CTTATGTGCTGGGCTT 4103	CTTAACCAACCTGCTTACTTGCCT	990
ro 168	snLeuThrGlnGlnLeuPro	157
TA	TCTT	054
rTyrThrLysProArg 156	TrpSerT	140
AATTGCTTGTTTT. 40	TTGTT	(ii)
eAspCvsPheG 14	uValGlnProGlyGlnSerValGlySerAlaVa	123
TCAGTTG 4035	GCTTATCCAATAGAGAGAGCAGCCTTTCTGGACCTCAGT	995

	_ 0	9	<u> </u>	** ** ** **	** ** ** **	** ** ** ** ** **	 ·				_		
llign seg 1/1 to reverse of: US-09-017-631-23 from: 1 to: 3601 13 CysSerLeuGlyLeuSerCysHisLeuTrpAspGlyAspVa 26 ::	lignment_block: US-09-899-471-2_COPY_21_440 x US-09-017-631-23/rev	lignment_scores: Quality: 101.50 Ratio: 0.495 Percent Similarity: 40.675 Percent Identity: 22.024	SOFTWARE: FastSE SEQ ID NO 23 LENGTH: 3601 TYPE: DNA ORGANISM: HOMO OPGANISM: HOMO -09-017-631-23	EARLIER APPLICATION NUMBER: US 08/113,080 EARLIER FILING DATE: 1993-08-26 EARLIER APPLICATION NUMBER: US 07/920,810 EARLIER FILING DATE: 1992-07-28 NUMBER OF SEQ ID NOS: 34	FILING DATE: 1998-02-03 APPLICATION NUMBER: US 08/80 FILING DATE: 1997-02-28 APPLICATION NUMBER: US 08/38 FILING DATE: 1995-02-02	ENERAL APPLICA APPLICA TITLE C TITLE C FILE RE	snAspAsp 403 :: ATGATGAT 5052	375 etAlaSerThrArgAlaAlaArgLeuGlyGluGluLeuLeu 388	363 aLeu	347 MetLeuLeuValGluMetLysThrGlyLeuAsnAsnThrSerValCysAl 363 :::::: :: :: :: 4858 TTGGTGCTGGTTCCTTTGACCACCAAAGTAGGTAGGTGCTGCAGGTGCAC 4907	334 CysSerTrpAlaAspSerLeuGlyProPheLysAspAsp 346	330GlnLeuGlnAla 333 4758 GGCAAAACTGGCTGATTTTGCGGTTGAACAAGAAGTAACAGCTGGAGACC 4807	4708 AATGCATCCTTGCAAGTCGATCGTGACGCTGCTCGTAGTCGCAGACTAAT 4757

303 2229	287 GlnSerProCysGlnProLeuValProProValProGlnLysAsnAlaTh
286 2270	270 laProCysCysLeuProGlyLysValThrLeuCysTrpGlnAlaProAsp ::::::
270 2317	254 .HisrleAlaArgLeuArgValLeuSerProGlyValTrpGlnLeuAspA :::::: :::
253 2367	G-T
243 2408	235 uArgValGluPhe
235 2458	219 LeuValProCysLeuCysIleGlnValTrpSerLeuGluProAspSerGl
218 2499	202 rpTytysAsnLeuThrGlyProGlnAsnIleThrLeuAsnHisThrAsp
202 2511	187 eLeuLeuTyrLéuArgProValProAspAlaLeuLysSerLeuT:::
187 2557	rGluGluGlnAspPheSerPh ::: ::::::::: :AAAGGGAAGGAATACGGACA
170 2577	154 ysProArgTyrGlnLysGluLeuAsnLeuThrGlnGlnLeuProAspGly
154 2615	141 .AlaSerLeuGlyAlaGluValGlnIleTrpSerTyrThrL :::
140 2656	125 ValGlnProGlyGlnSerValGlySerAlaValPheAspCysPheGlu; ::::::
124 2697	ArgCysAlaLeuLeuGluValGlnValProAlaAspLe ::: ::::::::::: CAGCTTCAGCTTTCCCCGGAGGAAATTGGAGTAGACTC
108 2747	91 uSerargAsnAlaSerLeuGlnAlaGlnValValLeuSerPheGlnAlaT 2747
91 2748	TrpAlaGluProGluGluAlaGl
75 2775	59 pCysklaLeuArgValArgValValValHisLeuAlaValHisGlyHis. ::: 2824 ACAAGCAATGTTGGTGAGGGAGGTGGTGGTGATATGCCCAGGTGGACACACC
59 2825	51 ValleuArgCysProGlnLysThrAs
50 2875	39 roValLeuValProThrArgLeuGlnThrGluLeu

313 2179 21179 316 32129 3225 2029 334 348 349 11979 352 3187 11829 372 372 372 372 372 372 372 372 372 372
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alignment_block: us-09-899-47/1-2\_COPY\_21\_440 \times us-08-883-795A-33/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION:
; LOCATION:
US-08-883-795A-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 40,200 REFERENCE/DOCKET NUMBER: 7841-TELECOMMUNICATION INFORMATION: 7812PHONE: (416) 361-1398
                                                                                                                    2747 TCCCCTGTGTACAGCTTCAGCTTTCCCCGGAGGAAATTGGAGTAGACTCG 2698
                                                                                                                                                                                               2748
                                                                                                                                                                                                                                                       2825 ACAAGCAATGTTGGTGAGGGAGGTGGTGGATATGCCCAGGTGGACACACC 2776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3016 TGCTCTCTGAATGCTTCCTGCTCTGGGCCCTCAAGTTGGCCCTGTGACAT 2967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (416) 364-7
TELEFAX: (416) 361-139
INFORMATION FOR SEQ ID NO:
                                                 2697 GAAGAGTTTGCGGAAAGTGTCAGCAGT.....
                                                                                                                                                                                                                                                                                                                                                                                                       2875 GAGCTGAGAGCCCCTCGACGGGGTTCAGGAGTGGCGGGGGGGAGGGTGTGGC 2826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2925 CCTGAGATGTCATTGCTGGCACTGGAGTGTCCATGGGACAGGCTGGCGCT 2876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2966 CCTTAGATCTCAGAGTTGC.....TCTCTGGACAGTTCCTCTGGCC 2926
                                                                                 125 ValGlnProGlyGlnSerValGlySerAlaValPheAspCysPheGlu.. 140
108 yrProlleAlaArgCysAlaLeuLeuGluValGlnValProAlaAspLeu 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM:
FEATURE:
NAME/KEY:
LOCATION:
LOCATION:
                                                                                                                                                                                                                                 91
                                                                                                                                                                                                                                                                                             76 TrpAlaGlu...ProGluGluAlaGlyLysSerAspSerGluLeuGlnGl 91
                                                                                                                                                                                                                                                                                                                                                       59 pCysAlaLeuArgValArgValValValHisLeuAlaValHisGlyHis. 75
                                                                                                                                                                                                                                                                                                                                                                                                                           51 ValLeuArgCysProGlnLys......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 lLeu ......CysLeuProGlySerLeuGlnSerAlaProGlyP 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 CysSerLeuGlyLeuSerCys......HisLeuTrpAspGlyAspVa 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39 ro.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: | nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                           uSerArgAsnAlaSerLeuGlnAlaGlnValValLeuSerPheGlnAlaT 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ...ValLeuValProThrArgLeu.........GlnThrGluLeu 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to reverse of: US-08-883-795A-33 from: 1 to: 3602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3602 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          join(625..637, 1201..1346, 1605..1691, 2303..2482,
2617..2772)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            join(625..637, 1201..1346, 1605..1691, 2303..2482,
2617..2772)
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0.495
40.675
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ER: 7841-062
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Gaps: 34
Percent Identity: 22.024
                                                                                                                                                                                                                                                                                                                                                                                                                                      .....ThrAs 59
                                                   .GATTGTTCGGAGTG 2657
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GUGULGAAGGATTUTUUGGUCATUTUGGCCTGGGATTATAGAC 1830 2748	358 91 uSerAr	.ValGluMet	Leu	YSSerTrpAlaAspSerLeuGlyProPheLysAspAspMetLeu 348 ::	ACTCTGTCACTGAGGCTGGAGTGGTGATCACAGCTCACTGCAG 2030 39 ro	ProAsnLeuCysValGlnValSerThr	13 CysSerL 	rValAsnGluProGlnAspPheGlnLeuVal313 : :: ::: :::: ::: #ACCAAGCTGAGCAAACAGAAGGTATGCAATAAGACTTGTTGAATGAA	70	gnment.	.HisileAlaArgLeuArgValLeuSerProGlyValTrpGlnLeuAspA 270 ; LENGTH: 3602 ; LENGTH: 3602 ; LENGTH: 3602 ; LENGTH: 3602 ; TYPE: DNA	rgGluAspProGlyAlaHisArgAsnLeuTrp 253 ; EARLIER FILTE	### PILE REFERENCE COURSENT APPLIES COURSE COURSE COURSE COURSE COURSE COU	rpSerLeuGluProAspSerGl 235 ::		. 2512 1729 CT seq_name: /	Leunigkrovatrroaspalateutysserteut 202	LeuLeuThrLeuAspYalSerGluGluGlnAspPheSerPh 187 ::::::::::::::::::::::::::::::::::::
	gAsnAlaSerLeuGlnAlaGlnValValLeuSerPheGlnAlaT 108	rpAlaGluProGluGluAlaGlyLysSerAspSerGluLeuGlnGl 91 -:::::: -:::::::::::::::::::::::	CysalaLeuArgValArgValValValHisLeuAlaValHisGlyHis. 75 :::	AlleuargCysProGlnLysThras 59	OGlnThrGluLeu 50	LeuCysLeuProGlySerLeuGlnSerAlaProGlyP 39 	ysSerLeuGlyLeuSerCysHisLeuTrpAspGlyAspVa 26 ::: GCTCTCTGAATGCTTCCTGCTCTGGGCCCTCAAGTTGGCCCTGTGACAT 2967	COPY_21_440 x US-09-018-138-1/rev to reverse of: US-09-018-138-1 from: 1 to: 3602	y: 101.50		n	FILING DATE: 1997-07-10 F SEQ ID NOS: 24 F SEXTSEQ for Windows Version 3.0	9	ENERAL INCOMPANTION: ENERAL INFORMATION: APPLICANT: Sytkowski, Arthur J. TITLE OF INVENTION: Production and Use of Recombinant TITLE OF INVENTION: Production and Use of Recombinant	m US/09018138	CCAA 1724 		:: :::::: ::: ::::::: :::: TCCCCCGATCATTCTCCCTTTCATCCAAAATCAGGCTCGCAAATGAGATT 1730 LeuGln 389

348 1980	YSSerTrpAlaAspSerLeuGlyProPheLysAspAspMetLeu :: ::::::: ::: ::: CCTCAAATTCCTGGGCTCAAGCGATCCTCCCGGCCTCAGCCTTCCAAATAT	33 4 2029
334 2030		326 2079
325. 2080	ProAsnLeuCysValGlnValSerThrProAsnLeuCysValGlnValSerThr	317 2129
316 2130	TGAATGAATGAGTGAGTGAGTGAATGAATGAATGTATTCCAT	314 2179
313 2180	rValAsnGluProGlnÁspPheGlnLeuVal	303 2229
303 2230	GlnSerProCysGlnProLeuValProProValProGlnLysAsnAlaTh :::	287 2270
286 2271	laProCysCysLeuProGlyLysValThrLeuCysTrpGlnAlaProAsp :::::	7
270 2318	.HisIleAlaArgLeuArgValLeuSerProGlyValTrpGlnLeuAspA ::::: ::: ccccgcaGGACAGCTTCCGACAGCAGGGCCAGGCCCTGCCAGACTTCTAC	25 4 2367
253 2368	rgGluAspProGlyAlaHisArgAsnLeuTrp	243 2408
243 2409	uArgValGluPheCysProPheA	235 2458
235 2459	LeuValProCysLeuCysIleGlnValTrpSerLeuGluProAspSerGl	219 2499
218 2500	rpTyrLysAsnLeuThrGlyProGlnAsnIleThrLeuAsnHisThrAsp	202 2511
202 2512	eLeuLeuTyrLeuArgProValProAspAlaLeuLysSerLeuT::: 	187 2557
187 2558	AspAsnValLeuLeuThrLeuAsp	171 2577
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154 2616	.AlaSerLeuGlyAlaGluValGlnIleTrpSerTyrThrL :::	141 2656
140 2657	ValGlnProGlyGlnSerValGlySerAlaValPheAspCysPheGlu:::::: :::	125 2697
124 2698	yrProlleAlaArgCysAlaLeuLeuGluValGlnValProAlaAspLeu	108 2747

•	ATTORNEY/ACENT INFORMATION: NAME: MURPHY JR, GERALD M REGISTRATION NUMBER: 28,977 REFERENCE/DOCKET NUMBER: 0230-111 TELEPHONE: (703) 205-8000 TELEPHONE: (703) 205-8000 TELEPHONE: (703) 205-8050 INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 3661 base pairs TYPE: nucleic acid STRANDENESS: single TOPOLOGY: linear MOLECULE TYPE: cDNA	
30 .	X: USA Z2040-0747 Z2040-0747 READABLE FORM: REPORM: FYPE: Floppy disk ER: IBM PC compatible ING SYSTEM: PC-DOS/MS-DOS RE: Patentin Release #1.0, Version #1. APPLICATION DATA: APPLICATION DATA: DATE: ELONGROUPE	
REGION-BINDING BIRCH	Seq_documentation_block: Sequence 5, Application US/08718388 Patent No. 6271362 GENERAL INFORMATION: APPLICANT: HARADA, MINORU APPLICANT: HARADA, NAONI TITLE OF INVENTION: GENE ENCODING IGG FC REGIO TITLE OF INVENTION: PROTEIN NUMBER OF SEQUENCES: 29 CORRESSONUENCE ADDRESS: ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH STREET: PO BOX 747 CITY: FALS CHURCH STATE: VA	
.::[::: WANTGAGATT 1730		
· · ·	TCAA Frva Frva GCCT	
	349 Leu	

alignment_scores:
Quality: 100.50 Length: 452
Ratio: 0.498 Gaps: 30
Percent Similarity: 44.690 Percent Identity: 22.345

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	242 eArgGluAspProGlyAlaHisArgAsnLeuTrpHisIleAlaArgLeuA 259 ::::::: ::	236 ArgValGluPheCysProPh 242	224 yslleGlnValTrpSerLeuGluProAspSerGlu	207 rGlyProGlnAsnIleThrLeuAsnHisThrAspLeuValProCysLeuC 224 : ::	191 LeuArgProValProAspAlaLeuLysSerLeuTrpTyrLysAsnLeuTh 207	174 euLeuThrLeuAspValSerGluGluGlnAspPheSerPheLeuLeuTyr 190 :::::	160 uLeuAsnLeuThrGlnGlnLeuProAspGlyAspAsnValL 174	148 GlnIleTrpSerTyrThrLysProArgTyrGlnLysGl 160 	131 alGlySerAlaValPheAspCysPheGluAlaSerLeuGlyAlaGluVal 147 ::: ::: 2205 TGGGGGCTGAGAACTTCACTGTCACTGTAGCCAATGAGCACCGGGGCAGC 2254	115 LeuLeuGluValGlnValProAlaAspLeuValGlnPro.GlyGlnSerV 131 :::::::: ::: ::: 2158AGGCACCTGCGAGTACCTGCTGAGTGCACCCTGCCCACCGGACCACCCT 2204	98 nAlaGlnValValLeuSerPheGlnAla.TyrProlleAlaArgCysAla 114 :::::::::::::::::::::::::::::::::::	82 AlaGlyLysSerAspSerGluLeuGlnGluSerArgAsnAlaSerLeuGl 98	72 alHisGlyHisTrpAlaGlu	58 rAspCysAlaLeuArgValArgValValValHisLeuAlaV 72 : ::: ::: :::	42 ValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnLysTh 58	28CysLeu.ProGlySerLeuGlnSerAlaProGlyProValLeu 41	13 CysSerLeuGlyLeuSerCysHlsLeuTrpAspGlyAspValLeu 27	Align seg 1/1 to: US-08-718-388-5 from: 1 to: 3661	US-09-899-471-2 COPY 21 440 x US-08-718-388-5
TELEPHONE: (703) 205-8000	EGISTRATION NUMBE EFERENCE/DOCKET N ECOMMUNICATION IN	FILING DATE: CLASSIFICATION: 536 ATTORNEY/AGENT INFORMATION:		PD 40	E: BIRCH, STEWART, KOLASCH AND BII PO BOX 747 ALLS CHURCH VA	ENTION: GENE ENCODING 19G FC ENTION: PROTEIN QUENCES: 29 CE ADDRESS:	ORMATION: : MORIKAWA, MINORU : HARADA, NAOKI	- 0 10	372leuProSerMetAlaSerThrArgAlaAlaArg 382 2913 ACGAGCTCTGCGGTGACTCCTGCGAGCCTGCCGAGCCTGCCGAGCCTGCCGAGCCTGCCGAGCCTGCCGAGCCTGCGAGCCTGCCGAGCCTGCCGAGCCTGCCGAGCCTGCCGAGCCTGCCGAGCCTGCCGAGCCTGCCGAGCCTGCCGAGCCTGCCGAGCCTGCCGAGCCTGCGAGCAGCAGCAGAGAGAG	358 snThrSerValCysAlaLeuGluProSerGlyCysThrPro 371 :: :::::::::::::::::::::::	ProPheLysAspAspMetLeuLeuValGluMetLys.ThrGlyLeuAsnA:::::::::::::::::::::::::::::::::::	325 hrTrpGluLysValGlnLeuGlnAlaCysSerTrpAlaAspSerLeuGly 341 ::: :: ::: ::: :::	312LeuValAlaGlyHisProAsnLeuCysValGinValSerT 325	300 LysasnalaThrValasnGluProGlnAspPheGln	CCGACGGCCCGCTGCCCCACGGCCTTGTGCCGCCCGCG	sValThrLeuCys : GCAAGAGTCC	TGCGGGGAATGTGTGCCAAGCCATGCCGTCGCCGTGCACCCCAGAGCA	AGCGGTGGGCGGAAGCCCGCCGGATGGCAGGTGGGCGCGCGC	alLeuSerProGlyVal

FEAN WILL STORY ST	ELEFAX: (703) 205-8050 MATION FOR SEQ ID NO: 6: UNIONCE CHARACTERISTICS: ENGTH: 7842 base pairs FFE: nucleic acid FRANDENESS: double POLOGY: linear ECULE TYPE: CDNA MAE/KEY: CDS CCATION: 21.7802 3-388-6 2-3	
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13	ysSerLeuGlyLeuSerCysHisLeuTrpAspGlyAspValLeu 27	
28 6011	41	
0	oGlnLysTh 58 	
58 6111	ValHisLeuAlaV 72 ::: TCTGCACACCTGCCAG 616	
i i	HisTrpAlaGluProGluGlu 81 :::::	
Ñ	G1 98 AT 625	
Ñ	leAlaArgCysAla 114	
115 6293	LeuLeuGluValGlnValProAlaAspLeuValGlnPro.GlyGlnSerV 131 :::::::: ::: ::: AGGCACCTGCGAGTACCTGCTGAGTGCACCCTGCCACGGACCACCCT 6339	
131 6340	alGlySerAlaValPheAspCysPheGluAlaSerLeuGlyAlaGluVal 147 :: ::: TGGGGGCTGAGAACTTCACTGTCACTGTAGCCAATGAGCACCGGGGCAGC 6389	
148 6390	GlnileTrpSerTyrThrLysProArgTyrGlnLysGl 160	
160 6440	uLeuAsnLeuThrGlnGlnLeuProAspGlyAspAsnValL 174 : ::: ::: ::: ::: ::: ::: CCTGACACTGACTGCCCGCTGGCCCCGGAAGCTACAGGTGGACGGCGTGT 6489	
174 6490	euLeuThrLeuAspValSerGluGluGlnAspPheSerPheLeuLeuTyr 190 ::::: TCGTCACTCTG	
191	LeuArgProValProAspAlaLeuLysSerLeuTrpTyrLysAsnLeuTh 207	

	PO BOX 747	
	NDENCE ADDR	
	UMBER OF SEQUENCES: 29	
(2	INVENTION:	
	APPLICANT	
	O. 6271362	
	seq_documentation_block: Sequence 8 Application US/08718388	
	seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-718-388-8	
95	G 70	
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7047	AGCCACT	
371	erGlyCysThrPro	
0	CAGCTCCGCGAGTGGAGGCGGCC	
358	euAsnA	
6986	TCAGGCCGCTGGGGCC	
341	SerTrpAlaAspSerLeuGly	
6954	6905 CGCCTGCCAAGTTCAGGGCCATCCTGGAGGCCTCTGTCCTGCAGTGGCCA	
325	snLeuCysValGlnValSerT	
6904	6879	
311	300 LysasnalaThrValasnGluProGlnAspPheGln	
6878	CCACGCCTTGTGCCGCCCGCG	
299	ProCysGlnProLeuValPro	
6834	6788 GCAAGAGTCCTTCGGCGGCCCGGACGCCTGCGGCGTGATCTCCGCCA	
287	laProA	
6787	TGTGTCCAAGCCATGCCCGTCGCCGTGCACCCCAGAGCA	
277	268LeuAspAlaProCysCysLeuProGlyLy	
6737	::::::::::::::::::::::::::::::::::::::	
267	259 rgValLeuSerProGlyValTrpGln	
6687		
259	242 eArgGluAspProGlyAlaHisArgAsnLeuTrpHisIleAlaArgLeuA	
6		
4	sPr	
6611	: CAGCTTCGTGCGCC	
235	224 ysIleGlnValTrpSerLeuGluProAspSerGlu	
6575	6539 CGGCGCCGACGTGGTGACCACAACCTCAGGGCTC	
224	GlyProGlnAsnIleThrLeuAsnHisThrA	
6538	6501 CCCTTCCAGCTGGACTCGCTCCTGCACGCACACCTGAG	

TACGTCACTCTGGATGGGCACCGATTCAA	13 CysSerLeuGlyLeuSerCysHisLeuTrpAspGlyAspValLeu 27	llgn seg 1/1 to: US-08-718-388-8 from: 1 to: 16382	lgnment_block: S-09-899-471-2_COPY_21_440 x US-08-718-388-8	ignment_scores: Quality: 100.50 Ratio: 0.498 Gaps: 30 Garcent Similarity: 44.690 Percent Identity: 22.345	08-718-388-8	KEY: CDS	OGY: linear E TYPE: cDNA	base pair acid double	FOR SEQ ID NO: CHARACTERISTICS:	NE: (703)	NAME: MURPHY JR REGISTRATION NUM REFERENCE/DOCKET	FILING DATE: CLASSIFICATION: 536 ATTORNEY/AGENT INFORMATION:	APPLICATION DATA: ATION NUMBER: US/08/718,388	A TYPE: Floppy disk IER: IBM PC compatible IING SYSTEM: PC-DOS/MS-DOS ARE: Patentin Release #1.0, Version #1.	Y: USA 22040-0747	CITY: FALLS CHURCH STATE: VA
The state of the s	TGACCGCTGTGTTCCCCTCAACAACGGCTGCGGCTGCGGCCAATGGCA 604 ValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnLysTh 58	CysSerLeuGlyLeuSerCysHisLeuTrpAspGlyAspValLeu	seg 1/1 to: US-08-718-388-8 from: 1 to: 16382 13 CysSerLeuGlyLeuSerCysHisLeuTrpAspGlyAspValLeu 1	ent_block: -899-471-2_COPY_21_440 x US-08-718-388-8 seg 1/1 to: US-08-718-388-8 from: 1 to: 16382 seg 1/1 to: US-08-718-388-8 from: 1 to: 16382 1 CysSerLeuGlyLeuSerCysHisLeuTrpAspGlyAspValLeu	ent_scores: Quality: 100.50 Quality: 0.498 Quality: 0.498 Ratio: 0.498 Raps: 30 nt Similarity: 44.690 Percent Identity: 22.345 ent_block: -899471-2_COPY_21_440 x US-08-718-388-8 seg 1/1 to: US-08-718-388-8 from: 1 to: 16382 seg 1/1 to: US-08-718-388-8 from: 1 to: 16382 seg 1/1 to: US-08-718-388-8 from: 1 to: 16382 seg 1/1 to: US-08-718-388-8 from: 1 to: 16382 seg 1/1 to: US-08-718-388-8 from: 1 to: 16382 seg 1/1 to: US-08-718-388-8 from: 1 to: 16382 seg 1/1 to: US-08-718-388-8 from: 1 to: 16382 seg 1/1 to: US-08-718-388-8 from: 1 to: 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-899-471-2_COPY_21_440 x US-08-718-388-8 seg 1/1 to: US-08-718-388-8 from: 1 to: 16382 13 CysSerLeuGlyLeuSerCysHisLeuTrpAspGlyAspValLeu	TELEPHONE: (703) 205-8000 TELEPHAX: (703) 205-8000 TELEPHAX: (703) 205-8000 TELEPHAX: (703) 205-8050 ORMATION FOR SEQ ID NO: 8: EQUENCE CHARACTERISTICS: LENGTH: 16382 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear OLECULE TYPE: cDNA EATURE: NAME/KEY: CDS LOCATION: 9.16223 718-388-8 ent_scores: Ouality: 0.498 EATURE: NAME/KEY: CDS LOCATION: 9.16223 718-388-8 ent_scores: Ouality: 44.690 Percent Identity: 22.345 ent_block: -899-471-2_COPY_21_440 x US-08-718-388-8 seg 1/1 to: US-08-718-388-8 from: 1 to: 16382 13 CysSerLeuGlyLeuSerCysHisLeuTrpAspGlyAspValLeu	REGISTRATION NUMBER: 28,977 REFERENCE/DOCKET NUMBER: 0230-111 FELECHAMINICATION INFORMATION: FELEPHONE: (703) 205-8000 TELEPAX: (703) 205-8000 TELEPAX: (703) 205-8050 ORMATION FOR SEQ ID NO: 8: EQUENCE CHARACTERISTICS: LENGTH: 16382 base pairs TYPE: nucleic acid STRANDEDNESS: double 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TTORNEY/AGENT INFORMATION: NAME: MURPHY JR, GERALD M REGISTRATION UNUMBER: 0230-111 FELECOMMUNICATION UNUMBER: 0230-111 FELECOMUNICATION UNUMBER: 0230-111 FELECOMUNICATION UNUMBER: 0230-111 FELECOMUNICAT	MEDIUM TYPE: FLORY disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-POS SOFTMARE: PATENITA PC-DOS/MS-POS SOFTMARE: PATENITA RELEASE #1.0, Version #1.30 URRENT APPLICATION NOMBER: US/08/718,388 FILING DATE: CLASSIFICATION: 536 TTORNET/AGENT INFORMATION: NAME: MURBER: 28,977 REFERENCE/DOCKET NUMBER: 0230-111 REFERENCE/DOCKET NUMBER: 0	OCOUNTRY: USA SIP: 22040-0747 OMOUTER READABLE FORM: MEDIUM TYPE: Ploppy disk COMPUTER: READABLE FORM: MEDIUM TYPE: Ploppy disk COMPUTER: IBM PC COMPATION OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PS-TON BATA: APPLICATION NUMBER: US/08/718,368 FILIND DATE: SOFTWARE: PS-TON NUMBER: US/08/718,368 FILIND DATE: APPLICATION NUMBER: US/08/718,368 FILIND DATE: APPLICATION NUMBER: US/08/718,368 FILIND DATE: CLASSIFICATION: SSG IM NO: 8 BOURNEE CHARACTERISTICS: TELEPHONE: (703) 205-8000 TELEFAX: (703) 205-8000 TELEFAX: (703) 205-8000 ORNATION FOR SEQ ID NO: 8 BOURNEE CHARACTERISTICS: TYPE: DUAL SEG IM NO: 8 BOURNEE CHARACTERISTICS: LENGTH: 16382 base pairs TYPE: DUAL TYPE: CDNA CANTON: 99.16223 718-388-8 ent_SCORTION: 99.16223 718-388-8 ent_SCORTION: 105-0 QUALITY: 100.50 QUALITY: 44.690 Percent Identity: 22.345 ENTURE: ARALO: 0.498 Seg 1/1 to: US-08-718-388-8 from: 1 to: 16382 Seg 1/1 to: US-08-718-388-8 from: 1 to: 16382 Seg 1/1 to: US-08-718-388-8 from: 1 to: 16382 13 CysSerieuGlyLeuSerCysHisLeuTrpAspGlyAspValLeu 11 1 1 1 1 1 1 1 1 1
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8: EQUENCE CHARACTERISTICS: LENGTH: 16382 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear OLECULE TYPE: CDNA EATURE: NAME/KEY: CDS LCCATION: 9.16223 718-388-8 ENTER: Quality: 100.50 Ratio: 0.498 CQBS: COPY_21_440 x US-08-718-388-8 Seg 1/1 to: US-08-718-388-8 from: 1 to: 16382 Seg 1/1 to: US-08-718-388-8 from: 1 to: 16382 13 CysSerLeuGlyLeuSerCysHisLeuTrpAspGlyAspValLeu	REGISTRATION NUMBER: 28,977 REFERENCE/DOCKET NUMBER: 0230-111 ELECOMMUNICATION INFORMATION: TELEPHONE: (703) 205-8000 TELEFAX: (703) 205-8000 TELEFAX: (703) 205-8000 TELEFAX: (703) 205-8050 ORMATION FOR SEQ ID NO: 8: EQUENCE CHARACTERISTICS: LENGTH: 16382 base pairs TYPE: nucleic acid STRANDENESS: double TOPOLOGY: linear OLECULE TYPE: CDN EATOURE: NAME/KEY: CDS LOCATION: 9.16223 718-388-8 ent_Scores: Ouality: 100.50 Ratio: 0.498 nt Similarity: 44.690 Percent Identity: 22.345 ent_block: -899-471-2_COPY_21_440 x US-08-718-388-8 seg 1/1 to: US-08-718-388-8 from: 1 to: 16382 13 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205-8050 ORMATION FOR SEQ ID NO: 8: EQUENCE CHARACTERISTICS: LENGTH: 16382 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: 11near OLECULE TYPE: CDNA EATURE: NAME/KEY: CDS LCCATION: 916223 718-388-8 ENLSCATION:	MEDIUM TIPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 URRENT APPLICATION NUMBER: US/08/718,388 FILING DATE: CLASSIFICATION NUMBER: US/08/718,388 FILING DATE: CLASSIFICATION NUMBER: US/08/718,388 FILING DATE: NAME: MURPHY JR, GERALD M REGISTRATION NUMBER: 28,977 REFERENCE/DOCKET NUMBER: 0230-111 FILECOMMUNICATION INFORMATION: RAPELICATION POR SEQ ID NO: 8: EQUENCE CHARACTERISTICS: LENGTH: 16382 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPPLOGY: linear OLECULE TYPE: CDNA EATURE: TYPE: CDNA RATIO: 0.498 Percent Identity: 22.345 FARING: 0.498 Percent Identity: 22.345 FARING: 0.498 FA	COUNTRY: USA, ZIP: 22040-0747 ZIP: 22040-0747 COMPUTER READABLE FORM: REDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOPTWARE: Patentin Release \$1.0, Version \$1.30 URRENT APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US/08/718,388 FILING DATE: REGISTRATION UNMBER: US/08/718,388 FILING DATE: NAME: MURPHY JR, GERALD M REGISTRATION UNMBER: 0230-111 ELECOMMUNICATION INFORMATION: TELEPHONE: (703) 205-8050 TELEPHONE: (703)
alHisGlyHisTrpAlaGlu	28CysLeu.ProGlySerLeuGlnSerAlaProGlyProValLeu 41	13 CysSerLeuGlyLeuSerCysHisLeuTrpAspGlyAspValLeu	seg 1/1 to: US-08-718-388-8 from: 1 to: 16382 13 CysSerLeuGlyLeuSerCysHisLeuTrpAspGlyAspValLeu 1	ent_block: -899-471-2_COPY_21_440 x US-08-718-388-8 seg 1/1 to: US-08-718-388-8 from: 1 to: 16382 13 CysSerLeuGlyLeuSerCysHisLeuTrpAspGlyAspValLeu	ent_scores: Quality: 100.50 Quality: 0.498 Gaps: 30 nt Similarity: 44.690 Percent Identity: 22.345 ent_block: -899-471-2_COPY_21_440 x US-08-718-388-8 seg 1/1 to: US-08-718-388-8 from: 1 to: 16382 13 CysSerLeuGlyLeuSerCysHisLeuTrpAspGlyAspValLeu	ent_scores: Quality: 100.50 Quality: 0.498 Gaps: 30 nt Similarity: 44.690 Percent Identity: 22.345 ent_block: -899-471-2_COPY_21_440 x US-08-718-388-8 seg 1/1 to: US-08-718-388-8 from: 1 to: 16382 13 CysSerLeuGlyLeuSerCysHisLeuTrpAspGlyAspValLeu	NAME/KEY: CDS INCATION: 9.16223 718-388-8 ent_scores: Quality: 100.50 Ratto: 0.498 Ratto: 0.498 Percent Identity: 22.345 ent_block: -899-471-2_COPY_21_440 x US-08-718-388-8 seg 1/1 to: US-08-718-388-8 from: 1 to: 16382 13 CysSerLeuGlyLeuSerCysHisLeuTrpAspGlyAspValLeu	TOPOLOGY: linear OLECULE TYPE: cDNA EATURE: EATURE: LACATION: 9.16223 718-388-8 ent_scores: Quality: 100.50 Ratio: 0.498	TYPE: INCLEIC ACID STRANDEDNESS: double TOPOLOGY: linear OLECULE TYPE: CDNA EATURE: CDNA EATURE: CDNA EATURE: CDNA EATURE: COATION: 9.16223 718-388-8 ent_scores: Quality: 100.50 Ratio: 0.498 Gaps: 30 nt Similarity: 44.690 Percent Identity: 22.345 ent_block: -899-471-2_COPY_21_440 x US-08-718-388-8 seg 1/1 to: US-08-718-388-8 from: 1 to: 16382 13 CysSerLeuGlyLeuSerCysHisLeuTrpAspGlyAspValLeu	ORMATION FOR SEQ ID NO: 8: EQUENCE CHARACTERISTICS: LENGTH: 16382 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear OLECULE TYPE: CDNA EATOURE: NAME/KEY: CDS LOCATION: 9.16223 718-388-8 ent_scores: Quality: 100.50 Ratto: 0.498 Ratto: 0.498 ratto: 0.498 ratto: 0.498 ratto: 0.498 ratto: 0.498 ratto: 0.50 Ratto: 0.498 ratto:	TELEPHONE: (703) 205-8000 TELEPHAX: (703) 205-8000 ORMATION FOR SEQ ID NO: 8: EQUENCE CHARACTERISTICS: LENGTH: 16382 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear OLECULE TYPE: CDNA EATORE: NAME/KEY: CDS LOCATION: 9.16223 718-388-8 ent_scores: Quality: 100.50 Ratio: 0.498 Ratio: 0.	NAME: MURCHY JR, GERALD M REGISTRATION NUMBER: 28,977 REFERENCE/DOCKET NUMBER: 0230-111 ELECOMMUNICATION INFORMATION: TELEPHONE: (703) 205-8050 ORMATION FOR SEQ ID NO: 8: EQUENCE CHARACTERISTICS: LENGTH: 16382 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear OLECULE TYPE: CDNA EATHOR: 9.16223 718-388-8 ent_scores: Quality: 100.50 Ratlo: 0.498 Ratlo: 0.498 Ratlo: 0.498 Ratlo: 0.498 Ratlo: 0.498 Ratlo: 0.498 Ratlo: 0.498 Ratlo: 0.498 Seg 1/1 to: US-08-718-388-8 from: 1 to: 16382 13 CysSerLeuGlyLeuSerCysHisLeuTrpAspGlyAspValLeu 11 CysSerLeuGlyLeuSerCysHisLeuTrpAspGlyAspValLeu 11	CLASSIFICATION: 536 TTORNEY/AGENT INFORMATION: NAME: MURPHY JR, GERALD M REGISTRATION UNBER: 20,977 REFERENCE/DOCKET NUMBER: 0230-111 RECOMMUNICATION INFORMATION: TELEPHONE: (703) 205-8050 TELEPHONE: (703) 205-8050 TELEFAX: (703) 205-8050 TELEFAX: (703) 205-8050 TELEFAX: (703) 205-8050 TELEFAX: (703) 205-8050 TELEFAX: (703) 205-8050 TELEFAX: (703) 205-8050 TELEFAX: (703) 205-8050 TELEFAX: (703) 205-8050 TELEFAX: (703) 205-8050 TELEFAX: (703) 205-8050 TELEFAX: (703) 205-8050 TELEFAX: (703) 205-8050 TELEFAX: (703) 205-8050 TELEFAX: (703) 205-8050 TELEFAX: (703) 205-8050 TYPE: NUMBER: 28,977 TIPE: NUMBER: 28,977 T	UNREET APPLICATION NUMBER: US/08/718,388 FILING DATE: CLASSIFICATION: 536 STORNEY/AGENT INFORMATION: NAME: WURPHY JR, GERALD M REGISTRATION NUMBER: 28,977 REFERENCE/DOCKET NUMBER: 0230-111 ELECOMMUNICATION INFORMATION: TELEPHONE: (703) 205-8000 TELEPHONE: (703) 205-8000 TELEPAX: (703) 205-8000 TELEPHONE: (703) 205-8000 TELEPHONE: (703) 205-8000 TELEPHONE: (703) 205-8000 TELEPHONE: 16382 base pairs TYPE: DI NO: 8: EQUENCE CHARACTERISTICS: LENGTI : 16382 base pairs TYPE: OLD NO: 8: EQUENCE CHARACTERISTICS: LENGTI : 16382 base pairs TYPE: OLD NO: 8: EQUENCE CHARACTERISTICS: LENGTI : 16382 base pairs TYPE: OLD NO: 8: EQUENCE CHARACTERISTICS: LENGTI : 16382 TYPE: OLD NO: 8: EQUENCE CHARACTERISTICS: LENGTI : 1623 TYPE: OLD NO: 8: EQUENCE CHARACTERISTICS: LENGTI : 1623 TYPE: OLD NO: 8: EQUENCE CHARACTERISTICS: LENGTI : 1623 TYPE: OLD NO: 8: EQUENCE CHARACTERISTICS: LENGTI : 1623 TYPE: OLD NO: 8: EQUENCE CHARACTERISTICS: LENGTI : 1623 TYPE: OLD NO: 8: EQUENCE CHARACTERISTICS: LENGTI : 1623 TYPE: OLD NO: 8: EQUENCE CHARACTERISTICS: LENGTI : 1623 TYPE: OLD NO: 8: EQUENCE CHARACTERISTICS: LENGTI : 16382 TYPE: OLD NO: 8: ENGTI : 16382 TYPE: OLD NO: 8: ENGTI : 16382 TYPE: OLD NO: 8: ENGTI : 16382 TYPE: OLD NO: 98: ENGTI : 16382 TYPE: OLD N	MEDIUM TIPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 URRENT APPLICATION LOATA: APPLICATION NUMBER: US/08/718,388 FILING DATE: CLASSIFICATION NUMBER: US/08/718,388 FILING DATE: CLASSIFICATION NUMBER: 0230-718 RAME: MURPHY JR, GERALD M REGISTRATION NUMBER: 0230-111 FELCOMMUNICATION INFORMATION: RAME: MURPHY JR, GERALD M REGISTRATION NUMBER: 0230-111 FELCOMMUNICATION INFORMATION: FELEPHONE: (703) 205-8000 TELEFAX: (703) 205-8000 TELEFAX: (703) 205-8050 T	COUNTRY: USA ZIP: 22040-0747 ZIP: 22040-0747 COMPUTER EADABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOCTWARE: Patentin Release #1.0, Version #1.30 URRENT APPLICATION DATA: APPLICATION NUMBER: US/08/718,388 FILING DATE: CLASSIFICATION: 536 FILING DATE: TYDREMY/AGENT INFORMATION: NAME: MURPHY JR, GERALD W REGISTRATION NUMBER: 0230-111 REFERENCE/DOCKET NUMBER: 0
rAspCysAlaLeuArgValArgValValValHisLeuAlaV 72 :	28CysLeu.ProGlySerLeuGlnSerAlaProGlyProValLeu 41	13 CysSerLeuGlyLeuSerCysHisLeuTrpAspGlyAspValLeu	seg 1/1 to: US-08-718-388-8 from: 1 to: 16382 13 CysSerLeuGlyLeuSerCysHisLeuTrpAspGlyAspValLeu	ent_block: -899-471-2_COPY_21_440 x US-08-718-388-8 seg 1/1 to: US-08-718-388-8 from: 1 to: 16382 seg 1/1 to: US-08-718-388-8 from: 1 to: 16382 13 CysSerLeuGlyLeuSerCysHisLeuTrpAspGlyAspValLeu	ent_scores: Quality: 100.50 Ratio: 0.498 Rat	ent_scores: Quality: 100.50 Ratio: 0.498 ont Similarity: 44.690 Percent Identity: 22.345 ent_block: -899-471-2_COPY_21_440 x US-08-718-388-8 seg 1/1 to: US-08-718-388-8 from: 1 to: 16382 13 CysSerLeuGlyLeuSerCysHisLeuTrpAspGlyAspValLeu	NAME/KEY: CDS INCATION: 9.16223 718-388-8 ent_scores: Quality: 100.50 Ratio: 0.498 Ratio: 0.498 Ratio: 0.498 Percent Identity: 22.345 ent_block: -899-471-2_COPY_21_440 x US-08-718-388-8 seg 1/1 to: US-08-718-388-8 from: 1 to: 16382 13 CysSerLeuGlyLeuSerCysHisLeuTrpAspGlyAspValLeu	TOPOLOGY: linear OLECULE TYPE: cDNA LEATURE: NAME/KEY: CDS LCCATION: 9.16223 718-388-8 ent_scores: Quality: 100.50	TYPE: INCLESC EACH STRANDEDNESS: double TOPOLOGY: linear OLECULE TYPE: CDNA EATURE: CATION: 9.16223 718-388-8 ent_scores: Quality: 100.50 Ratio: 0.498 Ratio: 0.	ORMATION FOR SEQ ID NO: 8: EQUENCE CHARACTERISTICS: LENGTH: 16382 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear OLECULE TYPE: CDNA EATURE: NAME/KEY: CDS LOCATION: 9.16223 718-388-8 ent_scores: Quality: 100.50 Ratio: 0.498 Ratio: 0.498 ratio: 0.498 ratio: 0.498 ratio: 0.498 ent_block: -899-471-2_COPY_21_440 x US-08-718-388-8 seg 1/1 to: US-08-718-388-8 from: 1 to: 16382 13 CysSerLeuGlyLeuSerCysHisLeuTrpAspGlyAspValLeu	TELEPHONE: (703) 205-8000 TELEPAX: (703) 205-8000 ORMATION FOR SEQ ID NO: 8: EQUENCE CHARACTERISTICS: LENCTH: 16382 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear OLECULE TYPE: CDNA EATOURE: NAME/KEY: CDS LOCATION: 9.16223 718-388-8 ent_scores: Quality: 100.50 Ratio: 0.498 ent_similarity: 44.690 Percent Identity: 22.345 ent_block: -899-471-2_COPY_21_440 x US-08-718-388-8 seg 1/1 to: US-08-718-388-8 from: 1 to: 16382 13 CysSerLeuGlyLeuSerCysHisLeuTrpAspGlyAspValLeu	NAME: MURCHY JR, GERALD M REGISTRATION NUMBER: 28,977 REFERENCE/DOCKET NUMBER: 0230-111 ELECOMMUNICATION INFORMATION: TELEPHONE: (703) 205-8000 TELEFAX: (703) 205-8000 ORMATION FOR SEQ ID NO: 8: EQUENCE CHARACTERISTICS: LENGTH: 16382 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear OLECULE TYPE: CDNA EATURE: NAME/KEY: CDS LCCATION: 916223 718-388-8 ent_scores: Quality: 100.50 Ratio: 0.498 Ratio: 0.498 ratio: 0.498 ratio: 0.498 ratio-chick: -899-471-2_COPY_21_440 x US-08-718-388-8 seg 1/1 to: US-08-718-388-8 from: 1 to: 16382 13 CysSerLeuGlyLeuSerCysHisLeuTrpAspGlyAspValLeu	CLASSIFICATION: 536 ITORNEY/AGENT INFORMATION: NAME: MUTPRY JR, GERALD W REGISTRATION UNBER: 28,977 REFERENCE/DOCKET NUMBER: 0230-111 ELECOMMUNICATION INFORMATION: TELEPHONE: (703) 205-8050 ORMATION FOR SEQ ID NO: 8: EQUENCE CHARACTERISTICS: LENGTH: 16382 base pairs TYPE: nucleic acid STRANDENESS: double TOPOLOGY: linear OLECULE TYPE: CDNA EATOURE: NAME/KEY: CDS LOCATION: 916223 718-388-8 ent_scores: Quality: 100.50 Ratio: 0.498 Ratio: 0.498 ratio 0.498 ratio 0.498 rest-block: -899-471-2_COPY_21_440 x US-08-718-388-8 seg 1/1 to: US-08-718-388-8 from: 1 to: 16382 13 CysSerLeuGlyLeuSerCysHisLeuTrpAspGlyAspValLeu	UNTRENT APPLICATION NUMBER: US/08/718,388 FILING DATE: CLASSIFICATION: 336 FILING DATE: CLASSIFICATION: 336 TITORNEY/AGENT INFORMATION: NAME: MURPHY JR, GERALD M REGISTRATION NUMBER: 0230-111 ELECOMMUNICATION INFORMATION: TELEPHONE: (703) 205-8000 TELEFAX: (703) 205-8000 TELEFAX: (703) 205-8000 TELEFAX: (703) 205-8000 TELEFAX: (703) 205-8050 ORMATION FOR SEQ ID NO: 8: EQUENCE CHARACTERISTICS: LENGTH: 16382 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear OLECULE TYPE: CDNA EATURE: NAMESKEY: CDS INCATION: 9.16223 718-388-8 ENT_SOURCE: 0.498 EATURE: 0.498 EATURE: 0.498 INCATION: 0.4	MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 URRENT APPLICATION NOTA: APPLICATION NUMBER: US/08/718,388 FILING DATE: CLASSIFICATION: NAME: MURPHY JR, GERALD M REGISTRATION: NAME: MURPHY JR, GERALD M REGISTRATION NUMBER: 28,977 REFERENCE/DOCKET NUMBER: 0230-111 ELECOMMUNICATION INFORMATION: TELEPHONE: (703) 205-8000 TELEPAX: (COUNTRY: USA ZIP: 22040-0747 ZIP: 22040-0747 ZIP: 22040-0747 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOPTWARE: Patentin Release #1.0, Version #1.30 URRENT APPLICATION NOMER: US/08/718,388 FILING DATE: CLASSIFICATION NUMBER: US/08/718,388 FILING DATE: MAME: MURPHY JR, GERALD M REGISTRATION NUMBER: 0230-111 RELECOMMUNICATION NUMBER: 0230-111 RELECOMMUNICATION NOMER: 0230-111 RELECOMMUNICATION NOMER: 0205-8050 OPELETAX: (703) 205-8050 OPELETAX: (703)
ValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnLysTh 58		13 CysSerLeuGlyLeuSerCysHisLeuTrpAspGlyAspValLeu	n seg 1/1 to: US-08-718-388-8 from: 1 to: 16382 13 CysSerLeuGlyLeuSerCysHisLeuTrpAspGlyAspValLeu 11	ent_block: -899-471-2_COPY_21_440 x US-08-718-388-8 seg 1/1 to: US-08-718-388-8 from: 1 to: 16382 seg 1/1 to: US-08-718-388-8 from: 1 to: 16382 13 CysSerLeuGlyLeuSerCysHisLeuTrpAspGlyAspValLeu	ent_scores: Quality: 100.50 Quality: 100.50 Gaps: 30 nt Similarity: 44.690 Percent Identity: 22.345 ent_block: -899-471-2_COPY_21_440 x US-08-718-388-8 seg 1/1 to: US-08-718-388-8 from: 1 to: 16382 seg 1/1 to: US-08-718-388-8 from: 1 to: 16382 13 CysSerLeuGlyLeuSerCysHisLeuTrpAspGlyAspValLeu	718-388-8 ent_scores: Quality: 100.50 Ratto: 0.498 Ratto: 0.4	NAME/KEY: CDS NAME/KEY: CDS LOCATION: 9.16223 718-388-8 ent_scores:	TOPOLOGY: linear OLECULE TYPE: CDNA EATURE: NAME/KEY: CDS LCCATION: 9.16223 718-388-8 ent_scores: Quality: 100.50 RatLo: 0.498 Caps: 30 nt Similarity: 44.690 Percent Identity: 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LCCATION: 916223 718-388-8 ent_scores: Quality: 100.50 Ratlo: 0.498 nt Similarity: 44.690 Percent Identity: 22.345 ent_block: -899-471-2_COPY_21_440 x US-08-718-388-8 seg 1/1 to: US-08-718-388-8 for CysSerLeuGlyLeuSerCysHisLeuTrpAspGlyAspValLeu	NAME: MURCHY JR, GERALD M REGISTRATION NUMBER: 28,977 REFERENCE/DOCKET NUMBER: 0230-111 ELECOMMUNICATION INFORMATION: TELEPHONE: (703) 205-8000 TELEFAX: (703) 205-8000 ORMATION FOR SEQ ID NO: 8: EQUENCE CHARACTERISTICS: LENCTH: 16382 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear OLECULE TYPE: CDN EATOURE: NAME/KEY: CDS LOCATION: 9.16223 718-388-8 ent_Scores: Quality: 100.50 Ratio: 0.498 Ratio: 0.498 nt Similarity: 44.690 Percent Identity: 22.345 ent_block: -899-471-2_COPY_21_440 x US-08-718-388-8 seg 1/1 to: US-08-718-388-8 from: 1 to: 16382 13 CysSerLeuGlyLeuSerCysHisLeuTrpAspGlyAspValLeu	CLASSIFICATION: 536 TTORNEY/AGENT INFORMATION: NAME: MURPHY JR, GERALD M REGISTRATION UNBER: 28,977 REFERENCE/DOCKET NUMBER: 0230-111 ELECOMMUNICATION INFORMATION: TELEPHONE: (703) 205-8050 OTALETAX: (703) 205-8050 OTALETAX: (703) 205-8050 OTALETAX: (703) 205-8050 OTALETON FOR SEQ ID NO: 8: EQUENCE CHARACTERISTICS: LENCTH: 16382 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear OLECOLE TYPE: CDN EATURE: NAME/KEY: CDS LOCATION: 9.16223 718-388-8 ent_Scores: Quality: 100.50 Ratio: 0.498 Ratio: 0.498 OTALITATION: 44.690 Percent Identity: 22.345 ent_block: -899-471-2_COPY_21_440 x US-08-718-388-8 seg 1/1 to: US-08-718-388-8 for Stranded Length: 10382 13 CysSerLeuGlyLeuSerCysHisLeuTrpAspGlyAspValLeu	APPLICATION NUMBER: US/08/718,388 FILING DATE: CLASSIFICATION: 536 CLASSIFICATION: 368 FILING DATE: CLASSIFICATION: 170, GERALD M REGISTRATION NUMBER: 28,977 REFERENCE/DOCKET NUMBER: 28,977 REFERENCE/DOCKET NUMBER: 28,977 REFERENCE/DOCKET NUMBER: 0230-111 ELECOMMUNICATION INFORMATION: TELEPHONE: (703) 205-8000 TELEPAX: (703) 205-8000 TELEPAX: (703) 205-8000 TELEPAX: (703) 205-8050 ORMATION FOR SEQ ID NO: 8: EQUENCE CHARACTERISTICS: LENCTH: 16382 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear OLECULE TYPE: CDNA EATURE: NAME/KEY: CDS LCCATION: 9.16223 718-388-8 ent_Scores: Quality: 100.50	MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFWMARE: Patentin Release #1.0, Version #1.30 URRENT APPLICATION DATA: APPLICATION NUMBER: US/08/718,388 FILING DATE: CLASSIFICATION: 536 FITORNEY/AGENT INFORMATION: NAME: MURBER: 28,977 REFERENCE/DOCKET NUMBER: 28,977 REFERENCE/DOCKET NUMBER: 0230-111 ELECOMMUNICATION INFORMATION: TELEPHONE: (703) 205-8050 ORMATION FOR SEQ ID NO: 8: EQUENCE CHARACTERISTICS: EQUENCE CHARACTERISTICS: LENGTH: 16382 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear OLECULE TYPE: CDNA EATURE: NAME/KEY: CDS LCCATION: 916223 718-388-8 ent_Staliay: 100.50 Ratio: 0.498 nt Similarity: 44.690 Percent Identity: 22.345 ent_Dlock: -899-471-2_COPY_21_440 x US-08-718-388-8 seg 1/1 to: US-08-718-388-8 seg 1/1 to: US-08-718-388-8 seg 1/1 to: US-08-718-388-8 SEGIFFERMENTAL STANGED	COUNTRY: USA ZIP: 22040-0747 ZIP: 22040-0747 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIAN Release #1.0, Version #1.30 URRENT APPLICATION DATA: APPLICATION NUMBER: US/08/718,388 FILING DATE: CLASSIFICATION NUMBER: US/08/718,388 FILING DATE: TELECHONE: (703) 205-8000 REGISTRATION NUMBER: 28,977 REFERENCE/DOCKET NUMBER: 0230-111 ELECOMMUNICATION INFORMATION: TELECHONE: (703) 205-8000 TELEFAX: (703) 205-8000 TELEFAX: (703) 205-8000 TELEFAX: (703) 205-8050 ORMATION FOR SEQ ID NO: 8: EQUENCE CHARACTERISTICS: LENGTH: 16382 base pairs TYPE: nucleic acid STRANDEDHESS: double TOPOLOGY: linear OLECULE TYPE: CDNA LEAVARE: CDS LCCATION: 916223 718-388-8 ENAME/KEY: CDS LCCATION: 916223 718-388-8 seq L/1 to: US-08-718-388-8 seg 1/1 to: US-08-718-388-8 seg 1/1 to: US-08-718-388-8 seg 1/1 to: US-08-718-388-8 seg 1/1 to: US-08-718-388-8 seg 1/1 to: US-08-718-388-8 SEG TTTGGGGGGCTGCCAGTGCGAGGGGGGGTTTCGTGTTAAGTGGC

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325 6943 342 6975 358 6998	76 888 88 23 23 00 67 67 12	242 6650 259 6676 268 6726		6328 148 6378 6378 160 6428 174 6478	— (2)
hrTrpGluLysValGlnLeuGlnAlac	GCAAGAGTCCTT	eArgGluAspProGlyAlaHisArgAsnLeuTrpH ::::::::::::::::::::::::::::::::::::	rGlyPro	TGGGGGCTGAGAACTTCACTGTAGC Gln lleTrpSerTyrThrLys	AGGC
LeuGly 3	CCA 6	SIleAlaArgLeuA :			· -
341 6974 358 359 6997 371 371	6822 299 6866 311 6892 325	259 6675 267 267 6725 6725 277 6775	224 224 6563 235 235 6599 6649	60 60 74 74 74 74 74 74 74 74	6327 147

372Leul 7036 ACGAGCTCTGCGGTGACT0	LeuProSerMetAlaSerThrArgAlaAlaArg 382
<pre>seq_name: /cgn2_6/ptodata/2,</pre>	/cgn2_6/ptodata/2/1na/6B_COMB.seq:US-09-301-665-3
<pre>seq_documentation_block: Sequence 3, Application US/093016 Patent No. 6207876</pre>	5/09301665
CANT: CANT: CANT: CANT: OF I	RODNEY E. RJIT K. , MICHAEL R. ADENOSINE DEAMINASE DEFICIENT TRANSGENIC MICE AND METHODS FOR THE USE THEREOF
APPLICATION PAPPLICATION PAPPLI	US/09/301,66 4-28 60/083,408
TLING DATE: 199 PLICATION NUMB TILING DATE: 199 SEQ ID NOS: 4	4-2 60 4-2
SOLTWARE: PATENTIN VET.: SEQ ID NO 3 LENGTH: 36741 TYPE: DNA ORGANISM: Homo sapiens US-09-301-665-3	2.0.
lignment_scores: Quality: 100.00 Ratio: 1.333 Percent Similarity: 45.732	Length: 164 Gaps: 9 Percent Identity: 25.610
lignment_block: US-09-899-471-2_COPY_21_440) x US-09-301-665-3
Align seg 1/1 to: US-09-3	301-665-3 from: 1 to: 36741
213 ThrLeuAsnHisThrAspl ::: ::: 21545 AGTTTGTCACACTCAGAT	ThrLeuAsnHisThrAspLeuValProCysLeuCysIleGlnValTrpSe 229 ::: ::: ::: ::
229 r	r
233 spSerGluArgValGluPh :: :: 21645 ATTCAGTGGCCCTTTT	spSerGluArgValGluPheCysProPheArgGluAspProGlyAlaHis 249 :: ::: ATTCAGTGGCCCTT:TTTCCAGCTCTGGGACTCAGGCCTGCCTCATTA 21691
250 ArgAsnLeuTrpHisIleAlaArgLeuArgVal ::::: ::: 21692 ACTGTCCTCACCCATTTCTCCTTCCAGTTC	ArgAsnLeuTrpHisileAlaArgLeuArgValLeuSerProGlyValTr 266 ::::: :::
266 pGlnLeuAspAlaProCys	pGlnLeuAspAlaProCysCysLeuProGlyLysValThrLeuCysTrpG 283 ::::::::: GCCTTTCAGGGGCCTCTC
283 lnAlaProAspGlnSer	InAlaProAspGlnSerProCysGln
292ProLeu\	ProLeuValProProValProGlnLysAsnAlaTh 303
303 rValAsnGluProGlnAsp	rValAsnGluProGlnAspPheGlnLeuValAlaGlyHisProAsnLeuC 320

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alignment_scores:
                                                                                                                                 ; RELEVANT RESIDUES IN SEQ ID US-08-026-138E-7
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    Sequence 7, Application
      Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21941 AGTTGGAGCAAGAGCCTTAACCCATGGTCTTCCCAGCTCATT 21982
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                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (212) 953-7733
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                 TISSUE LACE.

PUBLICATION INFORMATION:

AUTHORS: MASSAYOSHI MISHINA

AUTHORS: MASSAYOSHI MISHINA

CODING THE SAME

TITLE: NOVEL PROTEINS AND GENES CODING THE SAME

TITLE: NOVEL PROTEINS AND GENES CODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Masayoshi MISHINA
TITLE OF INVENTION: NOVEL PROTEINS AND GENES CODING THE SAME
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 22,389
REFERENCE/DOCKET NUMBER: F-/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 986-2340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Word Perfect 5:1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/C
FILING DATE: 26-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          335 SerTrpAlaAspSerLeuGlyProPheLysAspAspMetLeu 348
                                                                                                                                                                                                                                                                        MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            320 ysValGlnValSerThrTrpGluLysVal.....GlnLeuGlnAlaCys 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                 LENGTH: 3717 nuclei
TYPE: nucleic acid
STRANDEDNESS: doubl
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 30-JUN-
APPLICATION NUMBER:
FILING DATE: 12-AUG-
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Nigata-shi
                                                                                                                                                                                                                                    ORGANISM: mouse
TISSUE TYPE: bra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS v.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: JP 173155/1992
FILING DATE: 30-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: JP 39563/1992 FILING DATE: 26-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-026-138E-7
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                             Ratio
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    99.50
1.026
38.492
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                                                                                                                                                                                                                                                                                                                                  double strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C.Bruce
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Length: 252
Gaps: 16
Percent Identity: 24.206
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alignment_block: US-09-899-471-2_COPY_21_440 x US-08-026-138E-7

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eq_documentation_block:
    Sequence 24, Application US/09041886
    Patent No. 6235872
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GENERAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 260 ValLeuSerProGlyValTrpGlnLeu.....AspAlaProCysCy 273
                                                                                                                                                                          eHis 418
                                                                                                                                                                                                                 AGAAGAGGTCAGCAGGGAAGCTTGTGGGACACAAGGGTTTCCAAGGTCCT 3679
                                                                                                                                                                                                                                                 ...AspAspAsnMetGlySerLeuTrpAlaCysProMetAspLysTyrIl 417
                                                                                                                                                                                                                                                                                                                                                                     CCAGCCA...CAGTCCCTGGCTCATTGGAACTTGGGAGCCTCCATCACAC 3579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .....CysGlnProLeuValProProValProGlnLysAsnAlaThrVal 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGCGCGCGCCTGGGCCAGGGCCCCGCGCCCTCGGCACGCTTCCCTGCCC 3258
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                                                                                           /cgn2_6/ptodata/2/1na/6B_COMB.seq:US-09-041-886-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ......SerTrpAlaAspSerLeuGly 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ....TGGCAGAAGCCTTCACTCGATCCAA 3290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .TCTGCCTGCACACCCATACCCACCT 3488
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us-09-899-471-2_COPY_21_440 x us-09-041-886-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY:
; LOCATION:
US-09-041-886-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (619) 535-894
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
              129
                                                                                           112
                                                                                                                                                                                                             250
                                                                                                                                                                                                                                                                                          219
                                                                                                                                                                                                                                                                                                                                                                 169 GTCCTCCTCGACTGCTCCGCGGAGTCCGACCGAGGAGTTCCAGTGATCAA 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                      96
                                                                                                                                                                                                                                                 79
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                                                                                                                                                                                                                                                                                                                                                                                                       50 LeuValLeuArgCysProGlnLysThrAspCysAlaLeuArgVal.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/041,886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                       roGluGluAlaGlyLysSerAspSerGluLeuGlnGluSerArgAsnAla
                                                                                                                                                                                                                                                                                      GTGGAAGAAAGATGGCATTCATCTGGCCTTG...
            lnSerValGlySerAlaValPheAspCysPheGluAlaSerLeuGlyAla 145
                                                                                                                             TCTCTGCTGATACAAAACATACTTCATTCCAGACACCAC.....
                                                                                                                                                                    SerLeuGlnAlaGlnValValLeuSerPheGlnAlaTyrProIleAlaAr 112
                                                                                         gCysAlaLeuLeuGluValGlnValProAlaAspLeuValGlnProGlyG 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         California
                                                                                                                                                                                                                                                                                                                    ...ArgValValValHisLeuAlaValHisGlyHisTrpAlaGluP 79
                                                                                                                                                                                                             .....GGAATGGATGAAAGGAAGCAGCAACTTTCAAATGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                to: US-09-041-886-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rabizadeh,
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SYSTEM: PC-DOS/MS-DOS
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0.599
35.776
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20
19.612
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161	54 TACGGATA 1	115
35	19 euCysValGlnValSerThrTrpGluLysValGlnLeuGlnAlaCysSer 3	ω
153	02 aThrValAsnGluProGlnAspPheGlnLeuValAlaGlyHisProAsnL 3 :	3(11(
103	90 CysGlnProLeuValProProValProGlnLysAsnAl 3	105
289	4 euProGlyLysValThrLeuCysTrpGlnAlaProAspGlnSerPro 2	
274 1018	7 gLeuArgValLeuSerProGlyValTrpGlnLeuAspAlaProCysCysL 2	97
257 971	TATACCTGTGTTGTCACATATAAAAATGAGAATATTAGTGCCTCTGCAGA	92
921	72 GTGGAAGCAACTTGCTTATCTCCAATGTGACAGATGATGACAGTGGAATG	
255	255 2	25
871	GGAAGTCATCCAACTCAGGTCTAAAAAGTATTCTTTATTGG	80
255		2
821	TTGTGTTTCTGGCTATCCTCCACCAAGTTTTACCTGGTT	7:
255		2
255 771	253 rpHisIle	7 2
721	TGAAGCAGAAGTCAGAATTTTATCAGATCCAGGACTGCATAGACAGCTGT	σį
2	ProGlvAlaHisArgAsnLenT	Ņ
243	236 ArgValGluPheCysProPheArg	6 ×
235 621	pSerLeuGluProAspSerGlu ::: CCGACTCCAACCGGGGGACATT	υ N
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219	[leThrLeuAsnHisThrAspL	N
206 528	TyrLysAsnLe CAGAAGAAC	نر ج
189 498	70 TGCTACTCAAGTGTGAAGTCATTGGGGAG	4
469	CACAGCCTTCATGGGAGACACAG	ء د
173	61 uAsnLeuThrGlnGlnLeuProAspGlyAspAsnV	
161 419	146 GluValGlnIleTrpSerTyrThrLysProArgTyrGlnLysGluLe ::: :::	ωμ
369	AGGAGCTTTACCAATGTGAGGCATCTTTAGGAGAT	ω

1300	1250	365	1200	348	1162	336
GATGI	TCCCT	luPro	TGTGG	uLeuV	:	TrpAl
3/2 LeuProSerMetALaSerThrArgAlaAlaArgLeu 383 ::: ::: ::: ::: 1300 GATGTGGTCCCTGTCTTGGTTTCCAGCCGATTTGTCCGTCTC 1341	1250 TCCCTAAGCCTGCAATCCCAAGCTCCAGTGTCCTCCCCTTCGGCTCCCAGA 1299	365 luproSerGlyCysThrPro 371	1200 TGTGGCTGAAAATGAGGCTGGAAATGCCCAGACCAGTGCACAGCTCATTG 1249	348 uLeuValGluMetLysThrGlyLeuAsnAsnThrSerValCysAlaLeuG 365	CTTGGGGTGGTGAAGTCAGATGAAGGCTTTTATCAATG 1199	336 TrpAlaAspSerLeuGlyProPheLysAspAspMetLe 348
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Query: US-09-899-471-2_COPY_21_440
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-FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500 -DELOP-6.000
-DELEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500 -DELOP-6.000
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-NCPU-6 -ICPU-3 -LONGLOG -DEV_TIMEOUT-120 -MARN_TIMEOUT-30
-NO_XLPXY -WAIT -THREADS-1
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BI251117 602994315F1 NCI_CGAP_I
BI765330 603050641F1 NIH_MCC_I
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B1689749 60331625F1 NCI_CGAP_N
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                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                    further details.
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mumalia; Eutheria; Rodentia;
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                                                                                                                   /clone="1110025H02"
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5 603038380F1 NIH_MC
0 PMO-HN0073-200201
3 603057401F1 NIH_MC
7 603024690F1 NIH_MC
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BB609618 RIKEN full-length enriched, 18 CDNA clone 1110025H02 5', mRNA sequence. linear EST 26-OCT-2001 days embryo Mus musculus

Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222

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Sugahara

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Please visit our web site (http://genome.gsc.riken.go.jp) for 1-Length Mouse cDNAs Compared with Genome 12, 673-677 (2001)

/clone_lib="RIKEN full-length enriched, /dev_stage="18 days embryo" /lab_host="SOLR" 18 days embryo"

prepared and sequenced in Mouse Genome Encyclopedia XhoI; Site_2: SstI; cDNA library was

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BASE COUNT
ORIGIN
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                                                                                                                                  pSerLeuGluProAspSerGluArgValGluPheCysProPheArgGluA
                                                                                                                                                                                                                                                                                                                                                                                 CTGCAGGGGTCTTGAAGTCCGGGACAGCATCCAGAGCTGCTGGGTCCTGC 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    heAspCysPheGluAlaSerLeuGlyAlaGluValGlnIleTrpSerTyr 152
                                                                 spProGlyAlaHisArgAsnLeuTrpHisIleAlaArgLeuArgValLeu
                                                                                                        GTCGCTAGAGCCCAGACTCTGAGAGGGTCGAATTCTGCCCCCTTCCGGGAAG
                                                                                                                                                                            IleThrLeuAsnHisThrAspLeuValProCysLeuCysIleGlnValTr 228
                        SerProGlyValTrpGlnLeuAspAlaProCysCysLeuProGlyLysVa
                                                  ATCCCGGTGCACACAGGGACCTCTGGCACATAGCCAGGCTGCGGGTACTG
                                                                                                                                                             ATTACTTTAAACCACACAGACCTGGTTCCCTGCCTCTGCATTCAGGTGTG
                                                                                                                                                                                                                  CGGATGCTCTCAAATCCTTGTGGTACAAAAACCTGACTGGACCTCAGAAC
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|Plate: LLAM10997 row: g column:
|High quality sequence stop: 646.
| Location/Qualifiers
                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Bechnologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                               National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D**
                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 784)
NIH-MGC http://mgc.nci.nih.gov/.
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                                                                                                                                                                                               DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
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/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
                                                        /organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
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Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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                                                AlaCysSerTrpAlaAspSerLeuGlyProPheLysAspAspMetLeuLe
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Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLA
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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plate: LLAM11333 row: k column: 20
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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Site_2: Sall; Cloned unidirectionally. Primer: Ol
Average insert size 1.9 kb. Constructed by Life
Technologies: Note: this is a NCI_CGAP Library."
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/clone="IMAGE:5135755"
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/strain="FVB/N"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
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     Similarity:
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                    Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA sequence
BI251117
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                                                                                                                                                                                                                                                                                                                                                                                                                     found through the I.M.A.G.E. Consortium/LLNL at: http://lmage.llnl.gov http://lmage.llnl.gov column: 03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 839)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BI251117.1 GI:14800198
                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 836.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            house mouse
                                                                                                                            146
                                                                                                                                          /note-*Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH*
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5.009
90.576
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Gaps:
Percent Identity:
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KEYWORDS
SOURCE
ORGANISM
                      COMMENT
                                                                     REFERENCE
                                                                                                                                                                                                         seq_documentation_block:
LOCUS BI765330
                                                                                                                                                                                                                                             seq_name:
                                                                                                                                                    VERSION
                                                                                                                                                                ACCESSION
                                                                                                                                                                                         DEFINITION
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US-09-899-47/1-2_COPY_21_440 x BI251117
                               TITLE
JOURNAL
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                                                          AUTHORS
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                                                                                                                                                                                                                                                                                                                            TGCCTGACTGCAGGGTCTTGAAGTCCGGGACAGCATCCAGAGCTGCTGGG
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                                                                                                                                                                                                                                             gb_lest2:BI765330
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Ma
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 922)
                                                                                                            Homo sapiens
                                                                                                                                      EST
                                                                                                                                                                          mRNA sequence.
                                                                                                                                                                                         603050641F1 NIH_MGC_116 Homo
                                                                                                                                                                                                                                                                                                GlyAspAsnValLeuLeu 175
                                                                                                                                                  BI765330.1 GI:15756908
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iomo sapiens cDr
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                                         Mammalian Gene Collection
                                                                                                                                                                                     RNA linear
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IMAGE:5190442 5',
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                                                                                            Euteleostomi;
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BASE COUNT
ORIGIN
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| US-09-899-471-2_COPY_21_440 x BI765330
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207
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                                                                                                                                                                                                                                                                     206 T..
                                                                                                                                                                                                                                                                                                                                                                                                                                    106 TGCTGGCGCCTACGCACCTGCAGACAGAGCTGGTGCTGAGGTGCCAGAAG 155
                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                    73 sGlyHisTrpAlaGluProGluGluAlaGlyLysSerAspSerGluLeuG 90
                                                                                                                                                                                                                                                                                                                                                                       57 LysThrAspCysAlaLeuArgValArgValValValHisLeuAlaValHi 73 :::|||||||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                          40 alLeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGln 56
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cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov plate: LLMM1476 row: b column: 11 High quality sequence stop: 794.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: pooled colon, kidney, stomach; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."
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3.610
72.948
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TITLE JOURNAL COMMENT	ERENCE	SIC	docume S NITION	seq_name: g	313 12 847 To	298 Pro	281 ys 11 753 GC	264 yVa 703 GAG	248 Ala 654 GCA	231 lo 604 AJ	215 As 554 AA	198 ei 521 .	181 u 493 G	169 . 443 A	157 T 393 T	140 lu 343 AG
Harry, Gibbons, M., Pape, D., Harrey, M., Bowers, Y., Ferson, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R. The WashU-NCI Mouse EST Project 1999 Unpublished (1999) Contact: Marra M, WashU-NCI Mouse EST Project 1999 Gashington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800	nniata; Vertebrata; Euteleostomi; iurognathi; Muridae; Murinae; Mus Martin,J., Beck,C., Wylie,T.,	17857	tation_block: AI463827 422 Va32a03.y1 GuayWoodford Beier	AI463827	lAlaGlyHisProAsnLeuCysValGlnValSer 324	roGlnLysAsnAlaThrValAsnGluProGlnAspPheGlnLeuVa 313 :::	*STTPGlnAlaProAspGlnSerProCysGlnProLeuValProProVal 297 ::: ::: ::: ::: ::: :::	ValTrpGlnLeuAspAlaProCysCysLeuProGlyLysValThrLeuC 281 	aHisArgAsnLeuTrpHisIleAlaArgLeuArgValLeuSerProGl	1uProAspSerGluArgValGluPheCysProPheArgGluAspProGly 247	AsnHisThrAspLeuVal.ProCysLeuCysIleGlhValTrpSerLeuG 231 	euLysSerLeuTrpTyrLysAsnLeuThrGlyProGlnAsnIleThrLeu 214	uGluGlnAspPheSerPheLeuLeuTyrLeuArgProValProAspAlaL 198 :::::: GGAGCAGCTCGGGCCTCTCCCTGTAC	AspGlyAspAsnValLeuLeuThrLeuAspValSerGl 181 ::: ::: :: aacGTGTCAGCAGATGGTGAAAACGTGCATCTGGATTCTGAATGTCTCTGA 492	Tyr¢lnLysGluLeuAsnLeuThrGlnGlnLeuPro	lualaSerLeuGlyAlaGluValGinIleTrpSerTyrThrLysProArg 156 :: AGGCTGCCCTAGGGAGTGAGGTACGAATCTGGTCCTATACTCAGCCCAGG 392

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BASE COUNT
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US-09-899-471-2_COPY_21_440 x AI463827
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377 erThrArgAlaAlaArgLeu 383
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                                                                                                                        LysaspaspmetLeuLeuValGluMetLysThrGlyLeuAsnAsnThrSe 360
                                                                                                                                                                                                                                                  GTGCCACCAGTGCCCCAGAAGAACGCCACTGTGAATGAGCCACAAGATTT
                                                    rValCysAlaLeuGluProSerGlyCysThrProLeuProSerMetAlas
                                                                                                                                                                              AGAAGGTTCAGCTGCAAGCGTGCTTGTGGGCTGACCTCCTTGGGCCCTTC
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                                                                                                                                                                                                                                                                                    eGlnLeuValAlaGlyHisProAsnLeuCysValGlnValSerThrTrpG
                                                                                                                                                                                                                                                                                                                                                                                             AGTCTGTGCCTTGGAACACAGTGGCTGTACACCACTGCCCAGCATGGCCT
                                                                                                         AAGGATGATATGCTGNTAGTGGAGATGAAAACCGGCCTCAACAACACATC
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Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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97.143
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/db_xref="taxon:10090"
/clone="IMAGE:733036"
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/lab_host="SOLR (kanamycin resistant)"
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/tissue_type="kidney"
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233 pSerGluArgValGluPheCysProPheArg.GluAspProGlyAlaHis 249
                                                                                                                                                                                                              217 ThraspLeuValProCysLeuCysIleGlnValTrpSerLeuGluProAs
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                                                                                   52 CTCCGTTAGGACGAACATCTGCCCCTTCAGGGGAGGACCCCCCGCGCACAC
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1 (bases 1 to 935)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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High quality sequence stop: 813.
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/clone_lb="NIH_MGC_49"
/clone_lb="NIH_MGC_49"
/tissue_type="melanotic melanoma, high MDR (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="norgan; skin; Vector; pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using 2AP-CDNA synthesis kit (Stratagene) and Superscript
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4.306
84.390
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/db_xref="taxon:9606"
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GAGAATGTCACTGTG...GACGTTCTCGAGTTCCCATTGCTGAAAGGCCA 298
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                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consorti
                                                            found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov
Plate: LLAM10893 row: 1 column: 21
High quality sequence step: 765.
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Mammalia; Eutheria; Rodentia;
1 (bases 1 to 787)
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                            DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
                              Location/Qualifiers
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/organism="Mus musculus"
/strain="FVB/N"
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                                                                                                                                                                                                                                                                                                                                                                         99 aG1nValLeuSerPheG1nAlaTyrProIleAlaArgCysAlaLeuL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                 83 GlyLysSerAspSerGluLeuGlnGluSerArgAsnAlaSerLeuGlnAl
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                                                                    CAGCAGCTGGCTGACTGCAGGGGTCTT....
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                                                                                                   GlnGlnLeuProAspGlyAspAsnValLeuLeuThrLeuAspValSerGl 181
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229 c 259 g 171 t
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/clone_lib="NCI_CGAP_Mam6"
/sex="female, virgin"
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BI689749
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 829)
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237 c 272 g 175 t
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4.420
91.061
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/clone_lib="NCI_CGAP_Mam6"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
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/strain="FVB/N"
/db_xref="taxon:10090"
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Percent Identity:
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musculus cDNA clone IMAGE:5356237 5',
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                                                                                                                                                                                            Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae
1 (bases 1 to 397)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dub,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                               High quality sequence stop: 359
                                                                                                                                                                                                                                                                                 Tel: 314 286 1800
Fax: 314 286 1810
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Clone IMAGE:733036 5′, mRNA sequence.
ḥA403935
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                                                                                                                                                                                                                                                                                                                                                           Contact: Marra M/Mouse EST Project
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/db_xref="taxon:10090"
/clone="IMAGE:733036"
/clone_lib="GuayWoodford
/tissue_type="kidney"
                                                                                     /organism="Mus musculus"
/strain="C57BL/6J"
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                 Beier mouse kidney day 7"
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US-09-899-471-2_COPY_21_440 x AA403935
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                               TITLE
                                         AUTHORS
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                                                                                                                                                                                                                                                                                                                                              AGAAGGTTCAGCTGCAACG.TGCTTGTGGGCCTGACTCCTTGGGGCCCCTTC
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 855)
                                                                                                                                            mRNA sequence
BI770219
                      NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                          Homo sapiens
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                                                                                                                               BI770219.1 GI:15761797
                                                                                                                                                                  603053287F1 NIH_MGC_122
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alignment_block:
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                                 erValGlySerAlaValPheAspCysPheGluAlaSerLeuGlyAlaGlu
                                                                                                                                               LeuGlnAlaGlnValValLeuSerPheGlnAlaTyrProIleAlaArgCy 113
                                                                                                                                                                                      AGTTTGGAGGAGCAGCTGACTCAGGGGTGGAGGAGCCTAGGAATGCCTCT
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Plate: LLAM11508 row: m column:
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Clone distribution: MGC clone distribution information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Invitrogen). Research Genetics tracking this is a NIH_MGC Library."

268 c 265 g 175 t
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                               This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                 Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dub
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 499)
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AA238911
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                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                        quality sequence stop: 432.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                    mouseest@watson.wustl.edu
/clone_lib="Soares mouse NML"
/tissue_type="Liver"
/lab_host="DH10B"
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/db_xref="taxon:10090"
/clone="IMAGE:693774"
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LOCUS AV752013
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                        TITLE
                                                                                               AUTHORS
                                                                                                                                                                   ORGANISM
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Song, H., Peng, Y., Gu, Y., Yang, Y., Gao, G., Xiao, H., Xu, X., Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu, S., Yu, Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Ye, M., Zhang, Han, Z., Chen, Z., Hu, R. and Chen, J.

Homo sapiens NPD library cDNA clones
Unpublished (2000)
                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 843)
                                                                                                                                                                                                                                           AV752013 NPD Homo sapiens cDNA
AV752013
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ValGlnIleTrpSerTyrThrLysProArgTyrGlnLysGluLeuAsnLe
                                                     erValGlySerAlaValPheAspCysPheGluAlaSerLeuGlyAlaGlu 146
                                                                                                                                                                                                                                                                  lValHisLeuAlaValHisGlyHisTrpAlaGluProGluGlu......
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                                                                                                       SAlaLeuLeuGluValGlnValProAlaAspLeuValGlnProGlyGlnS 130
                                                                                                                                                            LeuGlnAlaGlnValValLeuSerPheGlnAlaTyrProIleAlaArgCy
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTCCAGGCCCAAGTCGTGCTCTCCTTCCAGGCCTACCCTACTGCCCGCTG
                                                                                                                                                                                                  AGTTTGGAGGAGCAGCTGACTCAGGGGTGGAGGAGCCTAGGAATGCCTCT
                                                                                                                                                                                                              .....AlaGlyLysSerAspSerGluLeuGlnGluSerArgAsnAlaSer
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                                                                                                                                                                                                                                                                                                       Quality:
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Shanghai Institute of Endocrinology, Rui-Jin Hospital
197 Rui-Jin II Road, Shanghai 200025, P. R. China
Tel: 86-21-64370045(ex.663332)
Fax: 86-21-64743206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mbshi@ms.stn.sh.cn
This clone is available at Shanghai Hematology Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shanghai
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66.779
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/db_xref="taxon:9606"
/clone="NPDBHC06"
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/dev_stage="Adult"
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                                                                                                                                           http://image.llnl.gov
Plate: LLAM11444 row: m column:
High quality sequence stop: 884.
                                                                                                                                                                                                Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, LTC.
Clone distribution: MCC clone #distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

| (bases 1 to 886)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/clone="IMAGE:5178409"
/clone_lib="NIH_MGC_115"
/lab_host="DH108"
                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                       Location/Qualifiers
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/note-*Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); source anonymous pool of 6 male brains, age range 23-2 male lung, age 27; and 1 male testis, age 69. Library

Library is

constructed by C.

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BASE COUNT
ORIGIN
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| US-09-899-471-2_COPY_21_440 x BI820026
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                                                             187
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204 LysasnLeuThrGlyProGlnasn 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AspAsnValLeuLeuThrLeuAspValSerGluGluGlnAspPheSerPh 187
                                                                                                                                                                              erValGlySerAlaValPheAspCysPheGluAlaSerLeuGlyAlaGlu 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lValHisLeuAlaValHisGlyHisTrpAlaGluProGluGlu...... 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGGAGAGGCTTGTGGGGGCCTCAGGACGCTACCCACTGCTCTCCGGGCCT
                                                          eLeu.LeuTyrLeuArgProValProAspAlaLeuLysSerLeuTrpTyr 203
                                                                                            GACAACGTGCATCTGGTTCTGAATGTCTCTGAGGAGCAGCACTTCGGGCT
                                                                                                                                                        CACACAGCAGTGCCTTGCCCTGCCCTGGCTCAACGTGTTCAGCAGATGGT
                                                                                                                                                                                                                      ValGlnIleTrpSerTyrThrLysProArgTyrGlnLysGluLeuAsnLe 163
                                                                                                                                                                                                                                                                                                                                                                                   sAlaLeuLeuGluValGlnValProAlaAspLeuValGlnProGlyGlnS 130
                                                                                                                                                                                                                                                                                                                                                                                                                   CTCCAGGCCCAAGTCGTGCTCTCCTTCCAGGCCTACCCTACTGCCCGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                  LeuGlnAlaGlnValValLeuSerPheGlnAlaTyrProIleAlaArgCy 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGTTTGGAGGAGCAGCTGACTTAGGGGTGGAGGAGCCTAGGAATGCCTCT 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .....AlaGlyLysSerAspSerGluLeuGlnGluSerArgAsnAlaSer 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ValLeuArgCysProGlnLysThrAspCysAlaLeuArgValArgValVa 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lnSerAlaProGlyProValLeuValProThrArgLeuGlnThrGluLeu 50
                                                                                                                                                                                                                                                                                     CTGTGGGCTCTGTGTATATGACTGCTTCGAGGCTGCCCTAGGGAGTGAG
                                                                                                                                                                                                                                                                                                                                                   CGTCCTGCTGGAGGTGCAAGTGCCTGCTGCCCTTGTGCAGTTTGGTCAGT 646
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3.797
79.646
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Percent Identity:
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KEYWORDS
SOURCE
ORGANISM
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US-09-899-471-2_COPY_21_440 x BF791762
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ORIGIN
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LOCUS BF791762
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                   861 AATCAGGTCCAGGGCCCCCAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
TTYTThTLYSPTOATGTTYTGlnLySGluLeuAsnLeuThTGlnGlnLeuP
                                                                                                                                                                                                               ValPheAspCysPheGluAlaSerLeuGlyAlaGluValGlnIleTrpSe
                                                                                                                                                                                                                                                                                                                                alGlnValProAlaAspLeuValGlnProGlyGlnSerValGlySerAla
                                                                                                                                                                                                                                                                                           TGCAAGTGCCTGCTGCCCTTGTGCAGTTTGGTCAGTCTGTGGGCTCTGTG
                                                                                                                                               GTATATGACTGCTTCGAGGCTGCCCTAGGGAGTGAGGTACGAATCTGGTC
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 946)
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BF791762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   602251953F1 NIH_MGC_84 Homo sapiens cDNA clone IMAGE:4344301 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BF791762.1 GI:12096816
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://image.llnl.gov
Plate: LLAM9962 row: j column:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA Library Preparation: Life Technologies, Inc.
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Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ratio:
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/tissue_type="adrenal cortex carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: adrenal gland; Vector: pCMV-SPORT6; Site_1:
/note="Organ: adrenal gland; Vector: pCMV-SPORT6; Site_1:
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/note="Organ: adrenal gland; Vector: pCMV-SPORT6; Site_1:
/note="Organ: adrenal
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3.432
77.344
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/db_xref="taxon:9606"
/clone="IMAGE:4344301"
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739	ACGGAGTGCTG.TGGGCTGACTCCTGGGGCT
342	rTrpGluLysValGlnLeuGlnAlaCysSerTrpAlaAspSerLeuGlyp
325 690	309 AspPheGlnLeuValAlaGlyHisProAsnLeuCysValGlnValSerTh
308	OLeuValProProValProGlnLysAsnAlaThrVal.AsnGluProGln
292 599	276 GlyLysValThrLeuCysTrpGlnAlaProAspGlnSerProCysGlnPr
275 551	259 rgValLeuSerProGlyValTrpGlnLeuAspAlaProCysCysLeuPro
259 501	242 eArgGluAspProGlyAlaHisArgAsnLeuTrpHisIleAlaArgLeuA
242 451	226 GlnValTrpSerLeuGluProAspSerGluArgValGluPheCysProPh
225 401	209 roGlnAsnIleThrLeuAsnHisThrAspLeuValProCysLeuCysIle
209 351	192 gProValProAspAlaLeuLysSerLeuTrpTyrLysAsnLeuThrGlyP:
192 302	176 ThrLeuAspValSerGluGluGlnAspPheSerPheLeuLeuTyrLeuAr ::: :::
175 252	168 roAspGlyAspAsnValLeuLeu

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3:IDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:AAS68625
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-DB-N_Geneseq_032802 -QFMM-fastap -SUFFIX-rng -GAPDF-12.000
-GAPEXT-4.000 -MINMATCH-0.100 -XGAPCD-10.000 -LOOPEXT-0.000
-GAPEXT-500 -QGAPEXT-0.050 -XGAPOP-10.000 -XGAPEXT-0.500
-FGAPOP-4.500 -GGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500
-FGAPOP-6.000 -FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500
-DELOP-6.000 -DELEXT-7.000 -START-1 -MATRIX-blosum62
-TRANS-human40.cd1 -LIST-45 -DOCALIGN-200 -THR_SCORE-pct
-TRANS-100 -THR_MIN-0 -ALIGN-15 -MODE-LOCAL -OUTFMT-pfs
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IDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:AAA61238
IDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:AAA51987
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//gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:AAS99515 + 2376.00 3114.10
//gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:AAS18130 + 2365.00 3999.90
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Percent Similarity:
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725

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G; 473 T; 0 other;

3723.00 5.349 99.713

Length: 698
Gaps: 0
Percent Identity: 99.570

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seq_documentation_block:
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/SIDS1/gcgdata/geneseq/geneseqn-embl/NAZUUL DAT:ANZ61611 +
/SIDS1/gcgdata/geneseq/geneseqn-embl/NAZUUL DAT:AAC99544 +
/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:AAT338U1 +
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The invention relates to primate and rodent DNAX cytokine receptor subunit (DCRS) polypeptides and the polypucleotides encoding them. The receptors, or their portions may be useful as phosphate labelling enzymes to label general or specific substrates. The subunits may also be functional immunogens to elicit recognising antibodies, or antigens capable of binding antibodies. A combination, e.g., including a DCRS can be used as an immunogen for the production of antisera or antibodies capable of distinguishing between other cytokine receptor family members. A purified DCRS can also be used as a reagent to detect antibodies generated in response to the presence of elevated levels of expression, or immunological disorders which lead to antibody production to the endogenous receptor. This sequence represents cDNA encoding the mouse DCRS7 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 17-20; 148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated antigenic human or mouse DNAX receptor subunit-like polypeptide useful for detecting antibodies generated in responpresence of increased protein levels or immunological disorders
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P-PSDB; AAU11354.
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284 ysProPheArgGluAspProGlyAlaHisArgAsnLeuTrpHisIleAla 300 	167 uCysIleGlnValTrpSerLeuGluProAspSerGluArgValGluPheC 284 	251 ThrGlyProGlnAsnIleThrLeuAsnHisThrAspLeuValProCysLe 267	234 yrLeuArgProValProAspAlaLeuLysSerLeuTrpTyrLysAsnLeu 250 	217 lleuLeuThrLeuAspValSerGluGluGlnAspPheSerPheLeuLeuT 234	201 SerCysTrpValLeuProTrpLeuAsnValSerThrAspGlyAspAsnVa 217 	184 hrGlnGlnLeuProAspCysArgGlyLeuGluValArgAspSerIleGln 200 	167 lGlnileTrpSerTyrThrLysProArgTyrGlnLysGlnLeuAsnLeuT 184 	151 valGlySerAlaValPheAspCysPheGluAlaSerLeuGlyAlaGluVa 167 	134 laLeuLeuGluValGlnValProAlaAspLeuValGlnProGlyGlnSer 150 	117 uGlnalaGlnValValLeuSerPheGlnAlaTyrProIlealaArgCysa 134 	101 GlualaglyLysSerAspSerGluLeuGlnGluSerArgAsnAlaSerLe 117 	84 alargvalvalvalhisLeualavalhisGlyhisTrpalaGluProGlu 100 	67 nThrGluLeuValLeuArgCysProGlnLysThrAspCysAlaLeuArgV 84	51 GlySerLeuGlnSerAlaProGlyProValLeuValProThrArgLeuGl 67 	34 erLeuGlyLeuSerCysHisLeuTrpAspGlyAspValLeuCysLeuPro 50 	17 1ValValSerLeuGluArgLeuMetGluProGlnAspThrAlaArgCysS 34 	1 MetProValSerTrpPheLeuLeuSerLeuAlaLeuGlyArgAsnProVa 17 	Align seg 1/1 to: AAS18132 from: 1 to: 2314
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584 1948	67 oAlaAlaValAlaGlnCysGlnGlnTrpLeuGlnLeuGlnThrValGluP 	
567 1898	gArgIleLeuGlnGluGlyGlyValValIleLeuLeuPheSerPr 	
550 1848	534 erargargGluLeuSeralaHisGlyAlaLeuAlagrpPheHisHisGln 	
534 1798	LeuTrpS CTGTGGA	
517 1748	501 LeuLeuHisSerAlaAspGlyAlaGlyTyrGluArgLeuValGlyAlaLe 	
500 1698	484 euLeuLysLysAspArgArgLysAlaAlaArgGlySerArgThrAlaLeu 	
484 1648	467 uValtrpLeuAlaCysLeuLeuLeuAlaAlaAlaLeuPhePhePheLeuL 	
467 1598	451 SerLeufrpAlaCysProMetAspLysTyrIleHisArgArgTrpValLe	
450 1548	434 spPheArgSerHisGlnCysMetGlnLeuTrpAsnAspAspAsnMetGly	
434 1498	417 oSerMetAlaSerThrArgAlaAlaArgLeuGlyGluGluLeuLeuGlnA 	
417 1448	401 ASNASNThrSerValCysAlaLeuGluProSerGlyCysThrProLeuPr 	
400 1398	384 euGlyProPheLysAspAspMetLeuLeuValGluMetLysThrGlyLeu 	
384 1348	367 1SerThrTrpGluLysValGlnLeuGlnAlaCysSerTrpAlaAspSerL 	
367 1298	351 ProdinaspPheGlnLeuValAlaGlyHisProAsnLeuCysValGlnVa 	
350 1248	334 ysGlnProLeuValProProValProGlnLysAsnAlaThrValAsnGlu 	
334 1198	317 sLeuProGlyLysValThrLeuCysTrpGlnAlaProAspGlnSerProC 	
317 1148	301 ArgieuargValleuSerProGlyValTrpGlnLeuAspAlaProCysCy 	

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         The invention relates to primate and rodent DNAX cytokine receptor subunit (DCRS) polypeptides and the polynucleotides encoding them. The receptors, or their portions may be useful as phosphate labelling enzymes to label general or specific substrates. The subunits may also be functional immunogens to elicit recognising antibodies, or antigens capable of binding antibodies: A combination, e.g., including a DCRS can be used as an immunogen for the production of antisera or antibodies capable of distinguishing between other cytokine receptor family members. A purified DCRS can also be used as a reagent to detect antibodies generated in response to the presence of elevated levels of expression, or immunological disorders which lead to antibody production to the procession of the presence of elevated levels of expression, or immunological disorders which lead to antibody production to the
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                                                                                                                                                                                                                                                                                               Disclosure; Page 20-21; 148pp; English.
                                                                                                                                                                                                                                                                                                                                       Isolated antigenic human or mouse DNAX receptor subunit-like polypeptide useful for detecting antibodies generated in responses of increased protein levels or immunological disordures.
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SNMGNMGNGARYTNMSNGCNCAYGGNGCNYTNGCNTGGTTYCAYCAYCAR
                                                                  uAlaSerAlaLeuSerGlnMetProLeuArgValAlaValAspLeuTrpS
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                                                                                                                                                   euLeuLysLysAspArgArgLysAlaAlaArgGlySerArgThrAlaLeu
                                                                                                                                                                                                  uValTrpLeuAlaCysLeuLeuLeuAlaAlaAlaLeuPhePhePheLeuL 484
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                                             NGCNWSNGCNYTNWSNCARATGCCNYTNMGNGTNGCNGTNGAYYTNTGGW
                                                                                          YTNYTNCAYWSNGCNGAYGGNGCNGGNTAYGARMGNYTNGTNGGNGCNYT 1550
                                                                                                      LeuLeuHisSerAlaAspGlyAlaGlyTyrGluArgLeuValGlyAlaLe
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ID AAC85027 standard;
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WPI; 2001-112618/12.
P-PSDB; AAB61880.
                                                                                                                                                                                                                                                                                                                                                                    Cytokine receptor; Zcytor14; human; inflammation; antiinflammatory; gene therapy; vaccine; ss.
                                                  Presnell
                                                                                                                    07-JUL-1999;
                                                                                                                                                   30-JUN-2000; 2000WO-US18383
                                                                                                                                                                                      18-JAN-2001.
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                                                                                  (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                      WO200104304-A1
                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                 Burkhead
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/product= "Zcytor14"
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New polypeptide encoding a human cytokine receptor Zcytor14,

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lignment_scores:
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US-09-899-471-5 x AAC85027
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Percent Similarity:
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                                                                                                 GATGAGGAAAAGTTTGGAGGAGCAGCTGACTCAGGGGTGGAGGAGCCTAG
                                                                                                                                                                                                                                                                                      alargvalvalvalhisteualavalhisGlyhisTrpalaGluproGlu 100
uGlyAlaGluValGlnIleTrpSerTyrThrLysProArgTyrGlnLysG
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                                          Glu.....AlaGlyLysSerAspSerGluLeuGlnGluSerAr 113
                                                                                                                                                                                                                                                                      TGCGTGTGGCTGTCCACTTGGCCGTGCATGGGCACTGGGAAGAGCCTGAA
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                                                                                                                                                                                                                                                                                                                               GACAGAGCTGGTGCTGAGGTGCCAGAAGGAGACCGACTGTGACCTCTGTC
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83.117
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463	447	430	413	397	380	363	347	330	313	297	280	263	247	230	213	197	180	Ūί
1506	1456	1409	1359	1309	1259	1209	1159	1109	1059	1009	959	909	859	809	759	730	704	
gArgTrpValLeuValTrpLeuAlaCysLeuLeuLeuAlaAlaAlaLeuP - :::	AspashMetGlySerLeuTrpAlaCysProMetAspLysTyrIleHisar :::::: :::	luLeuLeuGlnAspPheArgSerHisGlnCysMetGlnLeuTrpAsnAsp 	SThrProLeuProSerMetAlaSerThrArgAlaAlaArgLeuGlyGluG 	LysThrGlyLeuAsnAsnThrSerValCysAlaLeTGluProSerGlyCy :::	rpalaaspSerLeuGlyProPheLysAspAspMetLeuLeuValGluMet	uCys\valGlnvalSerThrTrpGluLysValGlnLeuGlnAlaCysSerT 	ThrvalAsnGluProGlnAspPheGlnLeuValAlaGlyHisProAsnLe	spGlnSerProCysGlnProLeuValProProValProGlnLysAsnAla ::: ::: GTGGGACCCCTGCCAGCCACTGGTCCCACCGCTTTCCTGGGAGAACGTC	PAlaProCysCysLeuProGlyLysValThrLeuCysTrpGlnAlaProA 	TrpHisIleAlaArgLeuArgValLeuSerProGlyValTrpGlnLeuAs	rgValGluPheCysProPheArgGluAspProGlyAlaHisArgAsnLeu :::::::::	UVA1 PTOCYSLeUCYSI1eG1nVa1TrpSerLeuG1uPTOAspSerG1uA 	TyrlysasnLeuThrGlyProGlnAsnIleThrLeuAsnHisThrAspLe:::	erPheLeuLeuTyrLeuArgProValProAspAlaLeuLysSerLeuTrp 	pGlyAspA TGGTGACA	InSerCysTrpValLeuProTrpLeu:::	luLeuAsnLeuThrGlnGlnLeuProAspCysArgGlyLeuGluValArg	GGAGTGAGGTACGAATCTGGTCCTATACTCAGCCCAGGTACGAG
480	463	446	430	413	396	380	363	346	330	313	296	280	263	246	230	213	196	703
1555	1505	1455	1408	1358	1308	1258	1208	1158	1108	1058	1008	958	908	858	808	758	729	

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seq_documentation_block:
ID AAS46223 standard; cE
XX
AC AAS46223;
XX
DT 18-DEC-2001 (first e
XX
DT 18-DEC-2001 (girst e
XX
DE Human DNA encoding PR
XX
KW PRO polypeptide; mamm
KW dog; cat; pig; goat;
KW blood; chondrocyte ce
KW adrenal; lung; breast
KW PCR primer.
XX
PN W0200168848-A2.
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                                                                                                 PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha; blood; chondrocyte cell; cell proliferation; cell differentiation; col adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
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| GTCTTCTCCCCGGTGCGGTGGCGCTGTGCAGCGAGTGGCTACAGGATG 1855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pArgValGluArgValThrGlnAlaLeuArgSerAlaLeuAspSerCys. 676:|||:::|||:::||||:::||||||||||
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                                                                                                                                                                                                                                                                                                                                                                                                                                          TCCATCCCCGGGGACTCCCGCGCGGGA
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                                                                                                     disorder;
                                                                                                                         colon;
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Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR primers for PRO polypeptides of the invention. The sequences of the invention can be used to detect the presence of a tumour in a mammal by comparing the level of expression of a PRO polypeptide in a test sample of cells from the animal and a control sample of normal cells, whereby a higher level of expression in the test sample indicates the presence of a tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep, plys, goats and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TNF) alpha release from human blood, when contacted with it. A specific polypeptide can be used to stimulate the proliferation or differentiation of chondrocyte cells. The PRO proteins can be used to determine the presence of tumours and also susceptibility to tumour development, particularly adrenal, lung, colon, breast, prostate, rectal, cervical, or liver tumours, in mammalian
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25-APR-
25-APR-
25-APR-
03-MAY-
17-MAY-
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                                                                                                                                                                                                                                      Novel nucleic acids encoding PRO polypegtides, used to diagnose the presence of tumours, such as prostate and breast tumours, in mammals to screen for modulators of the compounds
                                                                                                                                                                                                                                                                                                                                                        Pan
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2000WO-US23328.
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2000WO-US20710.
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2000WO-US15264.
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Wood WI, Zhang
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US-09-899-471-5 x AAS46223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 1ValValSerLeuGluArgLeuMetGluProGlnAspThrAlaArgCysS 34
                                                                                  AspSerIleGlnSerCysTrpValLeuProTrpLeuAsnValSerThrAs 213
                                                                                                                                                                   gAsnAlaSerLeuGlnAlaGlnValValLeuSerPheGlnAlaTyrProI 130
                                    pGlyAspAsnValLeuLeuThrLeuAspValSerGluGluGlnAspPheS
                                                                                                                  AACTCAACCACACAGCAGCTGCCT............
                                                                                                                                   luLeuAsnLeuThrGlnGlnLeuProAspCysArgGlyLeuGluValArg 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGGACATCGTGCTGCTCCGGGCCCCCGTGCTGGCGCCCTACGCACCTGCA 432
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erPheLeuLeuTyrLeuArgProValProAspAlaLeuLysSerLeuTrp
                                                                                                                                                                                                                                                                                                                  GAATGCCTCTCCAGGCCCAAGTCGTGCTCTCCTTCCAGGCCTACCCTA 632
                        TGGTGACAACGTGCATCTGGTTCTGAATGTCTCTGAGGAGCAGCACTTCG
                                                                      .....GCCCTGCCCTGGCTCAACGTGTCAGCAGA 837
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Gaps: 7
Percent Identity: 65.912
                        887
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246
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532 532	laLeuAlaSerAlaLeuSerGlnMetProLeuArgValAlaValAspLe	516	
	aLeuLeuLeuHisSerAlaAspGlyAlaGlyTyrGluArgLeuV	7.2	
17	TTGAAACAGGACGTCCGCTCGGGGGCCGCCAGGGGCCGCGCGGC	1685	
	hePhePheLeuLeuLeuLysLysAspArgArgLys	் ம் வ	
48 16	gArgTrpValLeuValTrpLeuAlaCysLeuLeu 	463 1585	
15	AspAsnMetGlySerLeuTrpAlaCysProMetAsp	447 1535	
15	luLeuLeuGlnAspPheArgSerHisGlnCysMetGlnLeuTrpAsnAsp 	430 1488	
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41 14	LysThrGlyLeuAsnAsnThrSerValCysAlaLeuGluProSerGlyCy::: :::	397 1388	
39 13	rpalaaspSerLeuGlyProPheLysaspAspMetLeuLeuValGluMet 	380 1338	
38 13	UCysvalGlnValSerThTTpGluLysValGlnLeuGlnAlaCysSerT 	363 1288	
36 12	ThrvalAsnGluProG	347 1238	
34 12	SpGlnSerProCysGlnProLeuValProProV	330 1188	
33 11	PAlaProCysCysLeuProGlyLysValThrLeuCysTrpGlnAlaProA	313 1138	
31 11	TrpHisIleAlaArgLeuArgValLeuSerProGlyValTrpGlnLeuAs	297 1088	
29 10	rgv	280 1038	
28 10	3 UVALPTOCYSLEUCYSILEGINVALTTPSETLEUGIUPTOASPSETGIUA 	263 988	
26 98	TyrLysAsnLeuThrGlyProGlnAsnIleThrLeuAsnHisThrAspLe	247 938	
93	GCCTCTCCCTGTACTGGAATCAGGTCCAGGGCCCCCCAAAACCCCGGTGG	888	

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seq_documentation_block:
ID AAS09515 standard; cDNA;
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WO200146420-A2
                                                                          mat_peptide
                                                                                                             sig_peptide
                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                             degenerative
                                                                                                                                                                                                                                                                         PRO20040; DNA 164625-2890; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; diabetes mellitus; allergic disease; asthma; demyelinating disease;
                                                                                                                                                                                                                                                                                                                Human; Interleukin-17 receptor; IL-17RH2; agonist; antagonist; PRO20040; DNA 164625-2890; systemic lupus erythematosus;
                                                                                                                                                                                                                                                                                                                                                                    Human cDNA encoding Interleukin 17 receptor, IL-17RH2
                                                                                                                                                                                                                                                                                                                                                                                                             24-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAS09515;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGCCCGGGGCGCACGCCCGCACGACGCCTTCCGCGCCTCGCTCAGCTG 2031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCCTGGCGTCGGCCCTGTGCCAGCTGCCGCTGGCCGTTGGCCGTAGACCTG 1831
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aLeuGlnGlyGlyCysSerThrSerAlaGlyArgProAlaAspArgValG 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGTGCTGCCCGACTTCTTGCAGGGCCGGCGGCGCCCGGCAGCTACGTGGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                         cartilaginous disorder;
                                                                      /*tag= b
293..2344
                                                                                                             233..292
                                                                                                                                                                 Location/Qualifiers 233..2347
                                   /label-
                                                                                                                          /*rag= a
/product= "IL-17RH2"
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                                 Mature_IL_17RH2
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alignment_scores:
Quality: 2376.00
| Ratio: 4.118
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US-09-899-471-5 x
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                                                                                                                                    Align seg 1/1
                                                                     233
                                                                                                                                                                                                                                                                                                                                             hypersensitivity, asthma, a transplantation associated disease, chronic linflammatory demyelinating polyneuropathy. Treating a degenerative cartilaginous disorder comprises administering a prol122 polypeptide agonist, or antagonist to the mammal. Numer examples of the diseases and disorders are given in the specific
                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence (DNA 164625-2890) encodes a PRO polypeptide (PRO20040) which is the human Interleukin 17 receptor, IL-17H2. A composition containing ant/agonists to the PRO polypeptides or individual components are useful for treating a mammal with an immune related disease, e.g. systemic lupus erythematosus, rheumatoid arrhiritis, osteoarrhiritis, juvenile chronic arrhiritis, a spondyloarrthropathy, systemic sclerosis, ar idiopathic inflammatory myopathy, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, a demyelinating disease, an autoimmune or immune-mediated skin disease, contact dermatitis, an allergic disease, e.g. food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-MAR-2000;
21-MAR-2000;
02-JUN-2000;
                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel PRO polypeptides homologous to interleukin-17, useful for the diagnosis and treatment of immune related disease e.g. rheumatoid arthritis and diabetes -
               17 lValValSerLeuGluArgLeuMetGluProGlnAspThrAlaArgCysS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1
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P-PSDB; AAU04956.
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24 - OCT - 2000;
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22-AUG-2000;
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                                                                               1 MetProValSerTrpPheLeuLeuSerLeuAlaLeuGlyArgAsnProVa
GGTCCTTTCTCGGAGAGGCTTGTGGGGCCTCAGGACGCTACCCACTGCT 332
                                                                ATGCCTGTGCCCTGGTTCTTGCTGTCCTTGGCACTGGGCCGAAGCCCAGT 282
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L, Li H, Hillan KJ, Tumas D, Van Lookeren M,
CK, Williams PM, Wood WI, Yansura DG;
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2000US-0213087.
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Vandlen RL;
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	313	TrpHisIleAlaArgLeuArgValLeuSerProGlyValTrpGlnLeuAs	297
	1 296	rgValGluPheCysProPheArgGluAspProGlyAlaHisArgAsnLeu :::::::::	280
·	1 280 1 1037	uValProCysLeuCysIleGlnValTrpSerLeuGluProAspSerGluA 	263 988
	263 r 987	TyrLysAsnLeuThrGlyProGlnAsnIleThrLeuAsnHisThrAspLe :::	247 938
	9246 937	erPheLeuLeuTyrLeuArgProValProAspAlaLeuLysSerLeuTrp	230 888
	s 230 : : 887	PG1yAspAsnValLeuLeuThrLeuAspValSerGluGluGlnAspPheS 	213 838
	s 213 1 A 837	AspSerIleGlnSerCysTrpValLeuProTrpLeuAsnValSerThrAs :::	197 809
	g 196 . 808	luLeuAsnLeuThrGlnGlnLeuProAspCysArgGlyLeuGluValArg AACTCAACCACACACAGCAGCTGCCT	180 783
	G 180 782	uGlyAlaGluValGlnIleTrpSerTyrThrLysProArgTyrGlnLysG :: :: :: AGGGAGTGAGGTACGAATCTGGTCCTATACTCAGCCCAGGTACGAGAAGG	163 733
,	e 163 732	ProGlyGlnSerValGlySerAlaValPheAspCysPheGluAlaSerLe	147 683
	n 146 682	leAlaArgCysAlaLeuLeuGluValGlnValProAlaAspLeuValGln 	130 633
	I 130 A 632	gAsnalaSerLeuGlnalaGlnValValLeuSerPheGlnAlaTyrPro	113 583
	r 113 582	GluAlaGlyLysSerAspSerGluLeuGlnGluSerAr:::	101 533
	u 100 A 532	alargValValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu 	84 483
	V 84 C 482	nThrGluLeuvalLeuArgCysProGlnLysThrAspCysAlaLeuArg 	67 433
	1 67 432	GlySerLeuGlnSerAlaProGlyProValLeuValProThrArgLeuG :::::: 	51 383
	o 50 T 382	erLeuGlyLeuSerCysHisLeuTrpAspGlyAspValLeuCysLeuPr 	34 333

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SVALLeuProAspPheLeuGlnGlyArgAlaThrG:			Trp\$erArgArgGluLeuSerAlaHlsGlyAla	laLeuAlaSerAlaLeuSerGlnMetProLeuArg	aLebLeuLeuHisSerAlaAspGlyAlaGlyTyrG ::: 	TTGAAACAGGACGTCCGCTCGGGGGCGGCCGCCAG	hePhePheLeuLeuLeuLysLysAspArgArgLy	gArgTrpValLeuValTrpLeuAlaCysLeuLeuLe 	AspAsnMetGlySerLeuTrpAlaCysProMetAs	luLeuLeuGlnAspPheArgScrHisGlnCysMet ACTTACTACAAGACCTGCAGTCAGGCCAGTGTCTG	SThiProLeuProSerMetAlaSerThrArgAlan	LysThrGlyLeuAsnAsnThrSerValCysAlaLe	rpalaaspSerLeuGlyProPheLysaspAspMet 	UCy\$ValGlnValSerThrTrpGluLysValGlr	ThryalasnGluProGlnAspPheGlnLeuVal	GTGGGGACCCCTGCCAGCCACTGGTCCCACCGCTT
31yArgTyrValG1yV 61 3GCAGCTACGTGGGGG 20 	AlaTrpLeuSerCy 5	::	AlaTrpPheHisH CTTGGTTTCACG	gValAlaValAspLeu 53 CGTGGCCGTAGACCTG 18	GluArgLeuValGlyA 51 	rgGlySerArgThrAl 49 ::: GGGGCCGCGCGGC 17	'S49 AGGGTGGCTGAGGCTC 16	LeuAlaAlaAlaLeuP 48 ::: TTTGCCGCTGCGCTTT 16	PLYSTYTILEHISAT 4	GlnLeuTrpAsnAsp 4 CAGCTATGGGAC 1	laArgLeuGlyGluG 4 	uGluProSerGlyCy 4 GGAACCCAGTGGCTG 1	LeuLeuValGluMet 3 ::: CTACTGTTGGAGACA 1	LeuGlnAlaCysSerT 3	AlaGlyHisProAsnLe 30	::: ::: TCCTGGGAGAACGTC 1
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18-FEB-2000;
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01-MAR-2000;
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The present sequence is the coding sequence for a human PRO polypeptide (secreted and transmembrane). The PRO protein, and PRO agonists, PRO antagonists or anti-PRO antibodies are useful for preparation of a medicament useful in the treatment of a condition which is responsive to the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO protein may also be employed as molecular weight markers for protein
                                                                                                   Eighty four nucleic acids encoding PRO polypeptides, useful in molecular biology, including use as hybridization probes, and i chromosome and gene mapping. -
                                                                                                                                                                                  Eaton DL, F
Grimaldi CJ,
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                                                                              Fig 161; 278pp;
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2000US-0187202.
2000US-0193397.
2000WO-US14042.
2000WS-0209832.
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| AGGGAGTGAGGTACGAATCTGGTCCTATACTCAGCCCAGGTACGAGAAGG
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                                           AspSerIleGlnSerCysTrpValLeuProTrpLeuAsnValSerThrAs
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                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                  Human DNAX cytokine receptor subunit 7 (DCRS7) cDNA.
                                                                                                                                                                                                                                                                          26-MAR-2002 (first entry)
                                                                         29-NOV-2001.
                                                                                               WO200190358-A2
                                                                                                                                                                                                                                                                                                                                                                                           SerSerSerGluAlaProGly
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CCGGGGACTCCCGCGCCCGGGA
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AGCAAGTGTCCCGGGCCCTTCAGCCAGCCCTGGATAGCTACTTCCATCCC
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| GCAGCGGCGCCAGACCCTGCAGGAGGGCGGCGTGGTGGTTGTTCT
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                                                                                                                                                                                                                            DNAX cytokine
                                                                                                                                                                                                                                                                                                                              standard; cDNA; 2308 BP.
                                                                                                                                                                                               ytokine receptor subunit 7; DCRS7; phosphate labelling; ss; protein therapy; immunological disorder.
                                                                                                                                                Location/Qualifiers 181..2292
                                                                                                                       /product=
                                                                                                                                       /*tag=
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24-MAY-2000; 2000US-206862P

23-MAY-2001; 2001WO-US16767

(SCHE)

SCHERING CORP

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Align seg 1/1 to:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         runctional immunogens to elicit recognising antibodies, or antigens be capable of binding antibodies. A combination, e.g., including a DCRS can be used as an immunogen for the production of antisera or antibodies capable of distinguishing between other cytokine receptor family members. A purified DCRS can also be used as a reagent to detect antibodies generated in response to the presence of elevated levels of expression, or immunological disorders which lead to antibody production to the endogenous receptor. This sequence represents cDNA encoding the human DCRS7 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to primate and rodent DNAX cytokine receptor subunit (DCRS) polypeptides and the polynucleotides encoding them. The receptors, or their portions may be useful as phosphate labelling enzymes to label general or specific substrates. The subunits may also be functional immunogens to elicit recognising antibodies, or antigens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated antigenic human or mouse DNAX receptor subunit-like polypeptide useful for detecting antibodies generated in response presence of increased protein levels or immunological disorders -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GATGAGGAAAAGTTTGGAGGAGCAGCTGACTTAGGGGGTGGAGGAGCCTAG
                                                                                                                                                                                                                                                                                                                      GlySerLeuGlnSerAlaProGlyProValLeuValProThrArgLeuGl
                                                                                                                                                                                                                                                                                                                                                                     leAlaArgCysAlaLeuLeuGluValGlnValProAlaAspLeuValGln
                                                                                                                                         Glu.....AlaGlyLysSerAspSerGluLeuGlnGluSerAr
                                                                                                                                                                           TGCGTGTGGCTGTCCACTTGGCCGTGCATGGGCACTGGGAAGAGCCTGAA
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luLeuLeuGlnAspPheArgSerHisGlnCysMetGlnLeuTrpAsnAsp 446
                                                   SThrProLeuProSerMetAlaSerThrArgAlaAlaArgLeuGlyGluG
                                                                                                                                           TACTTCACTACCCAGCAAAGCCTCCACGAGGGCAGCTCGCCTTGGAGAGT
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                                                                                                         LysThrGlyLeuAsnAsnThrSerValCysAlaLeuGluProSerGlyCy
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seq_documentation_block:
                                      seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAF93875
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BXXXB

AAF93875;

alignment_scores:
| Quality: 2219.00 | Ratio: 3.977 | Constitution | 71.722

Length: 778
Gaps: 10
Percent Identity: 57.841

alignment_block: US-09-899-471-5 x AAF93875

Align seg

1/1 to: AAF93875

from:

to: 2499

17 257

lValValSerLeuGluArgLeuMetGluProGlnAspThrAlaArgCysS

23-MAY-2001

(first entry)

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can be used in gene therapy. The polynucleotide sequences and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate secretory protein/membrane protein expression. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples. They may also be used to study the expression and function of secretory proteins/membrane polypeptides and their role in metabolism. The polypeptides may be used as antigens in the production of antibodies against them and in assays to
                                                                                                                   activity. The antibodies and antagonists may also be used as therapeutic agents to down regulate expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of the polypeptides in samples (e.g. by enzyme linked immunosorbant assay (ELISA). Examples of diseases which may be treated include rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA sequences of the invention. The invention also includes methods for the production of antibodies directed against the proteins, and cDNA sequences, which can be used in vaccines. The polynucleotide sequences can be used in gene therapy. The polynucleotide sequences and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding secretory proteins/membrane proteins, useful in gene therapy or as candidate target molecules in drug development - \,
                            Sequence 2499 BP; 418 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB88317 - AAB88419. Included in the invention are primers
AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention relates to nucleic acid sequences AAF93744 - AAF93916 which encode human secretory or membrane proteins represented by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; secretory protein; membrane protein; vaccine; gene therapy; rheumatoid arthritis; diabetes; ss.
                                                                                              arthritis and diabetes.
                                                                                                                                                                                                                                                                                            identify modulators (agonists and antagonists) of expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-093989/11.
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11-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID 263; 609pp + CD ROM; English.
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2000JP-0118775.
2000JP-0183766.
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                        821 C;
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764 G; 496 T; 0 other;
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	250Leu.ThrGlyProGlnAsnIleThrLeuAsn 259
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-	249 249
	1013 GAGGACTCACCCCAAGCAAGGGAAAATTGGTGGGGGAACTTCTGCCTTCC 1062
	249
2	963 GCCGATGCCTGTGCAAAGGACGCAGTGCCATATCAGAGAGGATCCTTGAA 1012
	249 249
	247 TyrlysAsn
	63
	13 pGlyAsp 13 TGGTGAC
	197 AspSerIleGinSerCysTrpValLeuProTrpLeuAsnValSerThrAs 213 :::
	758 AACTCAACCACACACAGCAGCTGCCT
	180 luLeuAsnLeuThrGlnGlnLeuProAspCysArgGlyLeuGluValArg 196
	163 uGlyAlaGluValGlnIleTrpSerTyrThrLysProArgTyrGlnLysG 180
	147 ProGlyGlnSerValGlySerAlaValPheAspCysPheGluAlaSerLe 163
	130 leAlaArgCysAlaLeuLeuGluValGlnValProAlaAspLeuValGln 146
	113 gAsnAlaSerLeuGlnAlaGlnValValLeuSerPheGlnAlaTyrProI 130
	101 GluAlaGlyLysSerAspSerGluLeuGlnGluSerAr 113 ::: ::::::::::::::::::::::::::::::
	84 alargvalvalvalHisLeuAlavalHisGlyHisTrpAlaGluProGlu 100 :: :::
	67 nThrGluLeuValLeuArgCysProGlnLysThrAspCysAlaLeuArgV 84
	51 GlySerLeuGlnSerAlaProGlyProValLeuValProThrArgLeuGl 67
	34 erLeuGlyLeuSerCysHisLeuTrpAspGlyAspValLeuCysLeuPro 50
	:::

545 1996	9 laValAspLeuTrpSerArgArgGluLeuSerAlaHlsGlyAlaLeuAla 	52 194
529 1946	gLeuvalGlyAlaLeuAlaSerAl	9
512 1896	6 SerArgThrAlaLeuLeuLeuHisSerAlaAspGlyAlaGlyTyrGluAr ::: :::	49 185
495 1849	2	49 180
491 1799	6 aAlaAlaLeuPhePhePheLeuLeuLeuLysLysAspArgArgLys	47 175
476 1749	0 TyrIleHisArgArgTrpValLeuValTrpLeuAlaCysLeuLeuLeuAl ::: :::	46 170
459 1699	3 euTrpAsnAspAspAsnMetGlySerLeuTrpAlaCysProMetAspLys	44 165
443 1652	luGluLeuLeuGlnAspPheArgSerHisGlnCys	42 165
426 1651	O ProSerGlyCysThrProLeuProSerMetAlaSerThrArgAlaAlaAr	41 161
409 1612	3 euValGluMetLysThrGlyLeuAsnAsnThrSerValCysAlaLeuGlu : : ::: 	39 156
393 1562	6 nAlaCysSerTrpAlaAspSerLeuGlyProPheLysAspAspMetLeuL 	3 7 151
376 1512	0 HisProAsnLeuCysValGlnValSerThrTrpGluLysValGlnLeuGl 	36 146
359 1462	3 InLysAsnAlaThrValAsnGluProGlnAspPheGlnLeuValAlaGly ::: ::: ::: :::	34 141
343 1412	6 pGlhAlaProAspGlnSerProCysGlnProLeuValProProValProG ::: :::	32 136
326 1362	0 TrpGlnLeuAspAlaProCysCysLeuProGlyLysValThrLeuCysTr :::::::::::	31 131
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293 1262	6 oAspSerGluArgValGluPheCysProPheArgGluAspProGlyAlaH 	27 121
276 1212	0 HlsThrAspLeuValProCysLeuCysIleGlnValTrpSerLeuGluPr 	26 116
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                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                           Cytokine receptor; Zcytor14; human; inflammation; rheumatoid arthritis; antiinflammatory; gene therapy; vaccine; variant; Zcytor14-1; ss.
                                                                                                                                                                                                                                                                                                                                                            08-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                        AAC85029
WPI; 2001-112618/12.
P-PSDB; AAB61881.
                                      Presnell SR,
                                                                                          07-JUL-1999;
                                                                                                                  30-JUN-2000; 2000WO-US18383.
                                                                                                                                              18-JAN-2001
                                                                                                                                                                        WO200104304-A1
                                                                                                                                                                                                                                                                                                                                    Human variant
                                                              (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCCTTTTCCGCACCGTGCCCGTCTTCACACTGCCCTCCCAACTGCCAGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:AAC85029
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                                                                                                                                                                                                                                                                                                                                  Zcytor14 protein Zcytor14-1 encoding
                                      Burkhead SK,
                                                                                        9905-0348854
                                                                                                                                                                                                                          Location/Qualifiers
2..1729
                                                                                                                                                                                                /product= "Zcytor14-1"
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                                      Pownder
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                                      SL;
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The invention provides a new human cytokine receptor desinated Zcytor14. CC Zcytor14 can be expressed by standard recombinant methodology. The CC encoding nucleic acid is useful for detecting the expression of a CC zcytor14 gene in a biological sample. Anti-Zcytor14 antibodies can be CC used to screen biological samples in vitro for the presence of Zcytor14. CC Proteins, polypeptides and peptides having Zcytor14 activity can be CC administered to a subject who lacks an adequate amount of this CC polypeptide, for treating inflammation and conditions such as rheumatoid CC arthritis. In contrast, Zcytor14 antagonists (e.g. anti-Zcytor14 CC antibodies) can be used to treat a subject who produces an excess of CC zcytor14. Zcytor14 nucleotide sequences can also be used to provide CC zcytor14 to a subject. The present sequence represents a cDNA encoding CC avariant of the human cytokine receptor Zcytor14, designated Zcytor14-1. CC The variant is a truncated form of the receptor polypeptide and lacks amino acid residues 1-113 of Zcytor14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polypeptide encoding a human cytokine receptor Zcytor14, treating inflammation e.g. rheumatoid arthritis -
Sequence
  1753 BP; 287 A; 584 C;
  548 G;
  334
     ₽;
     0 other;
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alignment_scores: Quality: alignment_block: US-09-899-471-5 x AAC85029 Align seg 1/1 Percent Similarity: 257 239 176 160 102 307 euGluValArgAspSerIleGlnSerCysTrpValBeuProTrpLeuAsn GGCCTACCCTACTGCCGCCTGCGTGCTGGAGGTGCAAGTGCCTGCTG nAlaTyrProIleAlaArgCysAlaLeuLeuGluValGlnValProAlaA uGlnAspPheSerPheLeuLeuTyrLeuArgProValProAspAlaLeuL GCAGCACTTCGGCCTCTCCCTGTACTGGAATCAGGTCCAGGGCCCCCCAA : GCCTGECTGAAC Ratio: ; ; 1888.50 4.053 78.451 from: 1 Percent Identity: 63.805 : : 276 176 143 193 159 101 51 126 406 259 356 209 151 226 256 238 201 243 306

456

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TrpPheHisHisGlnArgArgArgIleLeuGlnGluGlyGlyValValI1 562
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                                                                                                                                                                                                                                                                                                                                                               CCCAGTGGCTGTACTTCACTACCCAGCAAAGCCTCCACGAGGGCAGCTCG
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                                                                                                                                                                                                                                                                                                                                                                                                     TGTTGGAGACACGAGGCCCCCAGGACAACAGATCCCTCTGTGCCTTGGAA
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AC AAZ65269;
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       18-MAY-1998;
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18-MAY-1998;
18-MAY-1998;
18-MAY-1998;
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12-MAY-1998;
12-MAY-1998;
12-MAY-1998;
                                                                                                                                                                                                                                                                  Human; secreted protein; cancer; tumour; developmental abnormality; foetal deficiency; blood disorder; immune system disorder; inflammation; autoimmuhe disease; allergy; Alzhelmer's disease; cognitive disorder; schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder; atherosclerosis; diabetes; cardiovascular disorder; kidney disorder; digestive disorder; endocrine disorder; infection; AIDS; leukaemia; therapy; chromosome 3; ds.
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|CTAÇGTGGGGGCCTGCTTCGACAGGCTGCTCCACCCGGACGCCGTACCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTCCTGGGGGCCCTGCAGCAGCCTCGCGCCCCCGCGTTCCGGGCGGCTCCA
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98US-0085921
98US-0085922
98US-0085923
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980S-0085906
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(HUMA-) HUMAN GENOME SCI INC.

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This sequence was found to be present on human chromosome 3.

Chay76124 to AAY76223 represent the secreted proteins encoded by the 97 chuman genes. The genes and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions, ce.g. by protein or gene therapy. Also pathological conditions can be chiagnosed by determining the amount of the new polypeptides in a sample crown by determining the presence of mutations in the new genes. Specific cuses are described for each of the 97 genes, based on which tissues they care most highly expressed in, and include developing products for the care most highly expressed in, and include developing products for the care diagnosis or treatment of cancer, tumours, developmental abnormalities and ciscated discretes, blood disorders, diseases of the immune system, cardiovascular disorders, skin considers, schizophrenia, arthritis, asthma, psoriasis, sepsis, skin colisorders, atherosclerosis, diabetes, cardiovascular disorders. The sequences shown in AAY76224 to AAY76424 represent fragments of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ulignment_block:
US-09-899-471-5 x AAZ65269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: AAZ65269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated human genes and the secreted polypeptides they encode, useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders -
                                                                                                                              427
                                                                                                                                                                                                             377
                                                                                                                                                                                                                                                                                               327
                                                                                                                                                                                                                                                                                                                                                                                277
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1752 BP; 324 A; 555 C; 522 G; 347 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 308; 475pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-062296/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ruben SM, Florence K, Ni J, Rosen CA, Carter KC, Moore Olsen HS, Shi Y, Young PE, Wei F, Brewer LA, Soppet DR; Lafleur DW, Endress GA, Ebner R;
                                                                                                                                                                                                                                                                                        84
                                                                                                                                                                  67
                                                                                                                                                                                                                                           51 GlySerLeuGlnSerAlaProGlyProValLeuValProThrArgLeuGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                17 lValValSerLeuGluArgLeuMetGluProGlnAspThrAlaArgCysS
                                                                                                                     nThrGluLeuValLeuArgCysProGlnLysThrAspCysAlaLeuArgV 84
                                                           alArgValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu 100
Glu.....AlaGlyLysSerAspSerGluLeuGlnGluSerAr 113
                                        TGCGTGTGGMTGTCCACTTGGCCGTGCATGGGCACTGGGAAGAGCCTGAA 526
                                                                                                                                                                                                       GGTCCTTTCTCTGGAGAGGCTTGTGGGGCCTCAGGACGCTACCCACTGCT 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality: 1801.00
Ratio: 4.248
milarity: 85.484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from: 1 to: 1752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length: 496
Gaps: 4
Percent Identity: 69.556
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413	ThrGlyLeuAsnAsnThrSerValCysAlaLeuGluProSerGlyCy	Lys'	397
396 1425	laAspSerLeuGlyProPheLysAspAspMetLeuLeuValGluMet ::: ::: CTGACTCCCTGGGGCCTCTCAAAGACGATGTGCTACTGTTGGAGACA	rpa GGG	380 1376
380 1375	ValGlnValSerThrTrpGluLysValGlnLeuGlnAlaCysSerT 	uCys	363 1326
363 1325	alAsnGluProGlnAspPheGlnLeuVal ::::: GGACAAGGTTCTCGAGTTCCCATTGCTC	Thry IIII ACTG	347 1276
346 1275	InSerProCysGlnProLeuValProProValProGlnLysAsnAla 	spG GTG	330 1226
330 1225	ProCysCysLeuProGlyLysValThrLeuCysTrpGlnAlaProA CGGTGCTCGCTGCCCGCAGAAGCGGCACTGTGCTGGCGGGCTCCGG	PA1a	313 1176
313. 1175	HISILeAlaArgLeuArgValLeuSerProGlyValTrpGlnLeuAs ::: ::: ::: 	Trp	297 1126
296 1125	alGluPheCysProPheArgGluAspProGlyAlaHisArgAsnLeu 	rgVa GACG	280 1077
280 1076	PTOCYSLEUCYSILEGINVAITTPSETLEUGIUPTOASPSETGIUA	uVa GGT	263 1027
263 1026	LysAsnLeuThrGlyProGlnAsnIleThrLeuAsnHisThrAspLe	Tyr:	247 977
246 976	heLeuieuTyrLeuArgProValProAspAlaLeuLysSerLeuTrp;:	erP	230 927
230 926	AspAsnValLeuLeuThrLeuAspValSerGluGluGlnAspPheS	pGly TGGT	213 877
213 876	SerIleGlnSerCysTrpValLeuProTrpLeuAsnValSerThrAs - :::	Asp ::: AAC	197 827
196 826	elasnLeuThrGlnGlnLeuProAspCysArgGlyLeuGluValArg	luLeu AAYTC	180 777
180 776	ilyalaGluValGlnIleTrpSerTyrThrLysProArgTyrGlnLysG ::: ::: :::	uG1 AGG	163 727
163 726	GlyGlnSerValGlySerAlaValPheAspCysPheGluAlaSerLe ::: :::	ProG TTTG	147 677
146 676	laArgCysAlaLeuLeuGluValGlnValProAlaAspLeuValGln :::	leAl CTGC	130 627
130 _.	hlaSerLeuGlnAlaGlnValValLeuSerPheGlnAlaTyrProI 	gAsnA GAATG	113 577
576	GAGGAAAAGTTTGGAGGAGCAGCTGACTTAGGGGTGGAGGAGCCTAG	GAT	527

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eq_documentation_block:
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The invention provides a new human cytokine receptor desinated Zcytor14. Caytor14 can be expressed by standard recombinant methodology. The encoding nucleic acid is useful for detecting the expression of a Zcytor14 gene in a biological sample. Anti-Zcytor14 antibodies can be used to screen biological samples in vitro for the presence of Zcytor14. Proteins, polypeptides and peptides having Zcytor14 activity can be administered to a subject who lacks an adequate amount of this polypeptide, for treating inflammation and conditions such as rheumatoid arthritis. In contrast, Zcytor14 antagonists (e.g. anti-Zcytor14 antibodies) can be used to treat a subject who produces an excess of Zcytor14. Zcytor14 nucleotide sequences can also be used to provide Zcytor14 to a subject. The present sequence represents the human cytokine receptor Zcytor14 degenerate nucleotide sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                               Claim 8; Page 94-95; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human cytokine receptor 2cytor14 degenerate nucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polypeptide encoding a human cytokine receptor zcytor14, for treating inflammation e.g. rheumatoid arthritis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Presnell SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JUN-2000; 2000WO-US18383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCGCTGGGCCCTCGTGTGGCCTGCCCTACTCTTTGCCTGCGCT...T
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本意は大利性を含むなななななななななないというないない。それは大利は大利の人の人の人の人の人の人の人の人の人の人の人の人の人の人の人の人の人を表現した。

Sequence 2076 BP; 232 A; 273 C;

399 G;

265 T; 907 other;

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alignment_scores:
Quality:
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                                                                                                                                                                                                               551
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TyrLysAsnLeuThrGlyProGlnAsnIleThrLeuAsnHisThrAspLe
                            GNYTNWSNYTNTAYTGGAAYCARGTNCARGGNCCNCCNAARCCNMGNTGG
                                                        erPheLeuLeuTyrLeuArgProValProAspAlaLeuLysSerLeuTrp
                                                                                                                                                                   AspSerIleGlnSerCysTrpValLeuProTrpLeuAsnValSerThrAs
                                                                                                                                                                                                    ARYTNAAYCAYACNCARCARYTNCCN.....
                                                                                                                                                                                                                                                                                       uGlyAlaGluValGlnIleTrpSerTyrThrLysProArgTyrGlnLysG
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                                                                                                                    pGlyAspAsnValLeuLeuThrLeuAspValSerGluGluGlnAspPheS
                                                                                                                                                                                                                             luLeuAsnLeuThrGlnGlnLeuProAspCysArgGlyLeuGhuValArg
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                                                                                        YGGNGAYAAYGTNCAYYTNGTNYTNAAYGTNWSNGARGARCARCAYTTYG
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Percent Identity: 47.186
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                                                                              Isolated antigenic human or mouse DNAX receptor subunit-like polypeptide useful for detecting antibodies generated in responsence of increased protein levels or immunological disord
                                                                                                                                           WPI; 2002-106198/14.
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The invention relates to primate and rodent DNAX cytokine receptor subunit (DCRS) polypeptides and the polynucleotides encoding them. receptors, or their portions may be useful as phosphate labelling

them. The

enzymes

Disclosure; Page 15-16; 148pp; English.

to label general or specific substrates. The subunits may also be functional immunogens to elicit recognising antibodies, or antigens capable of binding antibodies. A combination, e.g., including a DCRS can be used as an immunogen for the production of antiscar or antibodies capable of distinguishing between other cytokine receptor family members. A purified DCRS can also be used as a reagent to detect antibodies generated in response to the presence of elevated levels of expression, or immunological disorders which lead to antibody production to the endogenous receptor. This sequence represents human DCRS7 reverse translation generic cDNA.

Sequence 2109 BP; 234 A; 267 C; 415 G; 269 T; 924 other;

lignment_scores:
Quality: 1645.00
Ratio: 3.697
7'--'larity: 63.031 lignment_block: US-09-899-471-5 x AAS18131 Align seg 1/1 to: 551 301 GAYGARGARAARTTYGGNGGNGCNGCNGAYYTNGGNGTNGARGARCCNMG 197 AspSerIleGlnSerCysTrpValLeuProTrpLeuAsnValSerThrAs 501 163 451 147 130 351 113 101 251 201 151 101 84 67 51 34 51 leAlaArgCysAlaLeuLeuGluValGlnValProAlaAspLeuValGln 146 Glu......AlaGlyLysSerAspSerGluLeuGlnGluSerAr 113 THMGNGTNGCNGTNCAYYTNGCNGTNCAYGGNCAYTGGGARGARCCNGAR 300 alArgValValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu 100 GlySerLeuGlnSerAlaProGlyProValLeuValProThrArgLeuGl 67 SNCCNGGNYTNWSNTGYMGNYTNTGGGAYWSNGAYATHYTNTGYYTNCCN GATHYTNWSNYTNGARWGNYTNGTNGGNCCNCARGAYGCNACNCAYTGYW 100 MetProValSerTrpPheLeuLeuSerLeuAlaLeuGlyArgAsnProVa luLeuAsnLeuThrGlnGlnLeuProAspCysArgGlyLeuGluValArg 196 nThrGluLeuValLeuArgCysProGlnLysThrAspCysAlaLeuArgV GGNGAYATHGTNCCNGCNCCNGGNCCNGTNYTNGCNCCNACNCAYYTNCA erLeuGlyLeuSerCysHisLeuTrpAspGlyAspValLeuCysLeuPro 50 **ARYTNAAYCAYACNCARCARYTNCCNGAYTGYMGNGGNYTNGARGTNTGG** NGGNWSNGARGTNMGNATHTGGWSNTAYACNCARCCNMGNTAYGARAARG RACNGARYTNGTNYTNMGNTGYCARAARGARACNGAYTGYGAYYTNTGYY 250 lValValSerLeuGluArgLeuMetGluProGlnAspThrAlaArgCysS 34 ATGCCNGTNCCNTGGTTYYTNYTNWSNYTNGCNYTNGGNMGNWSNCARTG AAS18131 from: 1 Length: 706
Gaps: 6
Percent Identity: 45.892 8 180 600 550 450 200 350 84

500	2 AlaAlaArgGlySerArgThrAlaLe	92
144	- F4 1	97
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430	ThrProLeuProSerMetAlaSerThrArgAlaAlaArgLeuGlyGl	13
413	7 LysThrGlyLeuAsnAsnThrSerValCysAlaLeuGluProSerGlyCy ::: ::::: ::: 0 MGNGGNCCNCARGAYAAYMGNWSNYTNTGYGCNYTNGARCCNWSNGGNTG	97
396 114	0 rpAlaAspSerLeuGlyProPheLysAspAspMetLeuLeuValGluMet ::: ::: 0 GGGCNGAYWSNYTNGGNCCNYTNAARGAYGAYGTNYTNYTNYTNGARACN	0 8
380 109	3 uCysValGlnValSerThrTrpGluLysValGlnLeuGlnAlaCysSerT	5 5
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31; 950	7 TrpHisileAlaArgLeuArgValLeuSerProGlyValTrpGlnLeuAs :	0 9
290 900	0 rgValGluPheCysProPheArgGluAspProGlyAlaHisArgAsnLeu ::::::::::	5 8
280 850	3 uValproCysLeuCysIleGlnValTrpSerLeuGluProAspSerGluA	0 6
26: 800	7 TyrLysAsnLeuThrGlyProGlnAsnIleThrLeuAsnHisThrAspLe :::	U1 45
24 75	0 erPheLeuLeuTyrLeuArgProValProAspAlaLeuLysSerLeuTrp ::	0 0
23 ₁	3 pGlyaspasnvalleuLeuThrLeuAspvalSerGluGluGlnAspPheS 1 YGGNGAYAAYGTNCAYYTNGTNYTNAAYGTNWSNGARGARCARCAYTTYG	5 1
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AAC85030 standard; cDNA; 1725 BP.
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                                                                                                                                              Cytokine receptor; Zcytor14; human; inflammation; rheumatoid arthritis; antiinflammatory; gene therapy; vaccine; variant; Zcytor14-1; ss.
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                           30-JUN-2000; 2000WO-US18383.
                                                          18-JAN-2001
                                                                                                                   Homo sapiens
 07-JUL-1999;
                                                                                     WO200104304-A1
                                                                                                                                                                                        Human 2cytor14 variant 2cytor14-1 degenerate nucleotide sequence
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                                                                                                                                                                                                                     (first entry)
99US-0348854.
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encoding nucleic acid is useful for detecting the expression of a Zcytor14 gene in a biological sample. Anti-Zcytor14 antibodies can be used to screen biological samples in vitro for the presence of Zcytor14. Proteins, polypeptides and peptides having Zcytor14 activity can be administered to a subject who lacks an adequate amount of this polypeptide, for treating inflammation and conditions such as rheumatoid arthritis. In contrast, Zcytor14 antagonists (e.g. anti-Zcytor14 antibodies) can be used to treat a subject who produces an excess of Zcytor14. Zcytor14 nucleotide sequence scan also be used to provide Zcytor14 to a subject. The present sequence represents a degenerate nucleotide sequence of a variant of the human cytokine receptor Zcytor14. The variant is a truncated form of the receptor
         Sequence 1725 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention provides a new human cytokine receptor desinated Zcytor14. Zcytor14 can be expressed by standard recombinant methodology. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 101; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polypeptide encoding a human cytokine receptor Zcytor14, treating inflammation e.g. rheumatoid arthritis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAB61881
                                                                                           polypeptide and lacks amino acid residues 1-113 of Zcytor14.
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    192 A;
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    226 C;
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332 G; 216 T; 759 other;
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alignment_block: alignment_scores: US-09-899-471-5 x AAC85030 Percent Similarity: Quality: 1314.50 Ratio: AAC85030 3.621 61.21**4** from: Length: 593
Gaps: 6
Percent Identity: 45.025 ç O:

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151 GARGUNGCHYTNGGNWSNGARGTNMGNATHTGGWSNTAYACNCARCUNG 143 spLeuvalGlnProGlyGlnSerValGlySerAlaValPheAspCysPhe 159 110 GlnGluSerArgAsnAlaSerLeuGlnAlaGlnValValLeuSerPheGl 126 201 176 160 126 nAlaTyrProIleAlaArgCysAlaLeuLeuGluValGlnValProAlaA 143 51 1 GARGARCCNMGNAAYGCNWSNYTNCARGCNCARGTNGTNYTNWSNTTYCA ValSerThrAspGlyAspAsnValLeuLeuThrLeuAspValSerGluGl NTAYGARAARGARYTNAAYCAYACNCARCARYTNCCN gTyrGlnLysGluLeuAsnLeuThrGlnGlnLeuBroAspCysArgGlyL 193 GlualaSerLeuGlyAlaGluValGlnIleTrpSefTyrThrLysProAr 176 uGlnAspPheSerPheLeuLeuTyrLeuArgProValProAspAlaLeuL 243 GTNWSNGCNGAYGGNGAYAAYGTNCAYYTNGTNYTNAAYGTNWSNGARGA euGluValArgAspSerIleGinSerCysTrpValLeuProTrpLeuAsn 209 RGCNTAYCCNACNGCNMGNTGYGTNYTNYTNGARGTNCARGTNCCNGCNG RCARCAYTTYGGNYTNWSNYTNTAYTGGAAYCARGTNCARGGNCCNCCNAGCNYTNCCNTGGYTNAAY 226 237 255 200 50

ZXZXXXXXXXXXXXXX

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                                                                                                                                                                                          aAlaAlaLeuPhePheLeuLeuLeuLysLysAspArgArgLys....
NGTNGGNGCNYTNGCNWSNGCNYTNTGYCARYTNCCNYTNMGNGTNGCNG
                       uValGlyAlaLeuAlaSerAlaLeuSerGlnMetProLeuArgValAlaV 530
                                                     MGNGCNGCNYTNYTNYTNTAYWSNGCNGAYGAYWSNGGNTTYGARMGNYT 1151
                                                                                                                                                                                                                                                    TyrIleHisArgArgTrpValLeuValTrpLeuAlaCysLeuLeuLeuAl 476
                                                                                                                                                                                                                                                                                            NYTNGGNGARTAYYTNYTNCARGAYYTNCARWSNGGNCARTGYYTNCARY 904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TNYTNGARACNMGNGGNCCNCARGAYAAYMGNWSNYTNTGYGCNYTNGAR
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                                                                                 ArgThrAlaLeuLeuHisSerAlaAspGlyAlaGlyTyrGluArgLe
                                                                                                              GGYTNMGNYTNYTNAARCARGAYGTNMGNWSNGGNGCNGCNGCNMGNGGN 110:
                                                                                                                                                                                                                                                                                                                        euTrpAsnAspAspAsnMetGlySerLeuTrpAlaCysProMetAspLys 459
                                                                                                                                                                                                                                                                                                                                                                       gLeuGlyGluGluLeuLeuGlnAspPheArgSerHisGlnCysMetGlnL 443
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                                                                                                                                                                                                                                   TAYATHCAYAARMGNTGGGCNYTNGTNTGGYTNGCNTGYYTNYTNTTYGC
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                                                                                                                                          .....AlaAlaArgGlySer 496
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                              antiinflammatory; antirheumatic; antiarthritic; immunosuppressive; antiinflammatory; antirheumatic; antiarthritic; immunosuppressive; antiinflammatory; antimeumatic; antiarthritic; virucide; anti-HIV; fungicide; antimatory; antiutagen; cardiovascular; antianaemic; aneemia; antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema; dermatological; antiallergic; antiasthmatic; antidabetic; cytostatic; neuroprotective; antidepressant; notradic; antiparkinsonian; infection; immunostimulant; gene therapy; antisense therapy; vaccine; inflammation; antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis; cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity; genetic disease; haematopoietic disorder; platelet disorder; asthma; the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength 
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1202 TNGAYYTNTGGWSNMGNMGNGARYTNWSNGCNCARGGNCCNGTNGCNTGG
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                                                                                                                                                                                                                                                                                                                       thrombodytopaenia; osteoporosis; severe combined immunodeficiency; allergic rhinitis; diabetes; multiple sclerosis; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               644 LeuAspAlaLeuGlnGlyGlyCysSerThrSerAlaGlyArgProAlaAs
                                                                                                                                                                                                                                                       neurological disorder;
                                                                                                                                                                                                                                                                                       Alzheimer's disease; Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human protein encoding cDNA sequence SEQ ID NO:640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer; ulcer; HIV infection; human immunodeficiency virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .ThrSerSerSerGluAlaProGly 684
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                                                                                                                                                                                                                                                                                   disease; neurodegenerative disorder
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WO200153455-A2 Homo sapiens.

26-JUL-2001.

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alignment_scores:
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cantilleer; osteopathic; dermatological; antiallergic; antiasthmatic;
cantillabetic; cytostatic; neuroprotective; antidepressant; nootropic;
cantillabetic; cytostatic; neuroprotective; antidepressant; nootropic;
cantillabetic; cytostatic; neuroprotective; antidepressant; nootropic;
cantillabetic; cytostatic; neuroprotective; antidepressant; nootropic;
cantillabetic; cytostatic; neuroprotective; antidepressant; nootropic;
cantillabetic; cytostatic; neuroprotectides and polynucleotides
cencoding them can be used in gene therapy, antisense therapy and vaccine
production, The proteins and polynucleotides are useful for screening for
cagonists or antagonists of a protein and for the treatment and diagnosis
cof disorders associated with the activity of a protein e.g. inflammation,
cof disorders associated with the activity of a protein e.g. inflammation,
consumptional cantillabetic shock, pancreatitis, cardiac dysfunction,
consumptional cantillabetic shock, pancreatitis, cardiac dysfunction,
canaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,
costeoporosis, severe combined immunodeficiency, eczema, allergic
costeoporosis, severe combined immunodeficiency, eczema, allergic
continuitis, asthma, diabetes, cancer, multiple sclerosis, depression,
continuitis, asthma, diabetes, cancer, multiple sclerosis, depression,
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continuitis, asthma, diabetes, cancer, multiple sclerosis, depression,
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continuitis, asthma, diabetes, cancer, multiple sclerosis, depr
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-DEC-1999; 99US-0471275.
21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552317.
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                                                                                             Isolated human polynucleotides encoding polypeptides, useful for treatment and diagnosis of e.g. cancer, ulcers and HIV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-DEC-2000;
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                                                                                                                                                                                                                                                                                                 nThrGluLeuValLeuArgCysProGlnLysThrAspCysAlaLeuArgV 84
                                                                                                                                                                                               lValValSerLeuGluArgLeuMetGluProGlnAspThrAlaArgCysS
GACAGAGCTGGTGCTGAGGTGCCAGAAGGAGACCGACTGTGACCTCTGTC
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                                                                                                                                                                         seq_name: /SIDS1/gcgdata/geneseq/geneseqn-embl/AA2001A.DAT:AAL02817
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                Human;
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                                          reproductive system
reproductive system related gene therapy; ds.
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                                                                      (first entry)
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                                        related antigen DNA SEQ
             antigen;
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            system disorder;
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470 uAl 11 15509 GGC	454 Ala 15474	445 15430 TTC		422 Thr ::: 15330 TCG	405 alc 15307 AGG	388 sAsp	372 Lys 15225 TAG	355 lnL 15196 AAG	338 lPr 15146 GAG	322 Val 1 15096 GTT	Align seg 1	alignment_block: US-09-899-471-5	alignment_sc	SQ Sequence	CC The presen CC number of CC in the pre CC including CC protein of CX	ps Disclosure;	PT Isolated	WPI;	Rosen	PA (HUMA-)
uAlaCysLeuLeuLeuAlaAlaAlaLeuPhePhePheLeuLeuLeuLysL 	AlaCysProMetAspLysTyrIleHisArgArgTrpValLeuValTrpLe ::: ::	ASDASPASDASNMETGlySerLeuTr ::::::::: TTCTCTGTGGAGGGTAAGTTTCTAACTCTTCTTCTTCTGGGTCTC	HisGlnCysMetGlnLeuTrp. 	ThrArgAlaAlaArgLeuGlyGluGluLeuLeuGlnAspPheArgSer:::::	alCysAlaLeuGluProSerGlyCysThrProLeuProSerMetAlaSer ::: :::	SASPASPMETLeuLeuValGluMetLysThrGlyLeuAsnAsnThrSerV ::::::	LysValGlnLeuGlnAlaCysSerTrpAlaAspSerLeuGlyProPheLy :::	InLeuValAlaGlyHisProAsnLeuCysValGlnValSerThrTrpGlu :::	IProProValProGlnLysAsnAlaThrValAsnGluProGlnAspPheG	ValThrLeuCysTrpGlnAlaProAspGlnSerProCysGlnProLeuVa ::: ::: 	1/1 to: AAL02817 from: 1 to: 16491	lock: 471-5 x AAL02817	_scores: Quality: 692.50 Length: 470 Ratio: 2.663 Gaps: 14 Similarity: 55.319 Percent Identity: 39.574	ce 16491 BP; 3837 A; 4251 C; 4180 G; 4223 T; 0	present invention provides the protein and coding sequences error of human reproductive system related antigens. These can be prevention and treatment of reproductive system disorders uding cancer. The present sequence is a genomic sequence ence ein of the invention.	SEQ ID NO 5505; 1297pp + Sequence L	nucleic acid molecule encoding a reproin preventing, treating or ameliorating	2001-465570/50.	CA, Barash SC, Ruben SM;) HUMAN GENOME SCI INC.
IL 487 NA 15558	æ 470 '™ 15508	rp 453	o. 444 C 15429	437 GC 15379	er 421 :: CC 15329	€V 405 - 	LY 388	lu 371 aG 15224	eg 355 15195	va 338 rg 15145				other;	g sequences of a . These can be used em disorders, sequence encoding a	₽ng	ductive system antigen a medical condition -			

. •	1 uAlaProGly 684 6 CGCGCGGGA 16415	681 16406
G1 681 CC 16405	77 GlnAlaLeuArgSerAlaLeuAspSerCysThrSerSerSerG :::: :::	667 16356
hr 666 :: CC 16355	lyCysSerThrSerAlaGlyArgProA	650 16306
:lyG 650 :AGC 16305	3 uPheSerLeuProThrGln : ::: 6 CTTCACACTGCCCTCCCAA	63 1625
Le 633 :: GT 16255	GlyLeuLeuHisProAspSerValPro 	617 16206
sp 616 - AC 16205	00 spPh¢LeuGlnGlyArgAlaThrGlyArgTyrValGlyValTyrPheAsp 	600 16156
OA 600 CG 16155	35GlyProHisAspAlaLeuAlaAlaTrpLeuSerCysValLeuPro :::	.58 1610
584 GC 16105	0 ValAlaGInCysGInGInTrpLeuGInLeuGInThrValGIuPro	57 1605
la 569 CG 16055	53 rgIleLeuGlnGluGlyGlyValValIIeLeuLeuPheSerProAlaAli ::	553 16006
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gAr 536 TCG 15955	0 AlaLeuSerGlnMetProLeuArgValAlaValAspLeuTrpSerAr :::	52 1590
er 519 CG 15905	3 isSerAlaAspGlyAlaGlyTyrGluArgLeuValGlyAlaLeuAlaS 	50 1585
uH 503 : CT 15855	AlaalaargGlySerargThralaLeuLeuLe 	492 15809
TCT 15808	9 CGCCCCCGGGGAGCCAGGCCTGTGCCAGCTCACCTCTTCCCTCCC	1575
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AA 1	9 ACTGGCTGCCTCCGCCCCTCTCCCCTAACAGGGTGGCTGAGGCTCTTG	
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491	91	49
491 GA 15608	7 ysaspargarglys	48 1555

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b_pr:HSA330055
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b_pr:HSNL1106R
b_pr:HSA335870
b_pat:AX350982
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-MODEL-frame+_p2n.model -DEV-xlh
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-DELEXT-7.000 -TARTIX-b-losum62 -TRANS-human40.cdi
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-NCPU-6 -1CPU-3 -LONGLOG -DEV_TIMEOUT-120 -WARRLTIMEOUT-30
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b_pr:HSA336001
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earch time (sec): 11857.370000
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AX073993 Sequence 161 from Pat
AX180776 Sequence 13 from Pate
AX350973 Sequence 7 from Pate
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ProGlnAspPheGlnLeuValAlaGlyHisProAsnLeuCysValGlnVa 36	ysGlnProLeuValProProValProGlnLysAsnAlaThrValAsnGlu 35 	SLeuProGlyLysValThrLeuCysTrpGlnAlaProAspGlnSerProC 33 	ArgLeuArgValLeuSerProGlyValTrpGlnLeuAspAlaProCysCy 31 	ysProPheArgGluAspProGlyAlaHisArgAsnLeuTrpHisIleAla 30 	uCyslleGlnValTrpSerLeuGluProAspSerGluArgValGluPheC 28 	ThrGlyProGlnAsnIleThrLeuAsnHisThrAspLeuValProCysLe 26 	YrLeuArgProValProAspAlaLeuLysSerLeuTrpTyrLysAsnLeu 25 		pgly regr	hrGlnGlnLeuProAspCysArgGlyLeuGluValArgAspSerIleGln 20	lGlnIleTrpSerTyrThrLysProArgTyrGlnLysGluLeuAsnLeuT 18 	ValGlySerAlaValPheAspCysPheGluAlaSerLeuGlyAlaGluVa 16 	laLeuLeuGluValGlnValProAlaAspLeuValGlnProGlyGlnSer 15 	uGlnAlaGlnValValLeuSerPheGlnAlaTyrProIleAlaArgCysA 13 	GluAlaGlyLysSerAspSerGluLeuGlnGluSerArgAsnAlaSerLe 11 	alargvalvalvalhisLeualavalhisGlyHisTrpAlaGluProGlu 10 	nThrGluLeuValLeuArgCysProGlnLysThrAspCysAlaLeuArgV 84	GlySerLeuGlnSerAlaProGlyProValLeuValProThrArgLeuGl 67
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651 CysSerTh	634 heserLe	617 YLeuLeu 1 2049 GCTGCTG	601 PheLeuG 1999 TTCCTGC	584 roglypr 1949 ccggcc	567 oAlaAla 1899 CGCGGCC	551 Argarga 1849 CGACGCC	534 erArgAr 1799 GCCGCCG	517 uAlaSer 1749 GGCGTCC	501 LeuLeuH 1699 CTCCTCC	484 euLeuLy 1649 TTCTAAA	467 uValTrp 1599 AGTATGG	451 SerLeuT 1549 TCGCTAT	434 spPheAr 1499 ACTTCCG	417 oSerMet 1449 CAGCATG	401 ASDASOT 1119 AACAACA	384 euGlyPr 1349 TGGGGCC	367 lSerThr 1299 GAGCACC	1249 CCACAAG
ırSerAlaGlyArgPr 	uProThrGlnLeuPro ::: CCCTCGCAGCTGCCG	HisProAspSerValP 	lnGlyArgAlaThrGl 	OHISASPALALEUALA 	ValAlaGlnCysGlnG grGGCGCAGTGTCAGC	xgIleLeuGlnGluGl GTATCCTGCAGGAGGG	gGluLeuSerAlaHis CGAGCTGAGCGCGCAC	AlaLeuSerGlnMetP 	isSerAlaAspGlyAl 	SLysAspArgArgLys AAAGGACCGCAGGAAA	LeuAlaCysLeuLeuL 	rpAlaCysProMetAs 	gSerHisGlnCysMet aTCACACCAGTGTATG	AlaŚerThrArgAlaA GCCTCCACGAGAGCTG	hrserValCysAlaLe	OPheLysAspAspMet CTTCAAGGATGATATG	TrpGluLysValGlnL TGGGAGAAGGTTCAGC	ATTTCCAGTTGGTGGC
oAlaAspArgValGlu 	AlaPheLeuAspAlaL 	roSerProPheArgVa. 	yArgTyrValGlyVal' 	AlaTrpLeuSerCysva 	InTrpLeuGlnLeuGl AGTGGCTGCAGCTCCA	yGlyValValIleLeu 	GlyAlaLeuAlaTrpP GAGCCCTAGCCTGGT	roLeuArgValAlaVa CACTGCGCGTGGCCGT	aGlyTyrGluArgLeu 	AlaAlaArgGlySerA 	euAlaAlaAlaLeuPh TGGCTGCGGCGCTTTT	PLYSTYTIleHiSATĠ 	GlnLeuTrpAsnAspA 	laArgLeuGlyGluGl 	uGluProSerGlyCys GGAACCCAGTGGCTGT	LeuLeuValGluMetL 	euGlnAlaCysSerTr TGCAAGCGTGCTTGTG	AGGCCACCCCAACCTC
ArgValThrG1	euGlnGlyGly TGCAGGGAGGC	lAlaProLeuP CGCCCCGCTCT	lTyrPheAspGl LFH CTACTTCGACGG	alLeuProAsp 1 * 1GCTACCCGAT	nThrValGluP	LeuPheSerPr CTCTTCTCGCC	heHisHisGln TCCACCACCAG	laspLeuTrpS GGACCTGTGGA	(ValGlyAlaLe GTGGGAGCACT	rgThrAlaLeu GCACGGCCTTG	ePhePheLeuL CTTCTTCCTCC	ArgTrpValLe CGCTGGGTCCT	\spAsnMetGly ACAACATGGGA	uLeuLeuGlnA GTTGCTGCAAG	ThrProLeuPr	ysThrGlyLeu AAACCGGCCTC	PAlaAspSerL GGCTGACTCCT	TGTGTCCAGGT
667	650 2148	634 2098	617 2048	1998	584 1948	567 1898	550 1848	534 1798	517 1748	500 . 1698	484 · 1648	467 1598	450 1548	434 1498	417 1448	400 1398	384 1348	1298

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus, clone MGC:6973
                                                                                                                                                                                                                                                                                                                                                                                            Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 6 Row: c Column: 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., I
A.M., Holloway, M., Telford, B, Hodgson, A., Bouck,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia DenceDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (21-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BC004759.1 GI:13435809 MGC.
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Muzny,D.M., Gibbs,R.A.
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                          /organism="Mus musculus"
/db_xref="taxon:10090"
/dlocate:6973 IMAGE:3154616"
/tissue_type="Mammary tumor. Brcal-/fl; MMTV-Cre model.
months old, gross tissue."
/clone_lib="NCI_CGAP_Mam3"
/lab_host="DH10B"
                                                                                                                                                                 /product="Unknown (protein for MGC:6973)"
/protein_id="AAH04759.1"
/db_xref="GI:33435810"
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IMAGE: 3154616, mRNA, complete cds.
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                                                                       lLeuLeuThrLeuAspValSerGluGluGlnAspPheSerPheLeuLeuT
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ACCTGCGTCCAGTCCCGGATGCTCTCAAATCCTTGTGGTACAAAAACCTG
                                                          CCTTCTGACACTGGATGTCTCTGAGGAGCAGGACTTTAGCTTCTTACTGT
                                                                                                                       AGCTGCTGGGTCCTGGCCTCAATGTGTCTACAGATGGTGACAATGT
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REMARK COMMENT

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OURCE EYWORDS ERSION CCESSION

FEATURES

CDS

1636	6	163
550	erArgArgCluLeuSerAlaHisGlyAlaLeuAlaTrpPheHisHisGln	53,
1636	6	163
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1636	6	163
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500 1636	4 eULeULYSLYSASPAIGAIGLYSAlaAlaArgGlySerArgThrAlaLeu 7 TTCTAAAAAA	162
484 1626	UValTrpLeuAlaCysLeuLeuLeuAlaAlaAlaLeuPhePhePheLeuL 	7 6
467 1576	SerLeuTrpAlaCysProMetAspLysTyrIleHisArgArgTrpValLe	່ ນັ່ນ
450 1526	4 spPheArgSerHisGlnCysMetGlnLeuTrpAsnAspAspAsnMetGly	43. 147
434 1476	7 oSerMetAlaSerThrArgAlaAlaArgLeuGlyGluGluLeuLeuGlnA 	41. 142.
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384 1326	7 1SerThrTrpGluLysValGlnLeuGlnAlaCysSerTrpAlaAspSerL 	7 6
367 1276	1 ProGlnAspPheGlnLeuValAlaGlyHisProAsnLeuCysValGlnVa 	35 122
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317 1126		7 0
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284 1026	57 uCysIleGlnValTrpSerLeuGluProAspSerGluArgValGluPheC 	26 97
267 976	1 ThrGlyProGlnAsnIleThrLeuAsnHisThrAspLeuValProCysLe	92

1 MetProValSerTrpPheLeuLeuSerLeuAlaLeuG	Align seg 1/1 to: AX350978 from: 1 to: 2094	alignment_block: US-09-899-471 5 x AX350978	alignment_scores: Ouality: 2756.00 Ratto: 4.984 Percent Similarity: 79.226 Percent Identity: 71.490	ASE COUNT 247 a 251 c 393 g 365 t 918 others ORIGIN	fied ***	Patent: WO 0190358-A 12 29-NOV-2001; SCHERING CORPORATION (US) Location/Qualifiers	REFERENCE 1 (sites) AUTHORS Gorman,D.M. TITLE Mammalian receptor proteins; related reagents and methods	X	seq_documentation_block: seq_documentation_block:	seq_name: gb_pat:Ax350978	684 lyCysCysGluGluTrpAspLeuGlyProCysThrThrLeuGlu 698	667 nAlaLeuArgSerAlaLeuAspSerCysThrSerSerSerGluAlaProG 684	651 CysSerThrSerAlaGlyArgProAlaAspArgValGluArgValThrG1 667	634 heSerLeuProThrGlnLeuProAlaPheLeuAspAlaLeuGlnGlyGly 650 	617 yLeuLeuHisProAspSerValProSerProPheArgValAlaProLeuP 634	601 PheLeuGInGlyArgAlaThrGlyArgTyrValGlyValTyrPheAspG1 617	584 roGlyProHisAspAlaLeuAlaAlaTrpLeuSerCysValLeuProAsp 600 	1636 1636	567 oAlaAlaValAlaGlnCysGlnGlnTrpLeuGlnLeuGlnThrValGluP 584	1636 1636	551 ArgArgIleLeuGlnGluGlyGlyValValIleLeuLeuPheSerPr 567
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|GARGCNGGNAARWSNGAYWSNGARYTNCARGARWSNMGNAAYGCNWSNYT 350
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                                                                                                                               yrLeuArgProValProAspAlaLeuLysSerLeuTrpTyrLysAsnLeu 250
                                                                                                                                                   RACNGARYTNGTNYTNMGNTGYCCNCARAARACNGAYTGYGCNYTNTGYG
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OCUS AX073993
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JS-09-899-471-5 x AX073993
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Ratio: 4.148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2255)
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                                                                                                                                                                                                                                                                                                                                                                                              AspAsnMetGlySerLeuTrpAlaCysProMetAspLysTyrIleHisAr 463
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Ratio: 4.118
milarity: 81.612
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Eaton, D.L., Filvaroff, E., Gerritsen, M.E., Goddard, A., Goddowski, P.J., Grimaldi, C.J., Gurney, A.L., Watanabe, C.K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 161 from Patent W00116318
AX092430
AX092430.1 GI:13444529
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/db_xref="taxon:9606"
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163/	7 ThrValAsnGluProGlnAspPheGlnLeuValAlaGlvHisProAsnTe	4
خة (0 spGlnSérProCysGlnProLeuValProProValProGlnLysAsnAla :::	33(
330 1187	3 pAlaProCysCysLeuProGlyLysValThrLeuCysTrpGlnAlaProA 	31; 113(
313 1137	7 TrpHislleAlaArgLeuArgValLeuSerProGlyValTrpGlnLeuAs ::: ::: :::	29; 1081
296 1087	0 rgValGluPheCysProPheArgGluAspProGlyAlaHisArgAsnLeu :::::::	28 103
280 1037	3 uValProCysLeuCysIleGlnValTrpSerLeuGluProAspSerGluA 	26: 98:
263 987	7 TyrLysAsnLeuThrGlyProGlnAsnIleThrLeuAsnHisThrAspLe :::	931
246 937	0 erPheLeuLeuTyrLeuArgProValProAspAlaLeuLysSerLeuTrp :::::	88
230 887	3 pGlyAspAsnValLeuLeuThrLeuAspValSerGluGluGlnAspPheS	21 83
213 837	7 AspSerIleGlnSerCysTrpValLeuProTrpLeuAsnV :::	19
196 808	0 luLeuAsnLeuThrGinGlnLeuProAspCysArgGlyLeu 	18 78
180 782	3 uGlyAlaGluValGl ::: :: 3 AGGGAGTGAGGTACG	16 73
163 732	7 P	14 68
146 682	30 leAlaArgCysAlaLeuLeuGluValGlnValProAlaAspLeuValGln 33 CTGCCGGCTGCGTGCTGGAGGTGCAAGTGCCTGCTGCCCTTGTGCAG	13 63
130 632	13 gAsnAlaSerLeuGlnAlaGlnValValLeuSerPheGlnAlaTyrProI 	11 58
113 582	1 GluAlaGlyLysSerAspSerGl ::: 3 GATGAGGAAAAGTTTGGAGGAGCAGCTGACTCAGG	10 53
100 532	84 alArgValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu:::	4 8
84 482	7 nThrGluLeuValLeuArgCysPro	43 6
432	:::::: 3 GGGACATCGTG	38

630 ValAlaProLeuPheSerLeuProThrGlnLeuProAlaPheLeuAspAl 646 :::::: ::: :::	ພ ພ
613 alTyrPheAspGlyLeuLeuHisProAspSerValProSerProPheArg 629 ::	61
596 svalleuproAspPheLeuGlnglyArgAlaThrGlyArgTyrValGlyV 613 	ω ώ
583 GluProGlyProHisAspAlaLeuAlaAla	ര് ര
566 erProAlaAlaValAlaGlnCysGlnGlnTrpLeudinLeuGlnThrVal 582 ::: 1932 CTCCCGGTGCGGTGGCGTGTGCA6CGAGTGGCTACAGAGTGTGCTCC 1981	ω 66
549 sGlnArgArgArgIleLeuGlnGluGlyGlyValValIleLeuLeuPhes 566 	54
533 TrpSerArgArgGluLeuSerAlaHisGlyAlaLeuAlaTrpPheHisH1 549 	53 83
516 laLeuAlaSerAlaLeuSerGlnMetProLeuArgValAlaValAspLeu 532 	8 →
499 aLeuLeuLeuHisSerAlaAspGlyAlaGlyTyrGluArgLeuValGlyA 516 	ωg
492AlaAlaArgGlySerArgThrAl 499	80 V9
480 hePhePheLeuLeuLeuLysLysAspArgArgLys	ω α
463 gArgtrpValLeuValTrpLeuAlaCysLeuLeuLeuAlaAlaAlaLaLeuP 480	46 58
447 AspAsnMetGlySerLeuTrpAlaCysProMetAspLysTyrIleHisAr 463 ::::: :::	53
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413 sThrProLeuProSerMetAlaSerThrArgAlaAlaArgLeuGlyGluG 430 	41 43
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380 rpAlaAspSerLeuGlyProPheLysAspAspMetLeuLeuValGluMet 396 	33 8
363 uCysValGinValSerThrTrpGluLysValGlnLeuGlnAlaCysSerT 380	36 28
1238 ACTGTGGACAAGGTTCTCGAGTTCCCATTGCTGAAAGGCCCACCCTAACCT 1287	ũ

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                                                                                      nThrGluLeuValLeuArgCysProGlnLysThrAspCysAlaLeuArgV 84
alArgValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu 100
                             GACAGAGCTGGTGCTGAGGTGCCAGAAGGAGACCGACTGTGACCTCTGTC 482
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Genentech, Inc. (US)
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Percent Identity: 65.912
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380 r	363 u 1 1288 c	347 T 1 1238 A	330 s 1188 G	313 p	297 T 1 1088 T	280 r 1038 d	263 u 988 G	247 T 938 C	230 e 888 G	213 p 838 T	197 /	180 1 783 A	163 u 733 A	147 F	130 633 (113 9 583 6	101 (533 (483
	CysValc	hrvalas	pGlnser ::: TGGGGAC	AlaProC GCACCGT	rpHisI1	gValGlu ::::: GACGAAC	Walproc GTTCCCT	YrLysas :: ACAAAAA	erPheLeu :::: CCTCTCC	Glyaspa GGTGACA	AspSerIl	LuLeuAsn 	IGLYALAG	roglyg Tregre	G – Ar	AsnAla AATGCC	Glu ::: GATGAGG	GCGTGT
SerLeuG	linvalse :: :AGGTGAA	nGluPr :::: CAAGGT	ProCys	ysCysL GCTCGC	eAlaAr CGCCCG	PheCys ::: ATCTGC	ysLeuC GCCTCT	nLeuTh CCTGAC	LeuTyr CTGTAC	snValI ACGTGC	eGlnSe	LeuThr CACACA	luValG : AGGTAC	Inserva AGTCTGT	gCysAla ::: CTGCGTC	SerLeuG CTCTCC		GCTGTC
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heLysAs ::	PGluLys GGAGAAG	PheGlnL TTCCCAT	euValPr TGGTCCC	yLysVal :::::: AGAAGCG	ValLeus ::: : CTGCTGA	rgGluAs GGGAGGA	nvalTrp GGTGTGG	GlnAsnI CAGATCA	rovalpr AGGTCCA	TCTGAAT	ValLeup ::: GCCCTGC	euProAs	PSerTyr GTCCTAT	Alavalp ::: : GTGGTAT	luValGl AGGTGCA	nValVal AGTCGTG	Lyssera ::: .GCAGCTG	CCGTGCA
PAspMet	ValGlnL ::: CTGCAGC	euValAl ::: TGCTGAA	oProVal	ThrLeu::: ::: GCACTO	~ ~	pProGly cccccgc	SerLeuG CCTCTGG	leThr	roAspAla AGGGCCCC	ValserG GTCTCTG	Ö — H	pCysAr	ThrLys ::: ACTCAG	heAspC :: ATGACT	nValPr AGTGCC	LeuSer CTCTCC	spSerG ACTCAG	ATGGGCA
LeuLeu	euGlnA !TGCAGG	aGlyHi AGGCCA	ProGla	STrpG CTGGC	yvalīr gagra	AlaHis GCACAC	luProA AACCTG	uAsnHi GAACCA	LeuLys CCAAAA	luGluG AGGAGC	uAsnVa CAACGT	GlyLeu	ProArgT CCCAGGT	ysPheGl GCTTCGA	OAlaAsp TGCTGCC	PheGlnA TTCCAGG	luLeuGl ::::: GGGTGGA	TGGGAA
ValGluMe :::	laCysSe	sProAsn CCCTAAC	LysAsnA ::: : GAGAACG	lnAlaPr F: GGGCTCC	pGlnLeu ccrccrc	ArgAsnLe ::: CAGAACCT	spSerGl	SThrAsp CACAGAC	SerLeuT 	lnAspPh AGCACTT	lserThr ::: GTCAGCA	luValæ	yrGlnLy ::: ACGAGAA	.uAlaSer ::: \GGCTGCC	Leuvald CTTGTGC	laTyrPr CCTACCC	nGluSer : GGAGCCT	GAGCCTG
et 39	ET 38	Le 36	la 34 :: TC 12	OA 330 GG 118	As 31 - GA 11	eu 29 TC 10	uA 28	Le 26	rp 24 GG 93	eS 23 : CG 88	As 21 11 GA 83	80	sG 18 	Le 16 	In 14 	OI 13	Ar 11 	AA 53
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                                                                                           aLeuGlnGlyGlyCysSerThrSerAlaGlyArgProAlaAspArgValG 663
                                                                                                                               ACCGTGCCGTCTTCACACTGCCCTACTGCCAGACTTCCTGGGGGC
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                            luArgValThrGlnAlaLeuArgSerAlaLeuAspSerCys.....Thr 677
                                                              ValAlaProLeuPheSerLeuProThrGlnLeuProAlaPheLeuAspAl 646
                                                                                                                                                                                              CCTGCTTCGACAGGCTGCTCCACCCGGACGCCGTACCCGCCCTTTTCCGC
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KEYWORDS
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Location/Qualifiers
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GDPCQPLYPPLSWENYTYDYNSSEKLQIQECLWADSIGPLKDDYLLLETRGPQDNRSI
CALEPSGCTSLPSKASTRAARLGEYLLQDLQSGQCLQLWDDDLGALWACPMDKYIHKR
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GTSAPGRGVGPGAGDGAGDGT*
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EKFGGAADLGVEEPRNASLQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVY
DCFEAALGSEVRIWSYTQPRYEKELNHTQQLPDCRGLEVWNSIPSCWALPWLNVSADG
DNVHLVLNVSSEQHFGLSLYWNQVQGPPKPRWHKNLTGPQIITLNHTDLVPCLGIQVW
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757 c 731 g
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FERLVGALASALCOLPLRVAVDLWSRRELSAQGPVAWFHAQRRQTLQEGGVVVLLFSP
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/db_xref="GI:18616350"
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ValAla	alTyrPhe! :: CCTGCTTC	SValle	GluPro. GGGCCCG	erProA	sGlnAr GCAGCG	Trpser	laLeuA CCTGG	aLeule	TTGAAAC	hePheP	gArgiri GCGCTG	Aspasn :::: GATGAC	luLeuL	STAPPT TACTTC	LysThr ::: CGAGGC	rpAlaAsp8 GGGCTGACT	uCysVa	ACTGTG
aProLeuPl : ::: GCCCGTCT	SAC H H	uProAs GCCGA	61 .	laAlav :: GTGCGG	gArgAr :: GCGCCA	ArgArg CGTCGT	laSerA CGTCGG	uLeuHi :: CCTCTA	CAGGAC	PheLeuL ::: :ATCCTCC	PValle ::: GGCCCT	MetGly ::: TTGGGA	euGlnA TACAAG	oLeuPr ACTACC	8 8	2 – 8	: 1G	GAC
neSe	GlyLeuLeuHisProAspSerValProS AGGCTGCTCCACCCGGACGCCGTACCCG	pPheLeu CTTCTTC	GGCCCACGCCCCACGACGCCTTCCGCGCCTC	erProAlaAlaValAlaGlnCysGlnGlnTrpLeuGh	lnArgArgArgIleLeuGlnGluGlyGlyValValIleLeuLeuPhe	TrpSerArgArgGluLeuSerAlaHisGlyAlaLeuAlaTrpPheHi 	laLeuSe CCCTGTO	SSETAL: : CTCAGC	AGGACGTCCGCTCGGGGG	heLeuLeuLysLysAspArgArgLys :: :CCTCCTTCTCAAAAGGATCACGCGAAAGGG	uValTr] . CGTGTG	snMetGlySerLeuTrpAlaCysProMetAspLysTyrIle	euGlnAspPheArgSerHisGlnCysMetGlnLeuTrp :::: ::: TACAAGACCTGCAGTCAGGCCAGTGTCTGCAGCTATGG	roLeuProSerMet CACTACCCAGCAA <i>E</i>	AsnAsn' ::: GACAAC	rLeuGlyProPheLysAspAspMetLeuLeuValGlu ::: ::: ::: CTGGGGCCTCTCAAAGACGATGTGCTACTGTTGGAG	lnValSerTh: ::::: GTGAACAG	:
rLeuProThrGlnLeuP : ::: ACTGCCCTCCCAACTGC	euHisPr CCACCC	iGlnGly CAGGGC	ProHis/ CGCACC	LnCysGI :: GTGCAC	JGlnGlu GCAGGAG	SerAlaH \GCGCGC	erGlnMe :: GCAGCT	aAspGly GATGAC	rceeee	YSLYSAS NAAAGGI	pLeuAla CTGGCC	TrpAlac rGGGCC1	rgSerHi :: AGTCAGO	tAlaSe AGCCTCC	ThrSerV	roPheLy	rTrpGlu : CTCGGAO	
hrGlnL :: CCCAAC	oAspSe :: GGACGC	ArgAla CGGGCG	SPALAI ACGCCT	InGlnTr :::: CGAGTG	iGlyGly GGCGGC	HisGlyA ::: :AGGGGC	etProLe :: GCCGCT	Alagly ::: TCGGGT	Alaa GGGCCC	spargar : : : \TCACGO	CysLeu TGCCTA	ysProb GCCCC	isGlnCy CCAGTO	ThrArg	AlCysi ::: CTCTGTG	/SASPAS NAGACGA	Lysval	
euProA TGCCAG	rValPr:	ThrGly cccgc	euAlaA :: I, TCCGCG	pLeuGL	Valval	laLeuA ::: CCGTGG	uArgVa } GCGCGT	TyrGlu ::: TTCGAG	AlaAlaArgGlyS CGGCCGCCAGGGGC.	gLys GAAAGG	LeuLeu ::: CTCTTT	letAspI TGGACA	SMetGl	AlaAla GCAGCT	laLeuG CCTTGG	PMetLe	GlnLeu CAGCTG	:
ProAlaPheLeuAsp CCAGACTTCCTGGGG	CC :: EI	ArgTyr AGCTAC	laTrpL JI	InLeuGlnThrVa ::: AGGATGGGGTGTC	IleLeu ::: GTCTTG	laTrpP CTTGGT	lAlava GGCCGT	ArgLeu GCCTG	. დ	TGGC	AlaAla GCCGCT	ysTyrI AATACA	nLeuTr GCTATG	ArgLeu CGCCTT	luProS AACCCA	uLeuVa :: ACTGTT	GlnAla CAGGAG	:
euAspAl TGGGGGC	ProPheArg TTTTCCGC	ValleuProAspPheLeuGlnGlyArgAlaThrGlyArgTyrValGlyV 	rpLeuSerCy EGCTCAGCTG	LeuGlnThrVal CTACAGGATGGGGTGTCC	LeuPheS CTCTTCT	heHisHi TTCACGC	laLeuhlaSerAlaLeuSerGlnMetProLeuArgValAlaValAspLeu 	aLeuLeuLeuHisSerAlaAspGlyAlaGlyTyrGluArgLeuValGlyA 	rArgThrAl ::: CGCGCGGC	TGAGGCTC	pValleuValTrpLeuAlaCysLeuLeuLeuAlaAlaAlaLeuP ::: :::	leHisAr :: TCCACAA	:pAsnAsp GGAC	MetAlaSerThrArgAlaAlaArgLeuGlyGluG 	yLeuAsnAsnThrSerValCysAlaLeuGluProSerGlyCy ::: ::: CCAGGACAACAGATCCCTCTGTGCCTTGGAACCCAGTGGCTG	lGluMet : GGAGACA	ThrTrpGluLysValGlnLeuGlnAlaCysSerT ::: ::: :AGCTCGGAGAAGCTGCAGCTGCAGGAGTGCTTGT	:
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1181 GTGGGGACCCCTGCCAGCCACTGGTCCCACCGCTTTCCTGGGAGAATGTC 1230

ThrValAsnGluProGlnAspPheGlnLeuValAlaGlyHisProAsnLe 363

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TrpHisIleAlaArgLeuArgValLeuSerProGlyValTrpGlnLeuAs 313

PAlaProCysCysLeuProGlyLysValThrLeuCysTrpGlnAlaProA 330

GCACCGTGCTCGCCGCAGAAGCGGCACTGTGCTGGCGGGGCTCCGG 1180

1031

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297

rgValGluPheCysProPheArgGluAspProGlyAlaHisArgAsnLeu 296

GGACGAACATCTGCCCCTTCAGGGAGGACCCCCGCGCACACCAGAACCTC 1080

230 erPheLeuLeuTyrLeuArgProValProAspAlaLeuLysSerLeuTrp 246

GCCTCTCCCTGTACTGGAATCAGGTCCAGGGCCCCCCAAAACCCCCGGTGG

930

163 uGlyAlaGluValGlnIleTrpSerTyrThrLysProArgTyrGlnLysG 180

AGGGAGTGAGGTACGAATCTGGTCCTATACTCAGCCCAGGTACGAGAAGG

730

581 CTGCCCCCTGCTGCTGCAGGTGCAAGTGCCTGCTGCCCTTGTGCAG

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leAlaArgCysAlaLeuLeuGluValGlnValProAlaAspLeuValGln 146

101 Glu.....AlaGlyLysSerAspSerGluLeuGlnGluSerAr 113

481 GATGAGGAAAAGTTTGGAGGAGCAGCTGACTTAGGGGTGGAGGAGCCTAG

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                                                                                                                                                                                                                                                                                                                                                                                                                                             Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 13 Row: 1 Column: 7
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Genomescan gene prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Vlotor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smallus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (09-APR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BC006411.1 GI:13623590
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        George Yang,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           448
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                                                                                                                                                                                                                                                                            AspSerIleGlnSerCysTrpValLeuProTrpLeuAsnValSerThrAs 213
                                                                                                                                                                                                    TTTGGTCAGTCTGTGGGCTCTGTGGTATATGACTGCTTCGAGGCTGCCCT
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                                                      AACTCAACCACACAGCAGCTGCCT.
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                                                                                                                                                                                                                      ProGlyGlnSerValGlySerAlaValPheAspCyaPheGluAlaSerLe 163
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                                                                                                                                                uGlyAlaGluValGlnIleTrpSerTyrThrLysProArgTyrGlnLysG
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                                                                                       luLeuAsnLeuThrGlnGlnLeuProAspCysArgGlyLeuGluValArg 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlySerLeuGlnSerAlaProGlyProValLeuValProThrArgLeuGl
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TITLE Secretory protein or membrane protein JOURNAL Patent: EP 1067182-A 263 10-JAN-2001; Helix Research Institute (JP)	ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 2499) AUTHORS Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Havashi,K.	IION Sequence 263 from Patent EP1067182	seq_name: gb_pat:AX136341 seq_documentation_block: LOCUS AX136341 2499 bp DNA linear PAT 30-MAY-2001	680 Ser	bb alThrGlnAlaLeuA ::::::: : 97 TGTCCCGGGCCCTTC	B nGlyGlyCysSerThrSerAlaGlyArgProAlaAspArgValGluArgV	632 ProLeuPheSerLeuProThrGlnLeuProAlaPheLeuAspAlaLeuGl 648 : ::: :::		98 uProAspPheLeuGlmGlyArgAlaThrGlyArgTyrYalGlyValTyrP	5 GlyproHisAspAlaLeuAlaAlaTrpLeuSerCysValLe	68 laAlavalAlaGlnCysGlnGlnTrpLeuGlnLeuGlnThrValGluPro ::	551 gArgArgIleLeuGlnGluGlyGlyValValIleLeuLeuPheSerProA 568	35 Arg 97 CGT	AserAlaLeuSerGlnMetProLeuArgYalAlaValAspLeuTrpSer	Ol uLeuHisSerAlaAspElyAlaGlyTyrGluArgLeuValGlyAlaLeuA 	CATCTGTTTCTCCGGCAGCGCCCCAGGGGCCGCGCGCTCTGCT	AGGGCCGCCCCGGGGAGCCAGGCTGTGCCAGCTCACCTCTTCCCTCCC

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, 100 Tr	08	147 Pa	130 le 608 C	113 g/ 558 G	101 G 508 G	84 a. 458 To	67 n' 1 408 G	51 G 358 G	34 e. 308 C	17 1: 258 G	. 1 M 1 208 A	Align seg	ignment_ S-09-899	.1gnment_	BASE COUNT	CDS	EATURES Source
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GlnGlnLeuProAspCysAr	InIleTrpSerTy :: SAATCTGGTCCT/	lGlySerAlava: ::: GGCTCTGTGGT/	LeuLeuGluVal(CTGCTGGAGGTG(lnAlaGlnValV AGGCCCAAGTCG	.AlaGlyLysSe: ::: ::GGAGGAGCAGC	HisLeuAlaVal	euArgCysProG : TGAGGTGCCAGA	rAlaProGlyPr TGCTCCGGGCCC	CysHisLeuTrp ::: TGCCGCCTCTGG	luArgLeuMetG ::: AGAGGCTTGTGG	PPheLeuLeuSe GTTCTTGCTGTC	AX136341 from:	.36341	3.977 71.722 Perc	/codon_start=1 /protein_id="cac39813.1" /protein_id="cac39813.1" /db_xref="G1:14272748" /db_xref="G1:14272748" /translation="MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDS /translation="MPVPWFLLSLALGRSPVVLSEDCDLCLRVAVHLAVHGHWEEPEDE EKFGGAADSGVEEPRNASLQAQVVLSFQAYETARCVLLEVQVPAALVQPGQSVGSVVY DCFEAALGSEVRIWSYTQPRYEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHF GLSLYWNQVQGPPKPRWHKNLVRPPPSQVHSHCRPMFVQRTQCHIREDP" GLSLYWNQVQGPPKPRWHKNLVRPPPSQVHSHCRPMFVQRTQCHIREDP" GLSLYWNQVGPPKPWHKNLVRPPPSQVHSHCRPMFVQRTQCHIREDP" GLSLYWNGVQGPPKPWHKNLVRPPPSQVHSHCRPMFVQRTQCHIREDP"	/organism="Homo /db_xref="taxon 208. 1011	ation/Qu .2499
g	YTThrLysProA ::: ATACTCAGCCCA	lPheAspCysPh ::: ATATGACTGCTT	SinvalProAla CAAGTGCCTGCT	alLeuSerPheG GCTCTCCTTCC	rAspSerGluLe : :GACTCAGGGGT	HisGlyHisTrp CATGGGCACTGG	lnLysThrAspC ::::: aGGAGACCGACT	oValLeuValPr ::: CGTGCTGGCGCC	AspGlyAspVal ::: ::: GACAGTGACATA	luProGlnAspī 	rLeuAlaLeuGl CTTGGCACTGGG	1 to: 2499		Length Gaps ent Identity	AC39812.1* 4272748* MPVPWFLLSLAI PVLAPTHLQTEI FWNASLOAQVVLS SYTOPRYEKELA SYTOPRYEKELA SPWHKNILVRPPE 64 g 496	n:9606"	rs
lyLeuGluValArg	rgTyrGlnLysG :::: GGTACGAGAAGG	eGluAlaSerLe ::: CGAGGCTGCCCT	AspLeuValGln GCCCTTGTGCAG	lnAlaTyrProI AGGCCTACCCTA	uGlnGluSerAr :::: GGAGGAGCCTAG	AlaGluProglu GAAGAGCCTGAA	ysAlaLeuArgV : GTGACCTCTGTC	OThrargLeuGl ::: TACGCACCTGCA	LeuCysLeuPro CTCTGCCTGCCT	hralaargCyss ::::::: CTACCCACTGCT	YArgAsnProVa ::; CCGAAGCCCAGT			778 10 10 157.841	GRSPVVLSLERI VLRCQKETDCDI FOAYPTARCVLI HTQQLPALPWLI SQVHSHCRPMPI t	•	
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409 1612	3 euValGluMetLysThrGlyLeuAsnAsnThrSerValCysAlaLeuGlu :::	.56
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326 1362	10 TrpGinLeuAspAlaProCysCysLeuProGlyLysValThrLeuCysTr 	31
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293 1262	76 oAspSerGluArgValGluPheCysProPheArgGluAspProGlyAlaH	27
276 1213	0 HisThrAspLeuVal	
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1112	63 TGGTTTCCTTGACTTTGGCCTCCTCCTCCTTCCTCCTTATCTTCTCCAACC	901
249		2,
249 1063	49 13 GAGGACTCACCCCAAGCAAGGGAAAATTGGTGGGGGAACTTCTGCCTTCC	101
1013		
249	49	2
249 962	47 TyrLysasn	9 2
246 912	30 erPheLeuLeuTyrLeuArgProValProAspAlaLeuLysSerLeuTrp	8 2
230 862	113 pGlyaspAsnValLeuLeuThrLeuAspValSerGluGluGlnAspPheS	80 N
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		643 PheLeuAspAlaLeuGlnGlyGlyCysSerThrSerAlaGlyArgProAl 659
		626 erProPheArgValAlaProLeuPheSerLeuProThrGlnLeuProAla 642 :: ::: ::: :::
,		609 gTyrValGlyValTyrPheAspGlyLeuLeuHisProAspSerValProS 626 ::: ::: ::: :::
Ali	·	593 TrpLeuSerCysValLeuProAspPheLeuGlnGlyArgAlaThrGlyAr 609
alig US-		579 euGlnThrValGluProGlyProHisAspAlaLeuAlaAla 592 :::
alig		562 eLeuLeuPheSerProAlaAlaValAlaGlnCysGlnGlnTrpLeuGlnL 579 :
BASE ORIG		546 TrpPheHisHisGlnArgArgArgIleLeuGlnGluGlyGlyValValI1 562
		529 laValAspLeuTrpSerArgArgGluLeuSerAlaHisGlyAlaLeuAla 545
		512 gLeuValGlyAlaLeuAlaSerAlaLeuSerGlnMetProLeuArgValA 529
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	·	492AlaAlaArgGly 495
FEAT		476 aAlaAlaLeuPhePhePheLeuLeuLysLysAspArgArgLys 491 ::::::
AC TI		460 TyrIleHisArgArgTrpValLeuValTrpLeuAlaCysLeuLeuLeuAl 476 ::: 1700 TACATCCACAAGCGCTGGGCCCTCGTGTGGCTGGCCTGCCT
of Of		443 euTrpAsnAspAspAsnMetGlySerLeuTrpAlaCysProMetAspLys 459
DEF] ACCE VERS	·.	nCysMetGlnL C
roce		1613 CCCAGTGGCTGTACTTCACTACCCAGCAAAGCCTCCACG 1651

CUS FINITION CESSION	AX073996 1753 bp DNA linear PAT 06-FEB-2001 Sequence 4 from Patent WO0104304.
ERSION EYWORDS DURCE	AX073996.1 GI:12710228 - human.
ORGANISM	HÓMO sapiens Eukarvota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
FERENCE	Primates; Catarrhini; Hominidae;
	Presnell, S.R., Burkhead, S.K. and Pownder, S.L.
TITLE	
JOURNAL	Patent: WO 0104304-A 4 18-JAN-2001;
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ignment_scores:	Dres:

alignment_scores:
Quality: 1888.50 Length: 594
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Align seg 1/1 to: AX073996 from: 1 to: 1753

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Patent: WO 0104304-A 3 18-JAN-2001;
ZymoGenetics, Inc. (US)
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                                                                                                                                                                                                                                       1 (bases 1 to 2076)
Presnell, S.R., Burkhead, S.K. and Pownder, S.
                                                                                                                                                                                                                                                          artificial sequence
1 (bases 1 to 2076
                                                                                                                                                                                                                                                                                            synthetic construct
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                                                                                                                                                                                                                                                                                                            synthetic construct.
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907 others
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RIGIN

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Ratio: 3.757
Tarity: 64.358
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US-09-899-471-5 x AX073995
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US-09-899-471-5 x AX350975
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ATGCCNGTNCCNTGGTTYYTNYTNWSNYTNGCNYTNGGNWGNWSNCARTG 50
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Sequence 9 from Patent W00190358.
AX350975
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unidentified unclassified.
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313 950	TrpHisileAlaArgLeuArgValLeuSerProGlyValTrpGlnLeuAs TrpHisileAlaArgLeuArgValLeuSerProGlyValTrpGlnLeuAs TGGCARGCNGCNMGNYTNMGNYTNYTNACNYTNCARWSNTGGYTNYTNGA	297 901
296 900	rgValGluPheCysProPheArgGluAspProGlyAlaHisArgAsnLeu ::::::::::	851
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246 750	· 70 I	230 701
230 700	pGlyaspAsnValLeuLeuThrLeuAspValSerGluGluGlnAspPheS 	213 .651
213 650	AspSerIleGlnSerCysTrpValLeuProTrpLeuAsnValSerThrAs :::: ::	197 601
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113 350	.AlaGlyLysSerAs ::: YGGNGGNGCNGCNGA	101 301
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34 100	1ValValSerLeuGluArgLeuMetGluProGlnAspThrAlaArgCysS::: ::: :::::: :::: ::::: :::::	17 51

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                                                                                                                                                                          roAlaAlaValAlaGlnCysGlnGlnTrpLeuGlnLeuGlnThrValGlu
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ACCESSION
VERSION
KEYWORDS
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TITLE
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                                                                                                                                                                                                                                                                    Percent Similarity:
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                                                                                                                1 GARGARCCNMGNAAYGCNWSNYTNCARGCNCARGTNGTNYTNWSNTTYCA
spLeuValGlnProGlyGlnSerValGlySerAlaValPheAspCysPhe
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Presnell,S.R., Burkhead,S.K. and Pownder,S. Human cytokine receptor
Patent: WO 0104304-A 6 18-JAN-2001;
ZymoGenetics, Inc. (US)
                                                                                                                                                                                                                                                                                                    Quality: 1314.50
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Sequence 6 from Patent W00104304.
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951	5 TNTGGGAYGAYYTNGGNGCNYTNTGGGCNTGYCCNATGGAYAAR	90
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409 804	3 euValGluMetLysThr 5 TNYTNGARACNMGNGGN	39 75
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376 704	60 H1sProAsnLeuCysValG1nValSerThrTrpG1uLysValG1nLeuG1 :::::	36 67
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326 605	0 TrpGlnLe	55
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193 237	176 gTyrGlnLysGluLeuAsnLeuThrGlnGlnLeuProAspCysArgGlyL ::: 201 NTAYGARAARGARYTNAAYCAYACNCARCARYTNCCN	2 1
176 200	60 GluAlaSerLeuGlyAlaGluValGlnIleTrpSerTyrThrLysProAr	: :
150	1 CNYTNGTNCARTTYGGNCARWSNGTNGGNWSN	<u> </u>

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Maddonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mienga, V., Morrow, J., Murphy, T., Naylor, J., White, J., Miranda, C., Mienga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Connor, R., Connor, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (01-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 26, 2000 this sequence version replaced gi:7132995. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Galagan,J., Gardyna,S., Ginde,S., Goy
Grand-Pierre,N., Grant,G., Hagos,B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Boguslavkly,L., Boukhgalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collin Collymore,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Boguslavkiy, L., Castle, A., Choepel, Y., Colangelo, M., Col
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 3, clone RP11-481H17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Young, G., Zainoun, J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D.,
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                                                                                                                                                                                                                                                    arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                             Quality co.

NOTE: This is a 'working draft' sequence. It currently consists of 22 contigs. The true order of the pieces is not known and their order in this sequence record is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Assembly program: Phrap; version 0.960731
Consensus quality: 156369 bases at least Q40
Consensus quality: 161786 bases at least Q30
Consensus quality: 163606 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing vector: Plasmid; n/a; %-0.1%% of reads 5.05173463177115Chemistry: Dye-terminator Big Dye; 100% of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing vector: M13; M77815; 95% of reads sequencing vector: Plasmid; n/a; %-0.f%% of reads
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Center clone name: 481_H_17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Insert size: 156000; agarose-fp
Insert size: 164520; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center code: WIBR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality coverage: 4.9 in Q20 bases; agarose-fp
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5655 6844: contig of 1190 bp in length 6845 6944: gap of 100 bp 6945 8557: contig of 1613 bp in length 8558 8657: gap of 100 bp 8658 11247: contig of 2590 bp in length 11248 11347: gap of 100 bp 11348 13427: contig of 2080 bp in length 113428 13527: gap of 100 bp
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|1348. .13427
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142057: contig of 17141 bp
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100510: contig of 24219 bp in
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111192: contig of 10582 bp in
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20876: contig of 3686
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66773: contig of 6876 bp
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76191: contig of 9318 bp in length
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contig of 7187
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	681 uhlaprogly 684
681 73359	667 GlnAlaLeuArgSerAlaLeuAspSerCysThrSerSerSerGl :::: :::
73309	650 lyCysserThrSerAlaGlyArgProAlaAspArgValGluArgValThr::: :::
650 73259	633 uPheSerLeuProThrGlnLeuProAlaPheLeuAghalaLeuGlnglyG : :: ::
73209	617 GlyLeuLeuHisProAspSerValProSerProPheArgValAlaProLe
616 73159	600 spPheLeuGlnGlyArgAlaThrGlyArgTyrValGlyValTyrPheAsp
73109	585GlyProHisAspAlaLeuAlaAlaTrpLeuSerCysValLeuProA
584 73059	570 ValalaGinCysGinGinTrpLeuGinLeuGinThrValGiuPro
1 569 3 73009	553 rg11eLeuGlnGluGlyGlyValValI1eLeuLeuPheSerProAlaAla ::
553 72959	536 gGluLeuSerAlaHisGlyAlaLeuAlaTrpPheHisHisGlnArgArgA
536 72909	520 AlaLeuSerGlnMetProLeuArgValAlaValAspLeuTrpSerArgAr :::
72859	503 isSeralaaspGlyAlaGlyTyrGluArgLeuValGlyAlaLeuAlaSer
1 503	492AlaAlaArgGlySerArgThrAlaLeuLeuLeuH
72762	72713 CGCCCCCGGGGAGCCAGGCCTGTGCCAGCTCACCTCTTCCCCTCCCCATCT
. 491	491
72712	72663 ACAGGACGTCCGCTCGGGGGGTGAGTGGGAGCAAGCGCTGGGCGGAGGGC
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72662	CAGGGTGGCTGAGGCTCTTGA
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72612	72563 GGACCAGAGTGGCTGTGGGAGTTCTCCGAGGGAAAGCGGCGGCCGAGCTC
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S.K., Chauko, J., Chur, C., Cox, Chen, Z., Chowdhry, I., Christoppulos, C., Cleveland, C.D., Cox, Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, Coyle, 
Submitted (03-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (01-NOV-2001) Human Genome Sequencing of Molecular and Human Genetics, Baylor College Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                         Worley, K.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (11-JUN-1999) Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,
Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F.,
Carter,M., Cavazos;S.R., Chavez,J., Chavez,J.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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(Cal Tech Human BAC Library B)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center, Department of Medicine, One
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on Nov 1, 2001 this sequence version replaced g1:16519453 INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email gc-help@bcm.tmc.edu

COMMENT

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones.

Overlapping clones are noted at the beginning and end of the only

NNOTATION OF FEATURES:

ocal mapping efforts a local database that includes STSs are identified using ePCR (Genome Res. 7:541-1 entries from dbSTS, 7:541-550) searches dbSTS, GDB, and

Repeats are identified using RepeatMasker (A. Smit and P. Green

unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not dentical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation

QUALSTAT-REPORT-

Number of N's in consensus :	Number of consensus changing edits:	Fraction of Phrap values less than 40 :	Average error rate (BCM-Phrap estimate):	Phrap values in estimate:	Contig length:	Summary Statistics
0	138	0.0295473	9.71965e-05	166919	168665	

<u>11-0</u>	0 00 0 00 0 00	857	80 00 05 05 05 05	851	850	847	841	8111	802	784	780	759	756	744	737	732	705	Position
ntnancnann(n)ngtctccann	nnntnancna(n)nnngtctcca	nannntnanc(n)annnngtctc	ttcanannnt(n)ancnannnngtc	ntttcanann(n)tnancnannn	gntttcanan(n)ntnancnann	cgggntttca(n)annntnancn	tagagacggg(n)tttcanannn	cnacgcccgg(n)taatttttg	tgcacaccac(n)acgcccggnt	agtagcnggg(n)ctacaggtgc	tcccagtagc(n)gggnctacag	tgccattntc(n)tgcctgagcc	tcatgccatt(n)tcntgcctca *	cgcntcccgg(n)ttcatgccat	caagcnccgc(n)tcccggnttc	cactgcaagc(n)ccgcntaccg	ctggagtgca(n)tggcgcgatc	Original+Context
gttagccaa(g)atggtctcaat	gtgttagcca(a)gatggtctca	cagtgttagc(c)aagatggtct	ttcacagtgt(t)agccaagatg	gtttcacagt(g)ttagccaaga	<pre>ggtttcacag(t)gttagccaag</pre>	cggggtttca(c)agtgttagcc	tagagacggg(g)tttcacagtg	ccacgcccgg(c)taatttttg	tgcacaccac(c)acgcccggct	agtagctggg(a)ctacaggtgc	tcccagtagc(t)gggactacag	tgccattctc(c)tgcctcagcc	tcatgccatt(c)tcctgcctca	cgcctcccgg(g)ttcatgccat	caageteege(e)teeegggtte	cactgcaagc(t)ccgcctcccg	ctggagtgca(g)tggcgcgatc	Edited+Context

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lignment_block:
JS-09-899-471-5 x AC007783/rev
                                                                                                           Align seg 1/1 to reverse of: AC007783 from: 1 to: 168665
                                 338 lProProValProGlnLysAsnAlaThrValAsnGluProGlnAspPheG 355
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18305
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53988
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2.663
55.319
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ccctcccctc(n)nnttccccct
cctcccctcn(n)nttccccctt
ctcccctcnn(n)ttcccccttt
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ccgcctnnca(n)cccaaggnnt
nncancccaa(g)gnntngggnt
cancccaagg(n)ntngggntan
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ancnannnng(t)ctccannccc
ncnannnngt(c)tccanncccc
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tttttcaaga(n)ggagtctcac
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gcctggctaa(n)tttttttt
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aggctgatct(n)gaactcctga
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gggntannnn(n)nttnagccnn
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gnntngggnt(a)nnnnnnttna
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                                                                                                                                                                                                        Length: 470
Gaps: 14
Percent Identity: 39.574
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gcgtgagcca(c)cgtgcctggc
cgtgagccac(c)gtgcctggc
aggctgatct(t)gaactcctga
ctggcgtggt(g)gtgggcct
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gggattacag(g)cgtgagccac
ggattacagg(c)gtgagccacc
gattacaggc(g)tgagccaccg
ttacaggcgt(g)agccaccgtg
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ctgacctcgt(g)atctgcccgc
tgacctcgtg(a)tctgcccgcc
gacctcgtga(t)ctgcccgcct
acctcgtgat(c)tgcccgcctt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cgiggiggig(g)gcgcctgtag
gtggtggtgg(g)cgcctgtagt
gcctggctaa(t)ttttttttt
                                                                                                                                                                                                                                                                                                                                                           ctccctcc(c)ctcccctt
                                                                                                                                                                                                                                                                                                                       tcccctcccc(c)tccccctttc
tttattttt(a)tttaattaat
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tgctgggatt(a)caggcgtgag
gctgggatta(c)aggcgtgagc
ctgggattac(a)ggcgtgagc
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ccgccttgcc(a)cccaaagtgc
tgccacccaa(a)gtgctgggat
ccacccaaag(t)gctgggatta
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ctcaatctcc(t)gacctcgtga
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agccaagatg(g)tctcaatctc
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tttttcaaga(c)ggagtctcac
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ctgcccgcct(t)gccacccaaa
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536 gGluLeuSerAlaHisGlyAlaLeuAlaTrpPheHisHisGlnArgArgA 553	Ū
520 AlaLeuSerGlnMetProLeuArgValAlaValAspLeuTrpSerArgAr 536 :::	52 13
503 isSeralaaspGlyAlaGlyTyrGluArgLeuValGlyAlaLeuAlaSer 519 	. — σ
492 AlaAlaArgGlySerArgThrAlaLeuLeuLeuH 503	44 (4
9285 CGCCCCCGGGGAGCCAGGCCTGTGCCAGCTCACCTATTCCCCCATCT 9	Ñ
9335 ACAGGACGTCCGCTCGGGGGGTGAGTGGGAGCAAGCGCTGGGCGGAGGGC 99286	a– ω
491 491	
9385 ACTGGCTGCCTCCGCCCCTCCCCTAACAGGGTGGCTGAGGCTCTTGAA 9	9938
	49
9435 GGACCAGAGTGGCTGTGGGAGTTCTCCGAGGGAAAGCGGCGGCCGAGCTC 5	9943
491 491	49
487 ysaspargarglys	9948
470 uAla¢ysLeuLeuLeuAlaAlaAlaLeuPhePhePheLeuLeuLysL 487 	UI A
9570 CCAGACATCCACAAGCGCTGGGCCTCGTGTGGCT 99	CS 4
A5A Alanus Drown the table transfer of the tra	١.
445	4 12
438HisGInCysMetGInLeuTrp. 444	4 0
422 ThrargalaalaargLeuGlyGluGluLeuLeuGlnaspPheargSer 437 ::: ::	7
405 alCysAlaLeuGluProSerGlyCysThrProLeuProSerMetAlaSer 421 ::: ::: 19737 AGGATGGTCTTGAT	4 1
388 saspaspmetLeuLeuValGluMetLysThrGlyLeuAsnasnThrSerV 405 :::::	-Ū ω
372 LysvalGlnLeuGlnAlaCysSerTrpAlaAspSerLeuGlyProPheLy 388 ::	ത ധ
355 InLeuValAlaGlyHisProAsnLeuCysValGlnValSerThrTrpGlu 371 ::	35 9984
	9989

	uAlaProGly 684 CGCGCCGGGA 98629	681 98638
681 98639	GlnAlaLeuArgSerAlaLeuAspSerCysThrSerSerSerGl::: :::	667 98688
98689	lyCysSerThrSerAlaGlyArgProAlaAspArgValGluArgValThr::: ::: ::::	650 98738
650 98739	uPheSerLeuProThrGlnLeuProAlaPheLeuAspAlaLeuGlnGlyG: :::	633 98788
633 98789	GlyLeuLeuHisProAspSerValProSerProPheArgValAlaProLe ::: ::: 	617 98838
616 98839	SpPheLeuGlnGlyArgAlaThrGlyArgTyrValGlyValTyrPheAsp 	88886 009
98889	GlyProHisAspAlaLeuAlaAlaTrpLeuSerCysValLeuProA :::	585 98938
58 4 98939	ValAlaGlnCysGlnGlnTrpLeuGlnLeuGlnThrValGluPro	570 98988
569 98989	rgIleLeuGlnGluGlyGlyValValIleLeuLeuPheSerProAlaAla ::	553 99038
99039	99088 TGAACTGAGCGCGCAGGGGCCCGTGGCTTGGTTTCACGCGCAGCGGCGCC	99088

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tabase: Issued_Patents_NA:*
tabase sequences: 383533
tabase length: 122816752
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ery length: 698
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QGAPOP-4.500 -QGAPEXT-0.050 -XGAPOP-10.000 -XGAPEXT-0.500
FGAPOP-6.000 -FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500
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0-/cgn2_1/USPT0_spco1/US09899471/runat_27092002_142439_17925/app_query.fasta_1.2519
DB-Issued_Patents_NA -OPMT-fastap -SUFFIX-rni -GAPOP-12.000
DB-Issued_Patents_NA -OPMT-fastap -SUFFIX-rni -GAPOP-17.000
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NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
USER=US09899471_@CGN1_1_132 -NCPU=6 -ICPU=3 -LONGLOO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of: US-09-899-471-5 to: Issued_Patents_NA:*
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RANS-human40.cd1 -LIST-45 -DOCALIGN-200 -THR_SCORE-pct
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                                    ptodata/2/1na/6B_COMB.seq:US-09-382-911-5 +
ptodata/2/1na/5A_COMB.seq:US-08-404-354B-1-
ptodata/2/1na/5A_COMB.seq:US-08-314-093B-1-
/ptodata/2/1na/5A_COMB.seq:US-08-435-655B-1-
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/ptodata/2/1na/5A_COMB.seq:US-08-336-257A-3-
/ptodata/2/1na/5A_COMB.seq:US-08-342-930-1+
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                                                                                                                                                                                                       /ptodata/2/ina/6B_COMB.seq:US-09-184-445-2
/ptodata/2/ina/5B_COMB.seq:US-08-841-483-3
                                                                                                                                                                                                                                            /ptodata/2/ina/5B_COMB.seq:US-09-060-836-
                                                                                                                                                                                                                                                                                /ptodata/2/ina/5B_COMB.seq:US-08-7
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                                                                                                                                                                                          /ptodata/2/ina/6B_COMB.seq:US-09-382-9
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GCCCTTTTGATACC
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/cgn2_6/ptodata/2/1na/6B_COMB.seq:US-09-103-840A-1
/cgn2_6/ptodata/2/1na/6B_COMB.seq:US-08-785-420-1
/cgn2_6/ptodata/2/1na/6B_COMB.seq:US-08-943-731-5 +
/cgn2_6/ptodata/2/1na/5A_COMB.seq:US-07-960-389-1 +
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APPLICANT: Strachan, Lorna
APPLICANT: Steeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: compositions In
TITLE OF INVENTION: and Methods Fo
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SEQ ID NO 226
LENGTH: 2165
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NUMBER OF SEO ID NOS: 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 laSerLeuGlnAlaGlnValValLeuSerPheGlnAlaTyrProIleAla 131
                                                                                                                                                                                                                                                        99 ProGluGluAlaGlyLys.SerAspSerGluLeuGlnGluSerArgAsnA 115
                                                                                                                                                                                                                  TGCCCGAGGTGCAGGCTGTTCGGGTGACTATTCCTGCAGGCCCCAAGGCC
                                                                                                                                                                                                                                                                                                                GTCACAAAAGTGTGGAGGACCTGAA.....TTCTCCTTTGATTTGC
                                                                                                                                                                                                                                                                                                                                                          y...GlnSerValGlySerAlaValPheAspCysPhgGluAlaSerLeuG 164
hraspGlyaspAsnValLeuLeuThrLeuAspValSerGluGluGlnAsp
                                                                               pSerIleGlnSerCys.....TrpValLeuProTrpLeuAsnValSerT
                                                                                                                                                                               LeuAsnLeuThrGlnGlnLeuProAspCysArgGlyLeuGluValArgAs
                                                                                                                                                                                                                                                                                                                                                                                                           AGGGCCCAGCCTTCAGCTGCAGAAGGAAGAAGAACATCTCCCTGAAGCAGG
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                                            . AGTGTGCGCCTTTGTTATCAGTGGGCACTGGAATGTGAAGACTTGAGTA
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o. 6150502
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Percent Identity:
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For Their Use
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2.5e+04
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	APPLICATION UMBER: US/08/620,694A ETIING DATE: 21 MARCH 1996
	COMPUTER: Apple Powe OPERATING SYSTEM: Apsocration of the soft of
	ZIP: 98101 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
	TATE: WA
11-1/	JENCES: 10 E ADDRESS:
	APPLICANT: Yao, Zhengbin APPLICANT: Spriggs, Melanie APPLICANT: Fanslow, William
	eq_documentation_block: Sequence 1, Application US/08620694A Patent No. 5869286 GENERAL INFORMATION:
,-	eq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-620-694A-1
	669 euArg\$erAlaLeuAspSerCysThrSerSerSerGluAlaPro 683 ::: :: ::: 1859 TTGAGGCTGCCAAAGATGACTACCAAGGCTCAACCAATAGTCCC 1902
669 1858	656 yArgProAlaAspArgValGluArgValThrGlnAlaL
656 1808	646 AlaLeuGlnGlyGlyCysSerThrSerAla
645 1758	629 rgValAlaProLeuPheSerLeuProThrGlnLeuProAlaPheLeuAsp ::: ::: ::: :::
629 1708	612 yValTyrPheAspGlyLeuLeuHisProAspSerValProSerProPheA :::
612 1658	596 CysValLeuProAspPheLeuGlnGlyArgAlaThrGlyArgTyrValGl
595 1632	579 euGlnThrValGluProGlyProHisAspAlaLeuAlaAlaTrpLeuSer
1584	1557 GCTCCTGTGGAACTGTGCGGGTCCCAGC
5 6	TrpPheHisHisGlnArgArgArgIleLeuGlnGluGlyGlyValVa
545 1506	529 laValAspLeuTrpSerArgArgGluLeuSerAlaHisGlyAlaLeuAla
529 1456	515 yAlaLeuAlaSerAlaLeuSerGlnMetProLeuArgValA
1406	1357 GTTTTACTCCTACATGCAGCGGACTCAGAGGCACAGCGACGCCTGGTGGG

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NAME/KEY:
LOCATION:
S-08-620-694A-1
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JS-09-899-471-5 x US-08-620-694A-1
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Ratio:
ercent Similarity:
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                               243 sSerLeuTrpTyr.....Lys&snLeuThr.....GlyProGlnAsnI 256
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ORGANISM: Mouse
STRAIN: HVS13 receptor
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PRIOR APPLICATION NUMBER: 1
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MOLECULE TYPE: CD
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PRIOR APPLICATION DATA:
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                         CysLeuCysIleGlnValTrpSerLeuGluProAsp.....
                                                                                                                                                    TGACAGCTGGATCCACCCCAAAAACCTGACCCCGTCTTCCCCCAAAAAAACA
                                                                                                                                                                                                                                                                         TGGCCCGGGCCGCGCCCCCGCGCTCCTCGACTTCCCGGCTCCCGGTC 246
                                                                                                                    TGCGCGCAGGAGGGGCTGAGCTGCAGAGTCAAGAATAGTACTTGTCTGGA 296
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                            TGGACCCTGCAGACAGATGCCAGCATCCTGTA 443
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Gaps: 32
Percent Identity: 20.763
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.....SerGluArg. 280
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491 1187	PhePheLeuLeuLeuLysLysAspArgArgLy	481 1138
480 1137	alLeuValTrpLeuAlaCysLeuLeuLeuAlaAlaAlaLeuPhe	466 1088
466 1087	ProMetAspLysTyrIleBisArgArgTrpV	456 1041
1040	CTAAATGACTGTTTGAGACACGCTGTGACTGTGEGGTGCCCAGTAATCTC	991
آف ا	ACTGGTGCTGCCATCACCACGTGCAGGTCCAGCCCTTCTTCAGCAGCTGC	
455	TrpAlaCys	453
452 940	rgSerHisGlnCysMetGlnLeuTrpAsnAspAspAsnMetGlySerLeu ::::::::::::::::::::::::::::::::::::	436 891
890	CALGSELINIAL GALGALGARG LEUGLYGLUGLULEULGLASPENEA: :::	841
840	GAATGAATCCACCCCTACCAGGTCCTGGAAAGTTTCTCCGACTCA	791
419	ALTICACCETOR ACTICACCETOR ACTICACCETOR ACTICACCETOR	.407
406	spMetLeuLeuValGluMetLysThrGlyLeuAsnAsnThrSerValCy	390
778	GACACACACATCTGCGAGTGG	757
390	IGInLeuGlnAlaCvsSerTrpAlaAspSerLeuGlvProPheLvsAspA	373
7	COURT A COURT OF THE COURT OF T	370 707
706	::: ::: CATCTTTGTGCCTGACTGTGAG	657
369	roAsnLeuCysValGlnValSer	361
361 656	ASn.AlaThrValAsnGluProGlnAspPheGlnLeuValAlaGlyHisP:::	345 634
344 633	laProAspGlnSerProCysGlnProLeuValProProValProGlnLys ::	328 604
0	CAGGAGTATGAAGTGACTGTT	583
328	nLeuAspAlaProCysCysLeuProGlyLysValT	311
311 582	5 LeuTrpHisIleAlaArgLeuArgValLeuSerProGlyValTrpGl	296 541
295 540	1 ValGluPheCysProPheArgGluAspProGlyAlaHisArgAsn	281 494
493	+ CCTCGAGGGTGCAGAGCTGTCCGTCCTGCAGCTGAACACCAATGAGCGGC	444

491 sAlaAlaArgGlySer..

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9q_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-022-255-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   664 ArgValThrGlnAlaLeuArgSerAlaLeuAspSerCysThrSerSerSe 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          650 lyCysSer......ThrSerAlaGlyArgProAlaAspArgValGlu 663
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                                                                   CORRESPONDENCE ADDRESS:
                                                                                                      APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17
                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                      PPLICANT:
                        STREET:
                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AlaAlaTrpLeuSerCysValLeuProAspPheLeuGlnGlyArgAlaTh 607
                                                                                                                                                                                                                                                                                                                                                                                 CAGTGCCCCG 1876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTGGCCGGCAGCTCAAGGAGGCTGTGCTTAGGTTCCAGGAGTGGCAAACC 1866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GATGCACCATGTCAGAGAGCTCACAGGGGACAATTACCTGCAGAGCCCTA 1816
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rGlyArgTyrValGlyValTyrPheAspGlyLeuLeuHisProAspSerV 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTGCAGCCATGAACATGATCCTGCCAGACTTCAAGAGGCCCAGCCTGCTT 1616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CACCCCTCTATGTGGAGGTGGTCCTAAAGTTCGCCCAGTTCCTGATCAC 1337
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Seattle
                 E: Immunex Corporation
51 University Street
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (206)
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
224 erGluGluGlnAspPheSerPheLeuLeuTyrLeuArgProValPro... 239
                                                                                                                                                                                          174
                                                                                                                                                                                                                                                   124 GCGATTCGGCGCTGCTGGCCACGGGTCGTCCCCGGGCCCCCTGGGATG
                                                                                                                                                                                                                                                                                            198 SerIleGlnSerCysTrp....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 7 AUGUST 1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 23 MARCH 19
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: USSN 0
FILING DATE: 21 MARCH 1996
APPLICATION NUMBER: USSN 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                        pLeuAsnValSerThrAspGlyAspAsnValLeuLeuThrLeuAspValS 224
                                                   TGCGCGCAGGAGGGCTGAGCTGCAGAGTCAAGAATAGTACTTGTCTGGA 296
                                                                                                                      TGGCCCCGGGCCGCCTCCCCGCGCTCCTCGACTTCCCGGCTCCGGTC 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
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42.290
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23 MARCH 1995
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                                                                                  .AspAlaLeuLy
                                                                                    243
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<pre>seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-022-696-1</pre>	680 rGluAlaPro 683 ::: 1867 CAGTGCCCCG 1876	19CysSerThrSerAlaGlyArgPressiaAspArgValGlu 663	624 alProSerProPheArgValAlaProLeuPheSerLeuPro.ThrGlnLe 640 ::: :::::::::::::::::::::::::	607 rGlyArgTyrValGlyValTyrPheAspGlyLeuLeuHisProAspSerV 624	591 AlaAlaTrpLeuSerCysValLeuProAspPheLeuGlnGlyArgAlaTh 607 ::: ::::::::::::::::::::::::::::::::	574 lnGlnfrpLeuGlnLeuGlnThrValGluProGlyProHisAspAlaLeu 590 ::::: ::: ::: ::: :::	567	556 GlnGluGlyGlyValValIleLeuLeuPheSer	539 erAlaHisGlyAlaLeuAlaTrpPhcHisHisGlnArgArgArgIleLeu 555 	-522 rGlnMetProLeuArgValAlaValAspLeuTrpSerArgArgGluLeuS 539 ::: ::: 1338 TGCCTGTGGCACTGAAGTAGCCCTTGACCTCCTGGAAGAGCAGGTTATCT 1387	507 GlyalaGlyTyrGluArgLeuValGlyAlaLeuAlaSerAlaLeuSe 522	497 ArgThrAlaLeuLeuLeuHisSerAlaAsp 506	491 salaalaargGlySer	481 PhePheLeuLeuLeuLysLysAspArgArgLy 491 ::::::	466 alLeuValTrpLeuAlaCysLeuLeuLeuAlaAlaAlaLeuPhe 480

seq_documentation_block:
; Sequence 1, Application US/09022696

991 CTAAATGACTGTTTGAGACACGCTGTGACTGTGCCCTGCCCAGTAATCTC 1040

455

453 ..TrpAlaCys.....

941 ACTGGTGCTGCCATCACCACGTGCAGGTCCAGCCCTTCTTCAGCAGCTGC 990

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890

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757 GACACACAGCATCTGCGAGTGG......778

756

390 spMetLeuLeuValGluMetLysThrGlyLeuAsnAsnThrSerValCys 406

.....ACTTCACCCTGT 790

634 GACCCAAACCACAATCCA.....AGAT 656 328 laProAspGlnSerProCysGlnProLeuValProProValProGlnLys 344

604CACCACCTGCCGAAGCCCATCCCTGATGGG 633

541 CGGTGGCGGTTTTCCTTCAGCCACTTTGTGGTAGATCCTGGC..... 582

540

.....SerGluArg. 280

311 nLeuAspAlaProCysCysLeuProGlyLysValThrLeuCysTrpGlnA 328

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207 pLeuAsnValSerThrAspGlyAspAsnValLeuLeuThrLeuAspValS 224	198 SerIleGlnSerCysTrpValLeuProTr 207 ::: ::: 124 GCGATTCGGCGCTGCTGGCCACGGGTCGTCCCCGGGCCCGCGCTGGGATG 173	lign seg 1/1 to: US-09-022-696-1 from: 1 to: 3288	lgnment_block: S-09-899-471-5 x US-09-022-696-1	lgnment_scores: Quality: 184.50 Ratio: 0.666 Gaps: 32 ercent Similarity: 42.290 Percent Identity: 20.763	NAME/REY: CDS LOCATION: 1212715 -09-022-696-1	ORGANISM: Mouse STRAIN: HVS13 receptor	ICAL: NO SE: NO	രെ	ğg	ID NO:	NE: (206)	DOCKET NUMBER:	ATTURNEY/AGENT INFORMATION: NAME: Perkins, Patricia Anne REGISTRATION NUMBER: 34.695	23 MARCH 1995 ON:	LICATION NUMB	PRIOR ADDITION: DRIOR ADDITION:	, 696	OPERATING SYSTEM: Apple Operating System 7.5.5 SOFTWARE: Microsoft Word for Apple, Version 6.0.1	PE: Floppy di	Y: USA 98101	WA	음날	TITLE OF INVENTION: NO. 6072037el Receptor That Binds IL-17 NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS:	APPLICANT: YaO, ZNENGDIN APPLICANT: Spriggs, Melanie APPLICANT: Fanslow, William	072037 ORMATIC

94	SGAAGAATTCCATCAGCGAGCTAATGTCACATTCACTCTAAGCAAGTTTC	891
5	gSerHisGlnCysMetGlnLeuTrpAsnAspAspAsnMetGlySerLe	436
4 3	tAlaSerThrArgAlaAlaArgLeuGlyGluGluLeuLeuGlnAspPheA : :::: ::: : ::: :	419 841
41 84	AlaLeuGluProSerGlyCysThrProLeu ProSerMe	407 791
79) TIC	779
40	rservalcy	390
77	CACACAGCATCTGCGAGTGG	757
39	ysSerTrpAlaAspSerLeuGlyProPhe	373
75	AGACCT	707
37	TrpGluLys	7
70	TOASTHEUCYS VALIGITY ALL SETTIFF. THEOTOGRAPH TOASTHEUCYS VALIGITY ALL SETTIFF. THEOTOGRAPH TOASTHEUCYS VALIGITY ALL SETTIFF. TOASTHEUCYS VALIGITY ALL SETTIFF. TOASTHEUCYS VALIGITY ALL SETTIFF.	707
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36	n.AlaThrValAsnGluProGlnAspPheGlnLeuValAlaGlyH1s 	
63	AAGCCCATCCCTGATGGG	604
34	euValProProValProGlnLys	328
90	CAGGAGTATGAAGTGACTGTT	583
3 0		211
5 O D	eAlaArgLeuArgValLeuSerProGlyValTrpGl ::::: ::::::::::::::::::::::::::::::	296
54	TCAAGTTCCAGTTTCTGTCCATGCTGCAGCATCACCGT	
29	GluPheCysProPheArgGluAspProGlyAlaHisArgAs :::	281
49	CCTCGAGGGTGCAGAGCTGTCCGTCCTGCAGCTGAACACCAATGAGCGGC	444
28	erGluAr	278
44	CYSLEUCYSLEGINVAITIPSETLEUGINFOASP	397
39	TATATCAATCTTAGTGTTTCCTCTACCCAGCACGGAGAATTAGTCCCT	
26	eThrLeuAsnHisThrAspLeuValPro	
34	TGAC	297
25	erLeuTrpTyrLysAsnLeuThrGlyProGlnAsn	243
29	ര് –	247
24	AspalaLe	240
24	GACTTCCC	197
23	erGluGluGlnAspPheSerPheLeuLeuTyrLeuArgProValPro	224

991 CTAAATGACTGTTTGAGACACGCTGTGACTGTGCCCTGCCCAGTAATCTC 1040

941 ACTGGTGCTGCCATCACCACGTGCAGGTCCAGCCCTTCTTCAGCAGCTGC

990 455

..TrpAlaCys.....

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    664 ArgValThrGlnAlaLeuArgSerAlaLeuAspSerCysThrSerSerSe 680
                                        GATGCACCATGTCAGAGAGCTCACAGGGGACAATTACCTGCAGAGCCCCTA 1816
                                                                                                                                                                                                                                        alProSerProPheArgValAlaProLeuPheSerLeuPro.ThrGlnLe 640
                                                                                                                                                                                                                                                                                                                                                                                                 AlaAlaTrpLeuSerCysValLeuProAspPheLeuGlnGlyArgAlaTh 607
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                                                                                                                        GAGGAGGTTTACTTCCGGATCCAGGACCTGGAGATGTTTGAACCCGGCCG 1766
                                                                                                                                                                                                 TCCCCGACCTCTTCAACATCACCTCCAGGTACCCACTCATGGACAGATTT 1716
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACATGGTGATGACTCCAAAATCAATGGCATCTTGCCCGTAGCAGACCTGA 1237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .....ArgThrAlaLeuLeuLeuHisSerAlaAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .....ProMetAspLysTyrIleHisArgArgTrpV
                                                                               .ThrSerAlaGlyArgProAlaAspArgValGlu 663
                                                                                                                                                                                                                                                                                                                                                                                                                                        .....AAGCCTGCT...GGGGACCTTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .....ProAlaAlaValAlaGlnCysG 574
                                                                                                                                                                                                                                                                                 1666
                                                                                                                                                                                                                                                                                                                      624
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                                                                             alignment_block:
US-09-899-471-5
                                                                                                                                                                                                                                                        ; NAME/KEY:
; LOCATION:
US-08-978-773-1
                                                                                                                                                                                               alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
                                        Align seg 1/1
                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Applica
Patent No. 6083906
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: NO ORIGINAL SOURCE: ORGANISM: MOU
                                                                                                                                                                                                                                                                                                                      FEATURE:
198 SerIleGlnSerCysTrp..
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION:
                                                                                                                                                                           Quality:
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                                                                                                                                                           Ratio:
                                        6
                                                                             x US-08-978-773-1
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                                        US-08-978-773-1
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O
                                                                                                                                    184.50
0.666
42.290
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1667

Percent Identity:

655 32 20.763

from:

6

..ValLeuProTr

1617

607

591

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seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-978-773-1
                                                                                                                                                                                                                                                                                 TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1867 CAGTGCCCCG 1876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1817 GTGGCCGGCAGCTCAAGGAGGCTGTGCTTAGGTTCCAGGAGTGGCAAACC 1866
                                                          IMMEDIATE SOURCE:
CLONE: IL-17 receptor
                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Troutt, Anthony
TITLE OF INVENTION: Method of Regulating Nitric Oxide Production
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      680 rGluAlaPro 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: USSN 60/052,525
FILING DATE: 27 NOVEMBER 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: Ap
OPERATING SYSTEM: Ap
                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                 : 3288 base pairs
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/08978773
                                                                                                                                                                                                                                                                                                                                                                                                                                      Perkins, Patricia Anne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Immunex Corporation
In the street
CDS
121..2712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Apple PowerMacintosh
SYSTEM: Apple Operating System 7.5.5
                                                                                                                                                                                                                                                                                                                                                        (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
                                                                                                                                                                                     cDNA to mRNA
                                                                                                                                                                                                                              single
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                                                                                                                                                                                                                                                                                                                                                                                                                34,693
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36	tAlaSerThrArgAlaAlaArgLeuGlyGluGluLeuLeuGlnAspPheA 4 ::::	419
40	: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::: :::: :::: :::: :::: :::: :::: :::: ::::! ::::! ::::! :::::! :::::! ::::::! ::::::	79
419	AlaLeuGluProSerGlyCysThrProLeuProSerMe	407
406 790	90 spMetLeuLeuValGluMetLysThrGlyLeuAsnAsnThrSerValCys 4	77
78	GACACACAGCATCTGCGAGTGG7	75
390	<pre>IGlnLeuGlnAlaCysSerTrpAlaAspSerLeuGlyProPheLysAspA ::: ::: </pre>	
156		707
173	GluLysVa 3	37
369 706	roAsnLeuCysValGlnValSerThr	361 657
556	GACCCAAACCACAAATCCA	ŝ
361	Asn.AlaThrValAsnGluProGlnAspPheGlnLeuValAlaGlyHisP	345
533	:::	604
776	laProAspGlnSerProCysGlnProLeuValProProValProGlnLvs	32
328 603	euAsPAlarroCysCysLeuProGIyLysValThrLeuCysTrpGlnA (::: CAGGAGTATGAAGTGAGTGTT	583
582	CGGTGGCGGTTTTCCTTCAGCCACTTTGTGGTAGATCCTGGC) 4 L
311	LeuTrpHisIleAlaArgLeuArgValLeuSerProGlyValTrpGl	296
540	TGTGTGTCAAGTTCCAGTTTCTGTCCATGCTGCAGCATCACCG	494
295	ValGluPheCysProPheArgGluAspProGlyAlaHisAr	281
193	CCTCGAGGGTGCAGAGCTGTCCGTCCTGCAGCTGAACACCAATGAGCGGC	444
280	8SerGluAr	27
277 443	CysLeuCysIleGlnValTrpSerLeuGluProAsp	266 397
396		347
265	leThrLeuAsnHisThrAspLeuValPro	256
346	TGACAGCTGGATCCACCCCAAAAACCATGACCCCGTCTTCCCCAAAAAAACCA	297
, i	SSerLeuTroTvrLvsAsnLeuThr GlvProGlnAsnT	243
243	TGCGCGCAGGAGGGCTGAGCTCAAGAATAGTACTTGTCTGCA	240
246	TGGCCCCGGGCCGCCCCCCCGCGCCTCCACTTCCCGGCTCCGGTC	197
239	erGluGluGlnAspPheSerPheLeuLeuTyrLeuArgProValPro	22
22 4 196	PLEUASDValSerThrAspGlyAspAsnValLeuLeuThrLeuAspValS 	174
173	GCGATTCGGCGCTGCTGGCCACGGGTCGTCCCCGGGCCCGCGCTGGGATG	12
	-	

650 1766	uProAlaPheLeuAspAlaLeuGln	640 1717
640 1716	alProserPropheArgValAlaProLeuPheSerLeuPro.ThrGlnLe	624 1667
624 1666	rGlyArgTyrValGlyValTyrPheAspGlyLeuLeuHisProAspSerV 	607 1617
607 1616	AlaAlaTrpLeuSerCysValLeuProAspPheLeuvInGlyArgAlaTh ::: ::::::::::::::::::::::::::::::::	591 1567
590 1566	InGlnTrpLeuGlnLeuGlnThrValGluProGlyProHisaspAlaLeu :::: ::: ACCACTGGAAGCCTGCTGGGAACCTTTTC	574 1538
574 1537	GTGGAAAGCTATCTTGGGTTGGGCTGAGCCTGCTGTCCAGCTACCGTGTG	567 1488
566 1487	GlnGluGlyGlyValValIleLeuLeuPheSer	556 1438
555 1437	erAlaHisGlyAlaLeuAlaTrpPheHisHisGlnArgArgArgIleLeu	539 1388
539 1387	rGlnMetProLeuArgValAlaValAspLeuTrpSerArgArgGluLeuS:::::::::::::::::::::::::::::::::::	522 1338
522 1337	GlyAlaGlyTyrGluArgLeuValGlyAlaLeuAlaSerAlaLeuSe	507 1288
.506 1287	CTCCCCCCACCCCTGAGGCCCAGGAAGGTCTGGATCGTCTACTCGGCCGAC	497 1238
496 1237	SAlaahaargGlySer	491 1188
491 1187	PhePheLeuLeuLeuLysLysAspArgArgLy ::::::	481 1138
480 1137	alLeuValTrpLeuAlaCysLeuLeuLeuAlaAlaAlaLeuPhe	466 1088
1087	AAATACCACAGTTCCCAAGCCAGTTGCAGACTACATTCCCCTGTGGG	456 1041
0	CTAAATGACTGTTTGAGACACGCTGTGACTGTGCCCCTGCCCAGTAATC	ō
σι		455
4:55	TypAlaCys	453 941
452 940	rgSerHisGlnCysMetGlnLeuTrpAsnAspAspAsnMetGlySerLeu ::::::::::::::::::::::::::::::::::::	436 891
89	GAGAACCACAGCTGCTTTGATGTCGTTA	841

LOCATION: 1212715 \$-09-022-253-1
CDs
STRAIN: HVS13 receptor
ORIGINAL SOURCE:
ANTI-SENSE: NO
TOPOLOGY: linear
c acid
LENGTH: 3288 base pairs
N FOR SEQ ID NO:
: (206)
TELEPHONE: (206)587-0430
BER: 34,69
NAME: Perkin
ATTORNEY /AGENT INFORMATION:
3 MARCH 1995
NSSU
PRIOR APPLICATION DATA:
AUGUST 199
ATION NUMBER: USSN
FILING DATE: 21-MARCH-1996
TION DATA:
ILING DATE:
APPLICATION NUMBER: US/09/022.253
ARE: Microsoft Word for Apple
SYSTEM: Apple Operating Sy
ER: Apple Powe
MEDITA TYPE: Floory Aisk
98101
OUNTRY
STATE: WA
CITY: Seattle
ADDRESSEE: Immunex Corporation
NDENCE ADDRESS
NUMBER OF SEQUENCES: 10
TOTAL TRANSPORT OF SOME SOME SOME SOME SOME SOME SOME SOME
: Spriggs,
CANT:
GENERAL INFORMATION:
equence 1, Appl
ed documentation block.
eq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-022-253-1
1867 CAGTGCCCCG 1876
:::::::::::::::::::::::::::::::::::::::
680 rGluAlaPro 683
1817 GTGGCCGGCAGCTCAAGGAGGCTGTGCTTAGGTTCCAGGAGTGGCAAACC 1866
oomatgyarrncunataLeuArgSerAlaLeuAspSerCysThrSerSerSe 680
ysSerThrSerAlaG

707 GCGTGAGCTCAGGCAGCCTTTGGGATCCCAACATC	61 roAsnLeuCysValGlnValSerThr ::: ::: 57 CATCTTGTGCCTGACTGTGAGGACAGC	345 Asn.AlaThrValAsnGluProGlnAspPheGln::: ::: 634 GACCCAAAACCACAAATCCA	328 laProAspGlnSerProCysGlnProLeuValPro	511 nLeuAspAlaProCysCysLeuProGlyLysValThrLeuC ::: % ::: 583CAGGAGTATGAAGTGACTGTT	LeuTrpHisIleAlaArgLeuAr	TGTGTGTCAAGTTCCAGTTTCTGTCCATGCT	CCTCGAGGGTGCAGAGCTGTCCGTCCTGCAGCTG	9 6	256 leThrLeuAsn	243 SSErLeuTrpTyrLysAsnLeuThrGlyProGlnAsnI :::	247 TGCGCGCAGGAGGGGCTGAGCTGCAGAGTCAAGA	224 erGluGluGlnAspPheSerPheLeuLeuTyrLeuArgProValPro	207 pLeuAsnValSerThrAspGlyAspAsnValLeu 	198 SerileGinSerCysTrp	Align seg 1/1 to: US-09-022-253-1 from:	alignment_block: US-09-899-471-5 x US-09-022-253-1	Percent Similarity: 42.290 Percent Iden
TrpGluLysVa 373		pPheGlnLeuValAlaGlyHisp 361	GInProLeuValProprovadProGlnLys 344 ::: Sil ::: ::: CACCACCTGCCGAAGCCCATCGTGGG 633	ThrLeuCysTrpGlnA 328	ProGlyValTrpGl 31 CCTGGC58	TOGLYAlaHisArgAsn 295	SerGluArg. 280 ::: GAACACCAATGAGCGGC 493	ASP	HisThrAspLeuValPro 26 ::: CACGGAGAATTAGTCCCT 39	GlyProGlnAsnI 25 ::: ::: GTCTTCCCCAAAAAACA 34	AGTCAAGAATAGTACTTGTCTGGA 29	yrLeuArgProValPro 23 ::: TCGACTTCCCGGCTCCGGTC 24	nValLeuLeuThrLeuAspValS 22		: 1 to: 3288		Gaps: 32 lentity: 20.763

373 lGlnLeuGlnAlaCysSerTrpAlaAspSerLeuGlyProPheLysAspA 390

591	574 1538	567 1488	556 1438	539 1388	522 1338	507 1288	497 1238	491 1188	481 1138	466 1088	456 1041	991	455	453 941	436 891	419 841	407 791	390 779	57
AlaAlaTrpLeuSerCysValLeuProAspPheLeuGlnGlyArgAlaTh 6 :::, :::::: :::	InGlnTrpLeuGlnLeuGlnThrValGluProGlyProHisAspAlaLeu 5 ::::		GlnGluGlyGlyValValIleLeuLeuPheSer	erAlaHisGlyAlaLeuAlaTrpPheHisHisGlnArgArgArgIleLeu 5 	rGlnmetProLeuArgValAlaValAspLeuTrpSerArgArgGluLeuS 5 : :: :::::::: ::: ::: :::	GlyAlaGlyTyrGluArgLeuValGlyAlaLeuAlaSerAlaLeuSe 5	ArgThrAlaLeuLeuLeuHisSerAlaAsp 5	sAlaAlaArgGlySer	PhePheLeuLeuLeuLysLysAspArgArgLy 4 :::::	alLeuValTrpLeuAlaCysLeuLeuLeuAlaAlaAlaLeuPhe 4	ProMetAspLysTyrIleHisArgArgTrpV 4 ::	GAGACACGCTGTGACTGTGCCCTGCCCAGTAATCTC 1	4	TrpAlaCys	rgSerHisGlnCysMetGlnLeuTrpAsnAspAspAsnMetGlySerLeu 4 ::::::::::::::::::::::::::::::::::::	tAlaSerThrArgAlaAlaArgLeuGlyGluGluLeuLeuGlnAspPheA 4 : ::	AlaLeuGluProSerGlyCysThrProLeuProSerMe 4 :::::: :::: GGAATGAATCCACCCCCTACCAGGTCCTGCTGGAAAGTTTCTCCCGACTCA	spMetLeuLeuValGluMetLysThrGlyLeuAsnAsnThrSerValCys 4	GACACAGAGCATCTGCGAGTGG7
507	<u>1</u> 566	574 · 1537	566 L487	555 1437	539 L387	522 1337	50 ⁶ L287	196 1237	491 1187	180 L137	166	040	155	990	152 940	36	419 840	90 6	78

п-17	APPLICANT: Yao, Zhengbin APPLICANT: Spriggs, Melanie APPLICANT: Fanslow, William TITLE OF INVENTION: No. 6100235el Receptor That Binds NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS: ADDRESSEE: Immunex Corporation STREET: 51 University Street CITY: Seattle WA COUNTRY: USA ZIP: 98101 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: Apple Power Macintosh OPERATING SYSTEM: Apple Operating System 7.5.5 SOFTWARE: Microsoft Word for Apple, Version 6.0.1 CURRENT APPLICATION NUMBER: US/09/022,260 FILING DATE: CLASSIFICATION DATA: APPLICATION NUMBER: US/09/022,260 FILING DATE: 23 MARCH 1995 CLASSIFICATION NUMBER: US/09/022,260 FILING DATE: 23 MARCH 1995 CLASSIFICATION NUMBER: 2617-B TELEPHONE: PETKINS, PATTICIA Anne REGISTRATION: NAME: PETKINS, PATTICIA Anne REGISTRATION: ATTORNEY/AGENT INFORMATION: ATTORNEY/AGENT INFORMATION: ATTORNEY/AGENT INFORMATION: ATTORNEY/AGENT ON NUMBER: 2617-B TELECOMMUNICATION INFORMATION: ATTORNEY/AGENT ON NUMBER: 2617-B TELEPHONE: (206)587-0430 TELEPHONE: (206)587-0430 TELEPHONE: (206)587-0430 TELEPHONE: US/09/023,260 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3288 base pairs TYPE: nucleic acid STRANDEDNESS: single
	CCCCG 187 2_6/ptoda 2_6/ptoda ion_block Applicati 100235 ORMATION:
680 1866	664 ArgyalThrGlnAlaLeuArgSerAlaLeuAspSerCysThrSerSerSerSerSerSerSerSerSerSerSerSerSer
663 1816	650 lyCysSerThrSerAlaGlyArgProAlaAspArgValGlu
650 1766	640 uProAlaPheLeuAspAlaLeuGln
640 · 1716	624 alproserpropheargValAlaproLeupheSerLeupro.ThrGlnLe
624 1666	607 rGlyArgTyrValGlyValTyrPheAspGlyLeuLeuHisProAspSerV

				0	_ 0	<u> </u>
328 laProAspGlnSerProCysGlnProLeuValProProValProG::: 604	TGTGTGTCAAGTTCCAGGAGTATGT LeuTrpHisIleAlaArgLeuArgVa CGGTGGCGGTTTTCCTTCAGCCACTTTGT nLeuAspAlaProCysCysLeuProGlyL	TGACAGCTGGATCCACCCCAAAAACCTGACCCCGTCTTCCC LeThrLeuAsn	07 pleuAsnValSerThrAspGlyAspAsnVal 74 GCTG	#11gnment_block: US-09-899-471-5 x US-09-022-260-1 Align seg 1/1 to: US-09-022-260-1 from: 1 to: 326 198 SerIleGinSerCysTrpValle ::: :::	: ity: 184.50 Length: tio: 0.666 Gaps: ity: 42.290 Percent Identity: 20.	TOPOLOGY: linear HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE: ORGANISM: MOUSE STRAIN: HVS13 receptor FEATURE: LOCATION: 1212715 GS-09-022-260-1
DValProGlnLys	yAlaHisargAsn	TCCCCAAAAACA TCCCCAAAAAACA TASPLeuValPro :::	LeuLeuThrLeuAspValS	o: 3 . Val	: 20	
344 633 361	295 540 311 582 328 603	346 265 396 396 280 493	2 2 2 4 5 2 2 4 5 2 2 4 5 5 5 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	207 173		

	PRIOR APPLICATION DATA: APPLICATION NUMBER: USSN 08/410,535 FILING DATE: 23 MARCH 1995 CLASSIFICATION: ATTORNEY/AGENT INFORMATION:	CLASSIFICATION: PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/620,694 FILING DATE: CLASSIFICATION.	COMPUTER READABLE FORM: COMPUTER READABLE FORM: COMPUTER: Apple Power Macintosh COMPUTER: Apple Power Macintosh OPERATING SYSTEM: Apple Operating System 7.5.5 SOFTWARE: Microsoft Word for Apple, Version 6.0.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/022,259 FILING DATE:	APPLICANT: Yao, Zhengbin APPLICANT: Spriggs, Melanie APPLICANT: Fanslow, William TITLE OF INVENTION: No. 6191104el Receptor That Binds IL-17 NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS: ADDRESSEE: Immunex Corporation STREET: 51 University Street CITY: Seattle STATE: WA COUNTRY: USA	<pre>seq_name: /cgn2_b/ptodata/2/ina/6B_COMB.seq:US-09-022-259-1 seq_documentation_block: ; Sequence 1, Application US/09022259 ; Patent NO. 101104 ; Patent NO. 101104</pre>	680 rGluAlaPro 683 ::: 1867 CAGTGCCCCG 1876	664 ArgValThrGlnAlaLeuArgSerAlaLeuAspSerCysThrSerSerSe 680 ::::::::::::::::::::::::::::::::::::	650 lyCysSerThrSerAlaGlyArgProAlaAspArgValGlu 663 :::	640 uProAlaPheLeuAspAlaLeuGln	624 alProSerProPheArgValAlaProLeuPheSerLeuPro.ThrGlnLe 640 :: :::::: ::: 1667 TCCCCGACCTCTCAACATCACCTCCAGGTACCCCACTCATGGACAGATTT 1716	607 rGlyArgTyrValGlyValTyrPheAspGlyLeuLeuHisProAspSerV 624	591 AlaAlaTrpLeuSerCysValLeuProAspPheLeuGlnGlyArgAlaTh 607 ::: :::::::::::::::::::::::::::::::	574 InGlnTrpLeuGlnLeuGlnThrValGluProGlyProHisAspAlaLeu 590 ::::: ::: ::: ::: ::: ::: ::: :::	567ProAlaAlaValAlaGlnCysG 574 ::::: : 1488 GTGGAAAGCTATCTTGGGTTGGGCTGAGCCTGTCCAGCTACGGTGTG 1537
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alignment_block:
US-09-899-471-5 x US-09-022-259-1
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Quality:
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3288 ---
541 CGGTGCCGGTTTTCCTTCAGCCACTTTGTGGTAGATCCTGGC..
                          296 LeuTrpHisIleAlaArgLeuArg...ValLeuSerProGlyValTrpGl 311
                                                                       494 TGTGTGTCAAGTTC.
                                                                                                           281
                                                                                                                                                                                   278
                                                                                                                                                                                                                                                 266 CysLeuCysIleGlnValTrpSerLeuGluProAsp.....
                                                                                                                                                                                                                                                                                           347
                                                                                                                                                                                                                                                                                                        256 leThrLeuAsn......HisThrAspLeuValPro 265
                                                                                                                                                                                                                                                                                                                                                                                 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     207 pLeuAsnValSerThrAspGlyAspAsnValLeuLeuThrLeuAspValS 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 GCGATTCGGCGCTGCTGGCCACGGGTCGTCCCCGGGCCCGCGCTGGGATG 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 26:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEPAX: (206)
                                                                                                                                           444 CCTCGAGGGTGCAGAGCTGTCCGTCCTGCAGCTGAACACCAATGAGCGGC 493
                                                                                                                                                                                                                                                                                                                                                               297 TGACAGCTGGATCCACCCCAAAAACCTGACCCCGTCTTCCCCAAAAAAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                  247 TGCGCGCAGGAGGGGCTGAGCTGCAGAGTCAAGAATAGTACTTGTCTGGA 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          197 TGGCCCCGGGCCGCCCCCGCGCCTCCTCGACTTCCCGGCTCCGGTC 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          224 erGluGluGlnAspPheSerPheLeuLeuTyrLeuArgProValPro... 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      174 GCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: cDNA to mRNA HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Perkins, Patricia Anne REGISTRATION NUMBER: 34,695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RGANISM:
                                                                                                                                                                                                                 GTGTTGCATGTTGAG...TGGACCCTGCAGACAGATGCCAGCATCCTGTA 443
                                                                                                                                                                                                                                                                                   TCTATATCAATCTTAGTGTTTCCTCTACCCAGCACGGAGAATTAGTCCCT 396
                                                                                                     YalGluPheCysProPheArgGluAspProGlyAlaHisArgAsn 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3288 base pairs nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HVS13 receptor
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121..2715
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0.666
42.290
                                                                     .. CAGTTTCTGTCCATGCTGCAGCATCACCGTAAG 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ......CTTCTGCTGCTGAACGTTC 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length: 655
Gaps: 32
Percent Identity: 20.763
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..........AspAlaLeuLy 243
                                                                                                                                                                               .....SerGluArg. 280
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	522 1337	GlyAlaGlyTyrGluArgLeuValGlyAlaLeuAlaSerAlaLeuSe	507 1288
	506 1287	CTCCCCCACCO	497 1238
•	496 1237	SAlaAlaArgGlySer	491 1188
	491 1187	PhePheLeuLeuLeuLysLysAspArgArgLy 	481 1138
	480 1137	alLeuValTrpLeuAlaCysLeuLeuAlaAlaAlaAlaLeuPhe 	466 1088
	466 1087	:ProMetAspLysTyrIleHisArgArgTrpV	456 1041
	1040	CTAAATGACTGTTTGAGACACGCTGTGACTGTGCCCTGCCCAGTAATCTC	991
	455		455
•	455 990	TrpAlaCys	941
	452 940	rgSerHisGlnCysMetGlnLeuTrpAsnAspAspAsnMetGlySerLeu:::::::::::::::::::::::::::::::::::	436 891
	890	GAGAACCACAGCTGCTTTGATGTCGTTAAACAAATATTTGCGCCCAGGCA	841
	419 840	AlaLeuGluProSerGlyCysThrProLeuP	791
	406 790	spMetLeuLeuValGluMetLysThrGl	390
	390 778	IGInLeuGlnAlaCysSerTrpAlaAspSerLeuGlyProPheLysAspA 	373 757
	373 756)TrpGluLysVa 	370 707
	369 706	roAsnLeuCysValGlnValSerThr	361 657
	361 656	ASn.AlaThrValAsnGluProGlnAspPheGlnLeuValAlaGlyHisP::: ::: GACCCAAACCACAAATCCAAGAT	345 634
	344 633	laProAspGlnSerProCysGlnProLeuValProProValProGlnLys	328 604
	328 603	nLeuAspAlaProCysCysLeuProGlyLysValThrLeuCysTrpGlnA ::: ::: }CAGGAGTATGAAGTGACTGTT	311 583

seq_documentat Sequence 1 Patent No. 6 GERRAL INF APPLICANT APPLICANT APPLICANT APPLICANT TITLE OF NUMBER OF CORRESPON ADDRESS STREET: COUNTRY COUNTRY COMPUTER MEDIUM COMPUTER MEDIUM COMPUTER COURTATI SOFTMAN APPLICAN APPLICAN	680 r 1867 c seq_name:	664 A 1817 C	650 1 1 1767 c	640 u 1717 c	624 a 1 1667 T	1617 c	591 ¢ : 1567 ¢	574 1 : 1538 A	567 . 1488 G	556 G 1438 G	539 e 1388 C	522 r 1338 1
ntation_block: 1, Application U. 2, 6197525 INFORMATION: CANT: Yao, Zhengl CANT: Spriggs, M. CANT: Fanslow, W. CANT: Fanslow, W. OF INVENTION: R OF SEQUENCES: SPONDENCE ADDRESS SPONDENCE ADDRESS EET: 51 Universi EET: 51 Universi EET: USA EET: USA INTRY: USA INTR	rGluAlaPro 683 ::: cAGTGCCCCG 1876 /cgn2_6/ptodata/2/ii	ArgValThrGlnAlaLeuArgSerAlaLeuAspSerCysThrSerSerSerSe 	lyCysSerThrSerAlaGlyArgProAlaAspArgValGlu	UPTOAlapheLeuAspAlaLeuGlnGlyG	alproSerProPheArgValAlaProLeuPheSerLeuPro.ThrGlnLe	rGlyargTyrValGlyValTyrPheAspGlyLeuLeuHisProAspSerV 	AlaÅlaTrpLeuSerCysValLeuProAspPheLeuGlnGlyArgAlaTh ::: ::::: ACTGCAGCCATGAACATGATCCTGCCAGACTTCAAGAGGCCAGCCTGCTT	InGlnTrpLeuGlnLeuGlnThrValGluProGlyP ::: ACCACTGGAAGCCTGCT.	ProAlaAlaValAlaGInCysGGTGGAAAAGCTATCTTGGGTTGGGCTGAGCCTGCTGTCCAGCTACGGTGTG	GlnGluGlyGlyValValIleLeuLeuPheSer	eralaHisGlyAlaLeuAlaTrpPheHisHisGlnAr 	rGlimetProleuargValalaValaspLeuTrpSerargArgGluLeus : :::::: ::::::::::::::::::::::::::::
9022257 9022257 nie iam 6197525el Receptor 5197525el Receptor 5197526el Receptor 519752	/2/ina/6B_COMB.seq:US-09	alThrGlnAlaLeuArgSerAlaLeuAspSerCysThrSerSerSe :: ::::: ::: :::::: :: :::::	ThrSerAlaGlyArgProAlaAspArgValGlu ::: ::: AGCTCACAGGGGACAATTACCTGCAGAGCCCTA	euGln ::: CAGGACCTGGAGATGTTTG	oSerProPheArgValAlaProLeuPheSerLeuPro.ThrGlnLe :::	/rPheAspGlyLeuLeuHis ::: ::: \CTTCAGTGGCATCTGTAGT	LLeuProAspPheLeuGlnG 	<pre>fhrValGluProGlyProHi ::: ::: AAGCCTGCTGG</pre>	ProAlaAlaValAlaGlnC ::: 	»LeuLeuPheSer ::: ATCCTGTGTTCCCGAGGCA	laHisGlyAlaLeuAlaTrpPheHisHisGlnArgArgArgIleLeu :::::::: :::::::: 	LaValAspLeuTrpSerArg : : :
That Binds IL-17	022-257-1	hrserserse 680 ::::::: GTGGCAAACC 1866	pArgValGlu 663 ::: CAGAGCCCTA 1816	GlyG 650 ::: ;AACCCGGCCG 1766	O.ThrGlnLe 640	ProAspSerV 624 ::: GAGAGGGATG 1666	HyArgAlaTh 607	roHisAspAlaLeu 590 ::: GGGGACCTTTTC 1566	AlaGlnCysG 574 ::: : CTACGGTGTG 1537	566 CCCAAGCAAA 1487	gArgArgIleLeu 555 :::::::::: GCAGGAGATGGTG 1437	ArgGluLeuS 539 ::: ::: CAGGTTATCT 1387

ALASSIFICATION

496	sAlaAlaArgGlySer	491
1187	GTGCTGATCATCTGTATGACCTGGAGGCTTTCTGGCGCGCCGATCAAGAGAA	1138
491	eLeuLeuLeuLysLysAspArgArgLy	481
480 1137	alLeuValTrpLeuAlaCysLeuLeuLeuAlaAlaAlaAlaLeuPhe	466 1088
1087	ATACCACAGTTCCCAAGCCAGTTGCAGACTACATTCCCCTGTGGG	
466	roMetAspLysTyrIleHishrgArgTrpV	456
	GACTGTTTGAGACACGCTGTGACTGTGCCCTGCCCAGTAATCTC	991
4 55		455
ټ	ATCACCACGTGCAGGTCCAGCCCTTCTTCAGCAGCTGC	941
G	rpAlaCys	. 453
4	GAAGAATTCCATCAGCGAGCTAATGTCACATTCACTCTAAGCAAGTTTC	9
452	erHisGlnCysMetGlnLeuTrpAsnAspAspAsnMetGlySerLeu	436
9	AACCACAGCTGCTTTGATGTCGTTAAACAAATATTTGCGCCCAGGCA	841
7 r v	GluLeuLeuGlnAspPheA	419
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9		. 779
406	LeuAsnAsnThrSerValCy	. 390
778	GACACACAGCATCTGCGAGTGG	757
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756	GCGTGAGCTCAGGCAGCCTTTGGGATCCCAACATCACTGTGGAGACCTTG	707
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361	sn.AlaThrValAsnGluProGlnAspPheGlnLeuValAlaGly ::	345
633		604
344	ProLeuValProProValProGl	328
603	Ω -	583
328	ysValThrLe	311
582	TTTTCCTTCAGCCACTTTGTGGTAGATCCTG	541
311	rpHisIleAlaArgLeuArgValLeuSerF	296
540	TGTGTCAAGTTCCAGTTTCTGTCCATGCTGCAGCATCACCGTAAG	494
295	alGluPheCysProPheArgGluAspProGlyAlaHisArg	281
493	CCTCGAGGGTGCAGAGCTGTCCGTCCTGCAGCTGAACACCAATGAGCG	444
280	SerGluA	278

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Sequence 6, Application US/09188930A Patent No. 6150502
                                                                                                                                                                                                                                                                                      q_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-188-930-6
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                 q_documentation_block:
                                                                                                                                                                                                                                                                                                                                         1867
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                                                                                                                                                                                                                                                                                                                                       CAGTGCCCCG 1876
                                                                                                                                                                                                                                                                                                                                                                  rGluAlaPro 683
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTGGAAAGCTATCTTGGGTTGGGCTGAGCCTGCTGTCCAGCTACGGTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GATGCACCATGTCAGAGAGCTCACAGGGGACAATTACCTGCAGAGCCCTA 1816
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; TYPE: DNA
; ORGANISM: Mouse
US-09-188-930-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132 ArgCysAlaLeuLeuGluValGlnValProAlaAspLeuValGlnProGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            362 TTTCCATCCCCTCCTCAGCCATC...TCCCACAGAGGCCAACGCACCAAA 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    115 laSerLeuGlnAlaGlnValValLeuSerPheGlnAlaTyrProIleAla 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             312 CCAGAGGAAGCTGCTAGGCAGCCCTTCCCTGTCTGAGGAAAGCCATCGAA 361
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                                    gAsnLeuTrpHisIleAlaArgLeuArgValLeuSerProGly.....
                                                                                                        GluArgValGluPheCysProPheArgGluAspProGlyAlaHis...Ar
                                                                                                                                                           spLeuValProCysLeuCysIleGlnValTrpSerLeuGluProAspSer 278
                                                                                                                                                                                                                                                                                                                                                                                                                                       hrAspGlyAspAsnValLeuLeuThrLeuAspValSerGluGluGlnAsp 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LeuAsnLeuThrGlnGlnLeuProAspCysArgGlyLeuGluValArgAs 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     y...GlnSerValGlySerAlaValPheAspCysPheGluAlaSerLeuG 164
GTGAGGCGCAAAAAGTGTCCCTTCCAGAGCTGGCCTGAAGCTTATGGCTC
                                                                                                                                                                                                                                 CAGAAAATTGTGTCTGGAGGCCACACTGTAGACCTGCCTTATGAAT 658
                                                                                                                                                                                                                                                                                  uTrpTyrLysAsnLeuThrGlyProGlnAsnIleghrLeuAsnHisThrA 262
                                                                                                                                                                                                                                                                                                                                                                   PheSerPheLeuLeuTyrLeuArgProValProAspAlaLeuLysSerLe 245
                                                                                                                                                                                                                                                                                                                                                                                                               GCCCTTTTGATACC.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGCCCGAGGTGCAGGCTGTTCGGGTGACTATTCCTGCAGGCCCCCAAGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lyAlaGluValGlnIleTrpSerTyrThrLysProArgTyrGlnLysGlu 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGGGCCCAGCCTTCAGCTGCAGAAGGAAGAAGAACATCTCCCTGAAGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTCACAAAAGTGTGGAGGACCTGAA.....TTCTCCTTTGATTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . AGTGTGCGCCTTTGTTATCAGTGGGCACTGGAATGTGAAGACTTGAGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to: US-09-188-930-6
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1.094
45.574
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	ZIP: 98101 OMPUTER READABLE FORM: MEDIUM TYPE: Floppy dis COMPUTER: Apple Power M OPERATING SYSTEM: Apple OPERATING SYSTEM: Apple SOFTWARE: Microsoft Wor						
	LIGORY CONTRIBUTE ASPICACION ASSISTANCE IN A SATE OF SEQUENCES:	JOB LEALLY					
341 lProGlnLysAsnAlaThrValAsnGluProGlnAspPheGlnLeuValA 358 ::::: ::: ::: :::::::::::	372 LysvalGlnLeuGlnAlaCys	372 LysvalGinLeuGinAlacys					
lProGlnLysAsnAlaThrValAsnGluProGlnAspPheGlnLeuValA ::::	380 pAlaAspSerLeu 384	1038 PALASPSETICU 384 1:::					
lproGlnLysAsnAlaThrvalAsnGluproGlnAspPheGlnLeuValA 358	_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-620-694A-9 _documentation_block: equence 9, Application US/08620694A atent No. 5869286 GENERAL INFORMATION: APPLICANT: Yao, Zhengbin APPLICANT: Spriggs, Melanie APPLICANT: Fanslow, William TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-1 NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS: ADDRESSEE: Immunex Corporation STREET: 51 University Street CITY: Seattle STATE: WA	name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-620-694A-9documentation_block:					
lProGlnLysAsnAlaThrvalAsnGluProGlnAspPheGlnLeuValA 358	ACRITISE 5, APPLICATION US/U8520594A atent No. 5869286 GENERAL INFORMATION: APPLICANT: Yao, Zhengbin APPLICANT: Spriggs, Melanie APPLICANT: Fanslow, William TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-1 NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS: ADDRESSE: Immunex Corporation STREET: 51 University Street CITY: Seattle STATE: WA	ACHURINE Y, APPLICATION US/UB520594A atent NO. 5869286 APPLICANT: Yao, Zhengbin APPLICANT: Spriggs, Melanie APPLICANT: Fanslow, William TITLE OF INVENTION: NO. 5869286el Receptor That Binds IL-1 CORRESPONDENCE ADDRESS: ADDRESSEE: Immunex Corporation STRRET: \$1 University Street STATE: WA COUNTRY: USA ZIP: 98101 COMPUTER: Apple Power Macintosh OPERATING SYSTEM: Apple Operating System 7.5.5 SOCTWARE: MADION DATA: APPLICATION UMBER: US/UB520,694A FILING DATE: 21 MARCH 1996 CLASSIFICATION: 435 FRIDR APPLICATION DATA: APPLICATION UMBER: USSN 08/538,765 FILING DATE: 7 AUGUST 1995 CLASSIFICATION: 435 FRIDR APPLICATION DATA: APPLICATION UMBER: USSN 08/538,765 FILING DATE: 23 MARCH 1995 CLASSIFICATION: 435 FRIDR APPLICATION UMBER: USSN 08/538,765 FILING DATE: 32 MARCH 1995 CLASSIFICATION: 435 FRIDR APPLICATION UMBER: USSN 08/538,765 FILING DATE: 37 AUGUST 1995 CLASSIFICATION UMBER: USSN 08/538,765 FILING DATE: 37 AUGUST 1995 CLASSIFICATION UMBER: USSN 08/538,765 FILING DATE: 37 AUGUST 1995 CLASSIFICATION UMBER: USSN 08/538,765 FILING DATE: 37 AUGUST 1995 CLASSIFICATION UMBER: USSN 08/538,765 FILING DATE: 37 AUGUST 1995 CLASSIFICATION UMBER: 35 AUGUST 1995 CLASSIFICATION UMBER: USSN 08/538,765 FILING DATE: 30 AUGUST 1995 CLASSIFICATION UMBER: 35 AUGUST 1995 CLASSIFICATION UMBER: 35 AUGUST 1995 CLASSIFICATION UMBER: 35 AUGUST 1995 CLASSIFICATION UMBER: 35 AUGUST 1995 CLASSIFICATION UMBER: 35 AUGUST 1995 CLASSIFICATION UMBER: 35 AUGUST 1995 CLASSIFICATION UMBER: 35 AUGUST 1995 CLASSIFICATION UMBER: 3617-B TELECOMMUNICATION 341 ProGlnLysAsnAlaThrvalAsnGluProGlnAspPheGlnLeuValA 358 B98CCCAACGCACAGCACAGAGTCAGAAGGATGGTATATCCTGG 940 358 laGlyHisProAsnLeuCysValGlnValSerThrTrpGlu 371	W	WAA USA 8101 8101 READABLE FORM: TYPE: Floppy disk R: Apple Power Macintosh NG SYSTEM: Apple Operating System 7.5.5 E: Microsoft Word for Apple, Version 6. PPLICATION DATA: TION NUMBER: US/08/620,694A DATE: 21 MARCH 1996 ICATION 235 LICATION DATA: TION NUMBER: USSN 08/538,765 DATE: 7 AUGUST 1995 ICATION: 435 LICATION DATA: TION NUMBER: USSN 08/410,535 DATE: 23 MARCH 1995 ICATION: 435 LICATION:	341 lproGlnLysAsnAlaThrValAsnGluProGlnAspPheGlnLeuValA 358 358		TION NUMBER: USSN 08/538.7 DATE: 7 AUGUST 1995 LICATION DATA: TION NUMBER: USSN 08/410,5 DATE: 23 MARCH 1995 LICATION: 435 LICATION: 435 LICATION: 435 LICATION: 435 LICATION: 435 LICATION: 435 LICATION: 435 LICATION: 147 LICAT
341 ProGlnLysAsnAlaThrValAsnGluProGlnAspPheGlnLeuValA 358 898CCCAAAGGCCACAGGAGTCAGAAGGATGGTATATCCTGG 940 358 laGlyHisProAsnLeuCysValGlnValSerThrTpGlu 371 941 AGAATGTGGACTTGCACCCCCAGCTCTGCTTTAAGTTCTCATTTGAA 987 372 LysValGlnLeuGlnAlaCys	WARKENY APPLICATION DATA: APPLICATION NUMBER: US/08/620, FILING DATE: 21 MARCH 1996 CLASSIFICATION: 435 RIOR APPLICATION DATA:	TION NUMBER: USSN 08/410,5 DATE: 23 MARCH 1995 DATE: 23 MARCH 1995 ICATION: 435 AGENT INFORMATION: PERKINS, PATITOR ANNE ATION NUMBER: 3695 CE/DOCKET NUMBER: 2617-B NICATION INFORMATION: NE: (206) 587-0430 : (206) IFOR SEQ ID NO: 9: CHARACTERISTICS: 323 base pairs nucleic acid DNESS: single Y: linear TYPE: CDNA to mRNA					
341 ProGlnLysasnAlaThrvalAsnGluProGlnAspPheGlnLeuValA 358 358 361 351 358 358 358 361 358 358 358 359 358 359 358 359 358 359 358 359 358 359 359 358 359	ON DATA: BER: US/08/620,694A 1 MARCH 1996 435 I DATA: BER: USSN 08/538,76 AUGUST 1995 435 CDATA:	AGENT INFORMATION: PERKINS, PATRICIA ANNE PERKINS, PATRICIA ANNE ATTON NUMBER: 241,695 CE/DOCKET NUMBER: 2617- NICATION INFORMATION: NE: (206)587-0430 : (206) : (206) : FOR SEQ ID NO: 9: CHARACTERISTICS: 3223 base pairs nucleic acid DNESS: single Y: Linear TYPE: CDNA to mRNA					
341 ProGlnLysasnAlaThrValAsnGluProGlnAspPheGlnLeuValA 358 358 1631y	ON DATA: ON DATA: BER: US/08/620,694 1 MARCH 1996 435 1 DATA: BER: USSN 08/538,7 AUGUST 1995 435 1 DATA: BER: USSN 08/410,5 3 MARCH 1995 3 MARCH 1995	CE/DOCKET NUMBER: 2617- NICATION INFORMATION: NE: (206) FOR SEQ ID NO: 9: CHARACTERISTICS: 323 base pairs nucleic acid DNESS: single Y: linear TYPE: CDNA to mRNA					
341 ProGliLysAsnAlaThrvalAsnGlubroclinaspheGliLeuvalA 358 898CCCAACGCCACAGCACAGAGTCCAGAGGATGTATATCTGG 940 358 laGlyHisProAsnLeuCysValGlnValSerThrTrpGlu 371 :::::! 1 :::: 941 AGAATGTGGACCTTGCACCCCCACCTGCTTTAAGTTCTCATTGAA 987 372 LysValGlnLeuGlnAlaCysSerTI 380 :::::: 988 AACAGCACCACGACGACGCCCACCTGCTTTAAGTTCTCCATTTGAA 987 372 LysValGlnLeuGlnAlaCysSerTI 380 ::::: 1 :::	APPLICATION UNMER: US/08/620,694 FILING DATE: 21 MARCH 1996 CLASSIFICATION: 435 CLASSIFICATION DATA: APPLICATION UNMER: USSN 08/538,7 FILING DATE: 7 AUGUST 1995 CLASSIFICATION A435 CLASSIFICATION A435 IOR APPLICATION UNMER: USSN 08/410,5 FILING DATE: 23 MARCH 1995 FILING DATE: 23 MARCH 1995 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 436 CLASSIFICATION: 436 CLASSIFICATION: 436 TORNEY/AGENT INFORMATION: A06 NAME: Perkins, Patricia Anne REGISTRATION NUMBER: 34,695 REFERENCE/DOCKET NUMBER: 34,695 REFERENCE/DOCKET NUMBER: 34,695	FOR SEQ ID NO: CHARACTERISTICS 3223 base pai nucleic acid DNESS: single Y: linear TYPE: CDNA to					
341 ProGlnLysAssAlaThrvalAssGolProGlnAspPheGlnLeuvalA 358 898CCCAACGCCACAGCACAGGAGTCAGAAGGATGGTATATCCTGG 940 358 laGlyHisProAsnLeuCysValGlnValSerThrTpGlu 371 941 AGAATCTGGACTTGCACCCCCACAGGAGTCAGAAGGATGGTATATCCTGG 940 359 laGlySerTragagagagagagagagagagagagagagagagagaga	REENT APPLICATION DATA: APPLICATION NUMBER: US/08/620,694 FILING DATE: 21 MARCH 1996 CLASSIFICATION: 435 IOR APPLICATION DATA: APPLICATION NUMBER: USSN 08/538,7 FILING DATE: 7 AUGUST 1995 CLASSIFICATION ATA: APPLICATION NUMBER: USSN 08/410,5 FILING DATE: 23 MARCH 1995 CLASSIFICATION: 435 CLASSIFICATION: 436 APPLICATION: 436 APPLICATION: 436 TORNEY/AGENT INFORMATION: NAME: PEIKINS, PATRICIA Anne REGISTRATION NUMBER: 34,695 REFERENCE/DOCKET NUMBER: 2617-B LECOMMUNICATION INFORMATION: TELEPHONE: (206)587-0430 PEFFERX: (206)587-0430	EDNESS: single GY: linear TYPE: cDNA to					
341 ProGlnLysAssAlaThrvalAssOclProGlnAspPheGlnLeuvalA 358 368 1aGly	TION NUMBER: USON 08/410,594 DATE: 21 MARCH 1996 ICATION: 435 LICATION DATA: TION NUMBER: USSN 08/538,7 DATE: 7 AUGUST 1995 ICATION DATA: LICATION DATA: LICATION DATA: LICATION UMBER: USSN 08/410,5 LICATION UMBER: USSN 08/410,5 LICATION UMBER: USSN 08/410,5 LICATION SARCH 1995 LICATION: 435 LICATION: 435 LICATION: 435 LICATION: 436 LICATION: 436 LICATION: 436 LICATION: 436 LICATION: 436 LICATION: 436 LICATION UMBER: 34,695 LICATION UMBER: 34,695 LICATION UMBER: 2617-B MICATION						

230 SerPheLeuLeuTyrLeuArgProValProAspAlaLeuLysSerLeuTr 246 ::: ::: 570 ACCGTTCACCACCTGCCCAACCCCATCCTGATGGGGACCCAAACCACAA 619
199 eGlnSerCysTrpValLeuProTrpLeuAsnValSerThra 213 :::
183 LeuThrGlnGlnLeuProAspCysArgGlyLeuGlagalArgAspSerII 199 ::::::::
166 luValGlnIleTrpSerTyrThrLysProArgTyrGlnLysGluLeuAsn 182
153 rAlavalPheAspCysPheGluAlaSerLeuGlyAlaG 166 :::
137 GluValGlnValProAlaAspLeuValGlnProGlyGlnSerValGlySe 153
124 erPheGlnAlaTyrProIleAlaArgCysAlaLeuLeu 136 :: :: :::
107 rGluLeuGlnGluSerArgAsnAlaSerLeuGlnAlaGlnValValLeuS 124 ::: ::: :::
91 AlaValHisGlyHisTrpAlaGluProGluGluAlaGlyLysSerAspSe 107 ::::: ::: ::
74 ysProgInLysThrAspCysAlaLeuArgValArgValValValHisLeu 90.
61 uValproThrArgLeuGlnThrGluLeuValLeuArgC 74
55 SerAlaProGlyProValle 61 ::::::::::::::::::::::::::::::::::::
Align seg 1/1 to: US-08-620-694A-9 from: 1 to: 3223
alignment_block: US-09-899-471-5 x US-08-620-694A-9
alignment_scores: Quality: 151.50 Length: 703 Ratio: 0.493 Gaps: 37 Percent Similarity: 43.670 Percent Identity: 21.479
N L IS-08-62

246 pTyrLysAsnLeuThrGlyProGlnAsnIleThrLeuAsnHisThrAspL 263

620 GTCCAAGAATTTC...

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Seq_documentation_block: Sequence 9, Application US/09022255 Patent NO. 6072033 GENERAL INFORMATION: APPLICANT: Yao, Zhengbin APPLICANT: Yao, Zhengbin APPLICANT: Spriggs, Melanie APPLICANT: Spriggs, Melanie APPLICANT: Spriggs, Melanie APPLICANT: Spriggs, Melanie APPLICANT: Spriggs, Melanie APPLICANT: Spriggs, Melanie APPLICANT: Spriggs, Melanie APPLICATION UNGER: 10 CORRESPONDENCE ADDRESS: 10 CORRESPONDENCE ADDRESS: 10 CORRESSEE: Immunex Corporation STREET: 51 University Street CITY: Seattle STATE: WA COUNTRY: USA ZIP: 98101 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: Apple Power Macintosh OPERATING SYSTEM: Apple Operating System 7.5.5 SOFTWARE: Microsoft Word for Apple, Version 6.0.1 CURRENT APPLICATION DATA: APPLICATION UNUMBER: US/09/022,255 FILING DATE: CLASSIFICATION UNUBER: US/09/022,255 FILING DATE: 21 MARCH 1996	654 eralaGlyArgProAlaAspargYalGlu.argValFhrGlnAlaLeuAr 670	GGACCTGTTCACTGCAGCCATGAACATGAATCCTCCCGGACTTCAAGAGGC 1yArgAlaThrGlyArgTyrValGlyValTyrPheAspGlyLeuLeuHis :::	GACCTGGGTGGGCCGTCAGAAGCAGGAGAAGCAGGAGAGCAACTCTAAGA 141 allleLeuLeuPheSerProAlaAlaValAlaGlnCysGlnGlnTrpLeu 577 :: ::: TCATCGTCCTGTGCTCCCGGGCAGGCGCGCGCGCAAGTGGCAGGCGCTCCTG 146 TCATCGTCCTGTGCTCCCGGGCAGGCGCGCGCAAGTGGCAAGCCGCTCCTG 146 ::: ::: :::: :::: :::: :::: ::::	ACGTGGTCCTGAAATTCGCCCAGTTCCTGCTCACCGCCTGCGGCACGAA ValalavalAspLeuTrpSerArgArgGluLeuSerAlaHisGlyAlaLe

1220 GCCCAGGAAGGTCTGGATCATCTACTCAGCCGACCACCCCCTCTACGTGG 1269

AAATACACCGATGGCCTGCCTGCGGCTGACCTGATCCCCCCACCGCTGAA 1219
....ArgThrAlaLeuLeuLeuHisSerAlaAspGlyAlaGlyTyrgluA 512

512 rgLeuValGlyAlaLeuAlaSer...AlaLeuSerGlnMetProLeuArg 527

1170

497

1076 CTCCATCCTGCTGGTGGGCTCCGTCATC.....CTGCTCATCGTCTGCA 1119

470 uAlaCysLeuLeuAlaAlaAlaLeuPhePhePheLeuLeuLysL 487

1120 TGACCTGGAGGCTAGCTGGGCCTGGAAGTGAAAAATACAGTGATGACACC 1169

487 ysAspArgArgLysAlaAlaArgGlySer......496

1053 GTG.....

1003 CAGAAATGCCAGACACTCCAGAACCAATTCCGGACTACATGCCCCTGTGG 1052

438 HisGlnCysMetGlnLeuTrpAsn.AspAspAsnMetGlySer.LeuTrp 453

.....TTTCCTGCC 1002

974 CCTCAGACACTCCGCGACTG....

741

CTGCGTGTGAGCT.....TCACCCTGTGGAACGAATCTACCCATTA 781

..... 653

280 ArgValGluPheCysProPheArgGluAspProGlyAlaHisArgAsnLe 296

263 euValProCysLeuCysIleGlnValTrpSerLeuGluProAspSerGlu 279

.....CTTGTGCCTGACTGTGAG 650

651 CAC....

654GCCAGGATGAAGGTAACCACGCCATGCATGAGCTCAGGCA 693

454 AlaCysProMetAspLysTyrIleHisArgArgTrpValLeuValTrpLe 470

.....TACTGGTTCATCACGGGCAT 1075

			-		<u>, p ==</u>	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	** ** ** ** ** ** *		
381 GAATGGACACTCCAGACAGAC	 91 AlavalHisGlyHisTrpAlaGluProGluGluAlaGlyLysSerAspSe 107 :::::: 261 TGCCTGGATGACAGCTGGATTCACCCTCGA	61 uValProThrArgLeuGlnThrGluLeuValLeuArgC 74 :::	Align seg 1/1 to: US-09-022-255-9 from: 1 to: 3223 55 SerAlaProGlyProValle 61 :::::: 120 GCTGTCCCGGGGCCCCTGCTGGGGCTGCTGCTGCTGCTGC	93.5/0 Percent Identity: 21. IS-09-022-255-9	9-022-255-9 nment_scores: Quality: 151.50 Ratio: 0.493 Gaps:	ANTI-SENSE: NC ORIGINAL SOURCE ORGANISM: Hu STRAIN: IL-1 FEATURE: NAME/KEY: CD LOCATION: 93	L'E	Perkins, Patricia ANTION NUMBER: 34 CE/DOCKET NUMBER: NICATION INFORMAT NE: (206)587-043	FILING DATE: 7 AUGUST 1995 PRIOR APPLICATION DATA: APPLICATION UNMBER: USSN 08/410,535 FILING DATE: 23 MARCH 1995 ATTORNEY/AGENT INFORMATION:

JArgTrpValLeuValTrpLe 470	rg
CGGACTACATGCCCCTGTGG 1052	G
pAsnMetGlySer.LeuTr	GlnCysMetGlnLeuTrpAsn.AspAspAs
TTTCCT	
eArgSe	rgLeuGlyGluG
CTGCCTCAATGACTG 973	30 CAAGTGCAGATCCAGCCCTTCTTCAGCAGCT.
of an and an analysis of the state of the st	04 rValcusalaiansinsprosersinsuurus
GlyLeuAsnAsnThrSe 4	300 LYSASPASPMETLEULEUVALGIUMETLYSTNT :::::::::::::::::::::::::::::::::::
GATÇÇA 8	62CAGAAGAGTTCCACCAGCG
AlaAspSerLeuGlyProPhe 387	71 luLysValGlnLeuGlnAlaCysSerTrpAlaA
	824 .TTGCTTTGAGCACATGCACATACCTGCGCCCA
.nVal	354 eGlnLeuValAlaGlyHisProAsnLeuCysVa
::: GGAGAACCACAG	TCCGCACAT
ValAsnGluPro	ValProGlnLysAsnAlaThrVa
ys.GinProLeu 337	ω.
AGACCCTGGAGGCCCACCAG 74	94 GCCTGTGGGACCCCCAACATCACCG
CysLeuProGlyLysValThrLe 324	08 lyValTrpGlnLeuAsp.AlaProCys
CGCCATGCATGAGCTCAGGCA 693	654GCCAGGATGAAGGTAACCACGCC
0	ArgValLeuSer
653	:
pProGlyAlaHisArgAsnLe 296	ValGluPheCysProPheArgGluAspP
SerLeuGluProAspSerGlu 279	· 0
	20 GTCCAAGAATTTC
nIleThrLeuAsnHisThrAspL 263	46 pTyrLysAsnLeuThrGlyProGlnAs
::: GATGGGGACCCAAACCACCA 61	TGCCCAAGCCCATCCCT
oAspAlaLeuLysSerLeuTr 246	rPheLeuLeuTyrLeuArgProValPro
ValSerGluGluGlnAspPhe 229 ::: ::: CAGGAATATGAGGTG 569	: 'al
CTTCAGCCACTTTGTGGTTG 54	GAGGCATCACCACAGGCGGTGGCGTTTTACCT
LenAsnValserThra 21	rCvsTrpValLeu
lyLeuGluValArgAspSerIl 199 ::: GGTTTGAGTTTCTGTCCAAACT 496	183 LeuthrGlnGlnLeuProAspCysArgGlyLeuG ::::::::
::: CTGCAGCTGAAC 452	430 AGTTATCTGTC

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q_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-022-696-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1620 GACGGCGACGTCCCCGACCTGTTCGGCGCGCGCGCGCGGTACCCGCTC..
                                                                                                                                                                                                                                          1704 GACCTGGAGATGTTCCAGCCGGGCCGCATGCACCGCGTAGGGGAGCTGT 1752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              604 lyArgAlaThrGlyArgTyrValGlyValTyrPheAspGlyLeuLeuHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1420 TCATCGTCCTGTGCTCCCGCGCGCACGCGCCCAAGTGGCAGGCGCTCCTG
                                                                                                                                                                                                                                                                                                                                                        654 erAlaGlyArgProAlaAspArgValGlu.ArgValThrGlnAlaLeuAr 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               621 ProAspSerValProSerProPheArgValAlaProLeuPheSerLeuPr 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sAspAlaLeuAlaAlaTrpLeuSerCysValLeuProAspPheLeuGlnG
                                                                                                                                                                                                                                                                                                                                                                                                                                        oThrGlnLeuProAlaPheLeuAspAlaLeuGlnGlyGlyCysSerThrS
                                                                                                                                                                                                                                                                                 gSerAlaLeuAspSerCysThrSerSerSerGluAlaProGlyCysCys 686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGACCTGTTCACTGCAGCCATGAACATGATCCTCCCGGACTTCAAGAGGC 1569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACGTGGTCCTGAAATTCGCCCAGTTCCTGCTCACCGCCTGCGGCACGGAA 1319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAGCCTGCTTCGGCACCTACGTAGTCTGCTACTTCAGCGAGGTCAGCTGT 1619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGCCGGGGGGCGCCTGCGGCTGCGACCACGGAAAGCCCCGTGGG 1519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GACCTGGGTGGGCCGTCAGAAGCAGGAGAATGGTGGAGAGCAACTCTAAGA 1419
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                                                                                                                                                                                                                                                                                                                         ......ATGGACAGGTTCGAGGAGGTGTACTTCCGCATCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .....GlnLeuGlnThrValGluProGlyPro...Hi
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                        6072037el Receptor That Binds
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US-09-899-471-5 x US-09-022-696-9
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Quality:
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LENGTH: 3223 base pairs
TYPE: nucleic acid
                                                             220
                                                                                                                                    170 GGCCCCGGGTGGCGCCTCCCTGCGACTCCTGGACCACCGGGCGCTGGTCT
                                                                                                                                                                                                                    120 GCTGTCCCGGGGCCTGCTGGGGCTGCTCCTGCGGCGTGCT
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US
FILING DATE: 23 MARCH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM:
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REGISTRATION NUMBER: 34,695
AlaValHisGlyHisTrpAlaGluProGluGluAlaGlyLysSerAspSe ::::::
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                                                           GCTCCCAGCCG..
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CH 1995
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                                                           GGGCTAAACTGCACGGTCAAGAATAGTACC
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Sequence 9, Application US/09022696 Patent No. 6072037

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GENERAL INFORMATION:

Zhengbin Melanie William

APPLICANT: APPLICANT:

ဝ္ဂ

INVENTION: SEQUENCES: Spriggs, Fanslow, Yao,

885	62CAGAAGAGTTCCACCAGCGATCCA
387	371 luLysValGlnLeuGlnAlaCysSerTrpAlaAspSerLeuGlyProPhe
861	III
371	uValAlaGlyHisProAsnLeuCysValGlnValSerThrTrpG
354 823	82 CCAGATCCTGCCACCAGTTTCCCGCACATGGAGAACCACAG
781	STETGAGCTTCACCCTGTGGAACGAATCTACCCATTA
	24 uCysTrpGlnAlaProAspGl
740	CAACATCACCGTGGAGACCC
N	yValTrpGlnLeuAsp.AlaProCysC
693	GAGCTCAGG
0	uTrpHisIleAlaArgLeuArgValLeuSerPro
653	
296	ValGluPheCysProPheArgGluAspProGlyAlaHisArgAsnI
650	
279	ıProAspSerGl
632	620 GTCCAAGAATTTC
263	urGlyProGlnAsnI
619	570 ACCGTTCACCACCTGCCCAAGCCCATCCCTGATGGGGACCCAAACCACCA
Ν	euTyrLeuArgProValPr
(J)	547 ACCCTGAC
229	\snValLeuLeuThrLeuAspValSer
546	GAGGCATCACCACAGGCGGTGGCGTTTTACCTTCAGCCACTTTGTGGTT
213	GlnSerCysTrpVall
496	:
	roAspCysArgGlyLeu
182 452	yrThrLys
4	2GCCAGCATCCT
166	rAlaValPheAspCysPh
401	C
153	alGlnProGlyGlnSerV
380	CAACAAGGAGACCTGTTCCCCGTGGCTCACAT
w	rPheGlnAlaTyrProIleAlaArgCysAlaLeuLe
12 4 339	10/ rGiuLeuGInGIUSerArgAsnAlaSerLeuGlnAlaGlnValValLeuS :::
290	TGCCTGGATGACAGCTGGATTCACCCTCGA

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654	oThrGlnLeuProAlaPheLeuAspAlaLeuGlnGlyGlyCysSerThrS	637
637 1667	ProAspSerYalProSerProPheArgValAlaProLeuPheSerLeuPr ::: :::	1620
620 1619	lyArgAlaThrGlyArgTyrValGlyValTyrPhe	604 1570
604 1569	SASPAIALEUAIAAIA :::::: GGACCTGTTCACTGCA	587 1520
587 1519		578 1470
577 1469	allleLeuLeuPheSerProAlaAlaValAlaGlnCysGlnGlnTrpLeu 	561 1420
561 1419	<pre>uAlaTrpPheHisHisGlnArgArgArgIleLeuGlnGluGlyGlyValV :::: ::: GACCTGGGTGGGCCGTCAGAAGCAGGAGATGGTGGAGAGCAACTCTAAGA</pre>	544 1370
544 1369	B ValAlaValAspLeuTrpSerArgArgGluLeuSerAlaHisGlyAlaLe ::: ::::: :::	528 1320
527 1319	rgLeuValGlyAlaLeuAlaSerAla ::: acGTGGTCCTGAAATTCGCCCAGTTCCTG	512 1270
512 1269	7ArgThrAlaLeuLeuLeuHisSerAlaAspGlyAlaGlyTyrGluA 	497 1220
1219	AAATACACCGATGGCCTGCCTGCCGGCTGACCTGATCCCCCCCC	1170
496	6	496
496 1169	7 ysaspargargLysalaalaargGlySer	487 1120
487 1119	0 uAlacysLeuLeuLeuAlaAlaAlaLeuPhePhePheLeuLeuLysL:::: :::::::::::::::::::::::::	107
470 1075	4 AlaCysProMetAspLysTyrIleH1sArgArgTrpValLeuValTrpLe :::	454 1053
453 1052	HisGinCysMetGlnLeuTrpAsn.AspAspAsnMet	438 1003
437 1002	1 erThrargAlaAlaArgLeuGlyGluGluLeuLeuGlnAspPheArgSer:::::	421 974
421 973	4 rValcysAlaLeuGluProSerGlyCysThrProLeuProSerMetAlaS :	404 930
404 929		388 886

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US-08-978-773-3
                                           lignment_block:
US-09-899-471-5 x US-08-978-773-3
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                                                                                     Quality:
Ratio:
Percent Similarity:
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                lign seg 1/1 to: US-08-978-773-3 from: 1 to: 3223
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                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
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ORGANISM: Hum
                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple PowerMacintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for PowerMacintosh, Version 6.0.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Troutt, Anthony
TITLE OF INVENTION: Method of Regulating Nitric Oxide Production
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION UMBER: USSN 60/052,525
FILING DATE: 27 NOVEMBER 1996
CLASSIFICATION: 530
CLASSIFICATION: 530
                                                                                                                                                                                                                                      CLONE: IL-17R
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CITY: Seattle
STATE: WA
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                                                                                                                                                                                                           NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2623-A
                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
TOPOLOGY: lir
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                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
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                                                                                     Length: 703
Gaps: 37
Percent Identity: 21.479
                         694 GCCTGTGGGACCCCAACATCACCG...TGGAGACCCTGGAGGCCCACCAG 740
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324 uCysTrpGlnAlaProAspGlnSerProCys.Gln.
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TrpGln	isIleA G		rocy 	GAAT	CACCA	AspAsn GAC	ATCACC	GlnGl ::::: GAACG	GlnIle :::::: TCTGTC	alPheAs	lGlnVa :: GACACT	ACCCAA	euGlnG TGACCC	H1SG1 GATGA	GlnLys CAGCCG	ro	aProG1 : cccggg
LeuAsp	laArgL : CCAGGA		hacvebr 	; ;	TyrLe CTGCC	ValLeu	Serc	nLeuPr	TrpSer	pCysp	lProAl:	CAAGGA	luserAr CCTCCTC	yHisTr CAGCTG	ThraspC	GCGCCT	yPro GCCCCT
.Alapr	euArgV :::: TGAAGG		Tiegin		uArgPr ::: CAAGCC	lLeuLeuThr	ysTrp GGTGG	oAspCy TG	TyrThr	heGluA G	aAspLe : AGAC	GlnAla ::: GACCTG	gAs CCC	PALAGI :: GATTCA	ysAla ::: GGG	Thrai	GCTGGG
oCysCys	alLeuS TAACCA		 p		OVALPr ::: CATCCC	LeuAs	alLeu ::: GTTTT	sArg { CGTC	LysPr	laSerL : CCAGCA	:uValGl	TyrPro ::: TTCCCC	nAlaSerI ::: AAAGGACC	uProG1 : :: CCCTCG	LeuArg ::: CTAAAC	rgLeuG GACTCC	GCTGCT
'sLeuPr	erPro. :: CGCCAT	: 8	CHARGO		OASPAL	spValSer	roTrp	yLeuG ::: GTTTG	oArgTyr	eu :: TCCTGT	nProGl	IleAla ::: :GTGGCT	euGln TGCAG	.uGluAl : :A	ValArg	lnThre	CCTGCT
oGlyLy	GCATG		TGTGCCT	, :		GluG1 ::: CAGGA	euAsr ::: GCCAC	luValArg AGTTTCTG	: 61	ACCTCG	yGlnSe	ArgCys	Alaginy : ATCCAGC	aGlyLy	ValVa GTCAA	luLeuVa ::: :ACCGGG	GCTCCT
'sValT}	GCTCAG		GACTG		SSerI ::: AAACC	GlnAs :: TATGA	ValserTh :: TTTGTGGT	Asps :::: TCCA	nLysGluLeu ::: .CTGCAGCTG	GlyA ;AGGGTG	erValG	sAlaLei	alval	sSerAs	lvalhis Gaatagt	/alLeuArgC ::: 3CGCTGGTCT	Va II NGGGCGT
hrLe 3	GCA 6	:	GAG	' : '	euTr 2	pPhe 2 ; GGTG 5	Thra 2 ::: GTTG 5	erIl 1 :::: AACT 4	ASn 1	AlaG 1 GCAG 4	lyse 1	Leu 1 ::: .ATC 3	Leus 1 :::: TTTG 3	pse ···	Leu		alLe 6
324	308	G (650	: ω α	246 519	229 569	213 546	961	182 152	166 129	101	136 380	124 339	107 290	90 260	74 219	51 169

....ProLeu 337

604	37 saspalaLeualaalaTrpLeuSerCysValLeuProAspPheLeuGlnG	583
1519	0 GGCCGGGGGCCTGTGCGGCTGCGCGACCACGGAAAGCCCGTGGG	1470
587	8	578
577 1469	1 allleLeuLeuPheSerProAlaAlaValAlaGlnCysGlnGlnTrpLeu:::	563 1420
561 1419	4 uAlaTrpPheHisHisGlnArgArgArgIleLeuGlnGluGlyGlyValV :::: ::: ::: GACCTGGGTGGGCCGTCAGAAGCAGGAGATGGTGGAGAGCAACTCTAAGA	7 4
544 1369	8 ValAlaValAspLeuTrpSerArgArgGluI ::: :::::::: GTGGCCCTGGACCTGCTGGAAGAGCAGGCCA	528 1320
527 1319	rgLeuValGlyAlaLeuAlaSerAlaLeuSerGlnMetProLeuArg ::: ::: :::	7
512 1269		497 1220
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4 96 1169	37 ysaspargarglysalaalaargGlySer	487 1120
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470 1075	AlaCysProMetAspLysTyrIleHis/ ::: GTG	454 1053
453 1052	38 HisGlnCysMetGlnLeuTrpAsn.AspAspAsnMetGlySer.LeuTrp ::::: ::: ::::::::::::::	438 1003
437 1002	erThrArgAlaAlaArgLeuGlyGluGluI ::::: CCTCAGACACTCCGCGACTG	421 974
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404 929	188 LysaspaspMetLeuLeuValGluMetLysThrGlyLeuAsnAsnThrSe 	381
387 885	71 luLysValGlnLeuGlnAlaCysSerTrpAlaAspSerLeuGlyProPhe ::: 62CAGAAGAGTTCCACCAGCGATCCA	371 862
371 861	eGlnLeuValAlaGlyHisi .TTGCTTTGAGCACATGCAC	35 4 824
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781		74:

MOLECULE TYPE: cDNA to mRNA	٠.
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: (206)	٠.
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REFERENCE/DOCKET NUMBER: 2	٠.
STRATION NUMBER: 34,	:
NAME: Perkins Patricia Anne	
FICATION:	
3 MARCH 1995	٠.
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PRIOR APPLICATION DATE:	
: 7 AUGUST 1995	٠.
ATION NUMBER: US	٠, .
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A:	٠.
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Apple Power Macintosh	
PE: Floppy disk	٠.
PUTER RE	ς,
910	٠
COMMERT: WA	
Seattle	٠.
: 51 University Stree	٠
Immunex Cor	
NUMBER OF SEQUENCES: 10	٠.
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Fanslow,	٠
APPLICANT: Yao, Zhengbin	
ENERAL INFORMATION:	٠.
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1667 1667	
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HYPOTHETICAL: NO		
ANTI-SENSE: NO ORIGINAL SOURCE: ORGANISM: Human STRAIN: IL-17 R (hCTLA8 receptor) FEATURE:		
NAME/ LOCAT 022-25		
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us-09-899-471-5 x us-09-022-253-9		
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107 rGluLeuGlnGluSerArgAsnAlaSerLeuGlnAlaGlnValValLeuS :::	InValValLeuS 124	
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324 740	308 lyValTrpGlnLeuAsp.AlaProCysCysLeuProGlyLysValThrLe:::::: ::: ::: :::	
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Hearch information block

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Nery length: 698

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9:43
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9.5e-70
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BE160122 601767822F1 NCI_CGAP_I
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BI765330 603050641F1 NIH_MGC_1
BI382622 UI-R-CW0s-CCd-b-11-0-1
BN210218 C0660H10-3 NIA MOUSE T
               | W13694 ma94902:II Soares mouse
| B1832635 60308201271 NIH_MCC_12
| BB760916 BB760916 RIKEN full-16
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| AA238911 mx92A04.rl Soares mous
| BM010292 603631169F1 NIH_MGC_4|
| A2995676 2M0281A07R Mouse 10kb
| BI770219 603053287F1 NIH_MGC_11
| BI820026 60307207F1 NIH_MGC_11
| BF161982 601767930F1 NCI_CGAP_I
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gb_est2:BI490389
gb_est2:BF791762
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                                                                                                                                           source
                                                                             /organism="Mus musculus"
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                     /db_xref="taxon:10090"
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seq_documentation_block:
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Carninci,P., Shibata,Y., Hayatsu.N., Sugahara,Y., Shibata,K., II
Carninci,P., Shibata,Y., Muramatsu.M. and Hayashizaki,Y.,
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
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RIKEN Mouse ESTS (Arakawa,T., et al. 2001)

Unpublished (2001)

On May 11, 1999 this sequence version replaced gi:4787313.
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                                                                                                                                                                                                                                                                                               Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. GenomecRes. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizaw, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashiakki, Y
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalla; Eutheria; Rodentia; Schurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 1039)
                          CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Grogenomic Sciences Center and Genome Science Laboratory in Division of Experimental Animal Research in Riken contributions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 [(11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahar,Y. and Hayashizaki,Y.
prepare mouse tissues
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Fax: 81-298-36-9098
                                                                                                                                                              Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
                                                                                                                                                                                                                      Computational Analysis of Full Labength Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
                                                                                                                                                                                                                                                                                        Hayashizaki,
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laAlaTrpLeuSerCysValLeuProAspPheLeuGlnGlyArgAlaThr
                      GlyGlyValValIleLeuLeuPheSerProAlaAlaValAlaGlnCysGl 574
                                                                                                                                   isGlyAlaLeuAlaTrpPheHisHisGlnArgArgArgIleLeuGlnGlu
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                                                                                                                         Email: genome resegsc.riken.go.jkk.
URL:http://genome.gsc.riken.go.jpk.
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1 (bases 1 to 1006)
Arakawa.T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
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                                 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 | (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                         1-7-22 Suehiro-cho,
Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yökohama, Kanagawa 230-0045, Jap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTS (Arakawa,T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
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BB609618 RIKEN full-length enriched, 18
cDNA clone 1110025H02 5', mRNA sequence
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Konno, H., Fukunishi, Y., Y. and Hayashizaki, Y.
                     Shibata, K.,
                   Itoh, M., Carninci, P.,
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ValSerGluGlnAspPhe.SerPheLeuTyrLeuArgProValP
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                                                                                                                                                      PCysArgGlyLeuGluValArgAspSerILeGlnSerCysTrpValLeup
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Ratio: 4.419
milarity: 83.807
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA was cleaved with xhoI and SstI."
278 c 320 g 218 t 6 ot
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/dev_stage="18 days embryo"
/lab_host="SOLR"
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  Mammalia; Eutheria;
1 (bases 1 to 697)
NIH-MGC http://mgc.
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Eukaryota; Metazoa;
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http://mgc.nci.nih.gov/
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                           Chordata;
Rodentia;
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US-09-899-471-5 x BI332055
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JOURNAL
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LeuGlyGluGluLeuLeuGlnAspPheArgSerHisGlnCysMetGlnLe 443
                                                  AlaCysSerTrpAlaAspSerLeuGlyProPheLysAspAspMetLeuLe
                                                                                                                                                                                                                                                                             pGlnLeuAspAlaProCysCysLeuProGlyLysValThrLeuCysTrpG 327
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                                                                                                                                                                                        GCGTGCTTGTGGGCTGACTCCTTGGGGCCCCTTCAAGGATGATATGCTGTT
                                                                                                                                                                                                                                                         ACCCCAACCTCTGTGTCCAGGTGAGCACCTGGGAGAAGGTTCAGCTGCAA
                                                                                                                                                                                                                                                                                                                               AAGAACGCCACTGTGAATGAGCCACAAGATTTCCATGTTGGTGGCAGGCC
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Ratio: 5.330
milarity: 99.138
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Contact: Robert Strausberg, Ph.D.
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Location/Qualifiers
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Plate: LLAM11333 row: k column: 20
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
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Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 212 c 205 g 139 t
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/strain="FVB/N"
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Gaps: 1
Percent Identity: 98.707
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REFERENCE
AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murili (bases 1 to 784)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
                                 Quality: 1187.00
                                                                                                                                                                                                                                                                                    riate: LLAM10997 row: g column: 04
High quality sequence stop: 646.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Plate: LLAM10997 row
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                    Ratio:
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92.520
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                                                                                                                                                                                                                                               /strain="FVB/N"
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Percent Identity: 89.370
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alignment_block: US-09-899-471-5 x BG968034

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DEFINITION
                                  seq_documentation_block:
Locus AI007139
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                                                                                                                                                                 spArgArg.LysAlaAlaArgGlySerArgThrAlaLeuLeuLeuHisSe 504
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IMAGE:1363899 5', mRNA sequence
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clone
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AUTHORS
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US-09-899-471-5 x AI007139
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Percent Similarity:
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                430
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sThrProLeuProSerMetAlaSerThrArgAlaAlaArgLeuGlyGluG
                                                                                                         LysThrGlyLeuAsnAsnThrSerValCysAlaLeuGluProSerGlyCy
                                      TACACCACTGCCCAGCATGGCCTCCACGAGAGCTGCTCGCCTGGGAGAGG
                                                                                             AAAACCGGCCTCAACAACACATCAGTCTGTGCCTTGGAACCCAGTGGCTG
                                                                                                                                                   to: AI007139
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from:

to: 775

430

102

413 52

446

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ACCESSION
                              Quality: 1095.00
|Ratio: 4.660
|milarity: 91.085
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dub
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 314 286 1800
Fax: 314 286 1810
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Contact: Marra M/Mouse EST Project
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A1007139.1
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                                                                                                                                                                                                                             T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Site_1: Not I; Site_2: Eco
RI; 1st strand cDNA was primed with a Not I - oligo(dT)
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/dev_stage="4 weeks"
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/clone="IMAGE:1363899"
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/strain="C57BL/6J"
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                       1 (bases 1 to 722)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                    mRNA sequence.
BF237179
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Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
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High quality sequence stop: 584.
Location/Qualifiers
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//db_xref="taxon:10090"
//db_xref="taxon:10090"
//clone_11b="NCI_CGAP_L19"
//clone_11b="NCI_CGAP_L19"
//lab_host="DH10B (T1 phage-resistant)"
//note="Organ: liver; Vector: pcWV-SpORT6; Site_1: l
Site_2: SalI; Cloned unidirectionally. Primer: Olic
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Sakai,C., Sakai,K., Saho,H., Sasaki
,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
Muramatsu,M. and Hayashizaki,Y.
Muramatsu,M. and Hayashizaki,Y., Calling A., Shiraki,Mouse ESTs (Arakawa,T., et al. 2001)
                                                                                                                                                                                                       encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Alizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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Contact: Yoshihide Hayashizaki
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Arakawa,T., Carninci,P., Fukuda,S.,
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                                                                           Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                Human Genome Sequences. Mamm. Genome. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                 sequencing
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Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y., Muramatsu, M. and Hayashizaki, Y., Mormalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura
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                                                                                                                                                                                                                                                                                                                                                                                             sequencing pipeline with 384 multicapillary (10 (11), 1757-1771 (2000)
                                                                                                                           Computational Analysis of Full-Length Mouse cDNAs Compared with Juman Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                               RIKEN integrated sequence analysis (RISA) system -- 384 - format
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                                                     e mouse tissues.
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                                                                                                                                                                                                                                                                                                                                                Hayashizaki,Y.
Location/Qualifiers
1. .643
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Y., Kira,A. and
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516 aLeuAjaSerAlaLeuSerGlnMetProLeuArgValAlaValAspLeuT
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rProAlaAlaValAlaGlnCysGlnGlnTrpLeuGlnLeuGlnThrValG
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3']. cDNA was cloned into the XhoI and BamHI sites.
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/clone="9330110N14"
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11371 row: m column: 03
High quality sequence stop: 836.
Location/Qualifiers
1 870
                                                                                                                       Quality: 1012.50
Ratio: 4.868
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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BI251117
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                             /note-*Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sal:
Site_2: NotI; Cloned unidirectionally. Primer: Oligo do
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
                                                                                                                                                                                                                                                                                                                                                                  /clone-"IMAGE:5150378"
/clone_lib-"NCI_CGAP_Mam5"
/tissue_type-"tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/strain="C57/B6"
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                                        Mus musculus
Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 620)
Arakawa.T., Carninci,P., Fukuda,S.,
Hiramoto,K., Hori,F., Ishii,Y., T
                                                                                                                                    BB637050 AIKEN full-length enriched, adult male aorta
BB637050 RIKEN full-length enriched, adult male aorta
BB637050 RIKEN full-length enriched, adult male aorta
                                                                                   house mouse.
                                                                                                             BB637050.1
                                                                                                             GI:16472835
                                      Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Furuno, M., Hanagaki, T., Hara, A. to, M., Kawai, J., Konno, H., Kouda
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wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahar
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Alzawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Please visit our web site further details. e mouse tissues.
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URL:http://genome.gsc.riken.go.jp/
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Unpublished (2001)
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                                                                                                          modified pBluescript
                                                                                                                                                                                                                                                                                                                                   contributed to prepare mouse tissues. 1st strand cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                             prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN, Division of Experimental Animal Research in Riken
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/db_xref="taxon:10090"
/clone="A530050M19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="Site_1: SalI; Site_2: BamHI; cDNA library
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/dev_stage="adult"
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(http://genome.gsc.riken.go.jp) for
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                                                                 mRNA sequence.
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                                                                                          EST. 26-OCT-2000
IMAGE:3484038 5',
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REFERENCE AUTHORS

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 562)
NIH-MGC http://mgc.nci.nih.gov/.

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BASE COUNT
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US-09-899-471-5 x BE290565
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Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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Contact: Robert St
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alignment_block:
US-09-899-471-5 x BF160122
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VERSION
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clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM9185 row: 1 column: 06
High quality sequence start: 2
High quality sequence stop: 632.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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95.652
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229 c 204 g 110 t.
                                                                                                                                                                                                                                                                                    /tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
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/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                              clone_lib="NCI_CGAP_Lu29"
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                                                     Identity:
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Mational Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                      mRNA sequence.
BG761977
BG761977.1 GI:14072630
                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 935)
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                                                                                           Hominidae;
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IMAGE:4858806 5',
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High quality sequence stop: 813.
Location/Qualifiers
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      154
Library. |
a 301 c
                                                                                  /tissue_type="melanotic melanoma, high MDR (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site_1: xhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned
into ECORI/XhoI sites using the following 5' adaptor:
GCCACGAG(G). Size-selected >500bp for average insert size
GCACGAG(G). Size-selected >510ng in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-CDNA synthesis kit (Stratagene) and Superscript
                                using ZAP-cDNA synthesis kit (Sururayundi RT (Life Technologies). Note: this is
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/clone="IMAGE:4858806"
/clone_lib="NIH_MGC_49"
189 t
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                                                           and Superscript
NIH_MGC
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alignment_block: US-09-899-471-5 x BG761977 alignment_scores: | Ratio: Percent Similarity: 344 LysAshAlaThrValAsnGluProGlnAspPheGlnLeuValAlaGlyH1 360 277 pSerĠluArgValGluPheCysProPheArg.GluAspProGlyAlaHis 293 261 ThraspLeuValProCysLeuCysIleGlnValTrpSerLeuGluProAs 102 CAGAACCTCTGGCAAGCCGCCCGACTGCGACTGCTGACCCTGCAGAGCTG AGTGCTTGTGGGCTGACTCCCTGGGGCCTCTCAAAGACGATGTGCTACTG GAGAATGTCACTGTG...GACGTTCTCGAGTTCCCATTGCTGAAAGGCCA sProAsnLeuCysValGlnValSerThrTrpGluLysValGlnLeuGlnA 377 pGlnLeuAspAlaProCysCysLeuProGlyLysValThrLeuCysTrpG laCysSerTrpAlaAspSerLeuGlyProPheLysAspAspMetLeuLeu GCTGCTGGACGCACCGTGCTCGCTGCCCGCAGAAGGGGCACTGTGCTGGC ACAGACCTGGTTCCCTGCCTCTGTATTCAGGTGTGGCCTCTGGAACCTGA Quality: to: BG761977 912.50 3.755 79.153 from: 1 Gaps: 8
Percent Identity: 62.866 to: 935 Length: 251 310 298 343 327 151 51 201

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FEATURES
                                                                                                                                                                                                                                     COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: gb_est2:BG917539
                                                                                                                                                                                                                                                                                                                                                                                    SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                   KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
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                                                                                                                                                                                                                                                                        AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                       CCESSION
                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
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CTGCGCTTTCCCTCATCCTCCTCTCAAAAAGGATCACCGCGAAAGGGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       laValAspLeuTrpSerArgArgGluLeuSerAlaHisGlyAlaLeuAla 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               euVal.GlyAlaLeuAlaSerAla.LeuSerGlnMetProLeuArgValA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATCCACAAGCGCTGGGCCTCGTGTGGCTGGCCTGCCTACTCTTTGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        euGlyGluGluLeuGlnAspPheArgSerHisGlnCysMetGlnLeu 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTGGAGAGTACTTACTACAAGACCTGCAGTCAGGCCAGTGTCTGCAGCTA
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                                                                                                                 Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                 NATIONAL INSTITUTES OF Health, Mammalian Gene Collection (MGC) Uppublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                mRNA sequence.
BG917539
BG917539.1 GI:14298015
                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1. (bases 1 to 787)
                                                                                                                                                                                                                                                                                                                                                                                                   EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      602817086F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:4946084 5',
                                                                                                                                                                                                                                                                                                                                                           Mus musculus
                                                                                     found through the I.M.A.G.E. Consortium/LLNL
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                  nouse mouse
                                                 quality sequence stop:
                                                 LLAM10893 row: 1 column: uality sequence stop: 765.
                              Location/Qualifiers
organism="Mus musculus"
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alignment_scores:
Quality:
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US-09-899-471-5 x BG917539
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ORIGIN
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                                                                                 ValArgValVal.ValHisLeu.AlaValHisGlyHisTrp.AlaGluPr
                                                                                                                                                                                                                                                                                                                                                                                GlySérLeuGlnSerAlaProGlyProValLeuValProThrArgLeuGl-67
                                                                                                                                                                                                                                                                                                                                                                                                                                uAsnLéuThrGlnGlnLeuProAspCysArgGlyLeuGluValArgAspS 198
                                                  laGlu.ValGlnIleTrpSerTyrThrLysProArgTyrGlnLysGluLe
                                                                                                                                                                                 erLeuGlnAlaGlnValValLeuSerPheGlnAlaTyrProIleAlaArg
                                                                                                                                                                                                                                   GGTCGTCTCTGGAGAGACTGATGGAGCCTCAGGACACTGCACGCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lValValSerLeuGluArgLeuMetGluProGlnAspThrAlaArgCysS
                                    CTGAGGGTACAGATCTGGTCCTACACGAAGCCCAGGGTACCAGAAAGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="organ: mammary; Vector: pCMV-SPORT6; Site_1:
Site_2: NotI; Cloned unidirectionally. Primer: Olic
Library constructed by Life Technologies. Investigat
providing samples: Jeffrey Green, M.D., NIH"
a 229 c 259 g 171 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /Clone="IMAGE:4946084"
/Clone_lib="NCI_CGAP_Mam6"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                908.00
4.563
93.427
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/db_xref="taxon:10090"
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Gaps:
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ORIGIN
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US-09-899-471-5 x BI765330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        eq_documentation_block:
                                                                                                                                                                                                                                                                                 Ratio:
ercent Similarity:
                                                                                                                                                                          lign seg 1/1 to: BI765330 from: 1
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198 erIleGlnSerCysTrpValLeu 205
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                                                                                                                                                                                                                                                                                                                        Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM11476 row: b column: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BI765330
BI765330.1 GI:15756908
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603050641F1 NIH_MGC_116 Homo
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NHH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                 147 a
                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Organ: pooled colon, kidney, stomach; Vector: pCMV-SPORF6; Site_1: NotI; Site_2: ECORV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library.*
                                                                                                                                                                                                                                                                               902.00
3.667
71.512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone="IMAGE:5190442"
clone_lib="NIH_MGC_116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lab_host="DH10B"
                                                                                                                                                                                                                                                                          Length: 344
Gaps: 7
Percent Identity: 56.977
                                                                                                                                                                        to: 922
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yo
of 2
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358 850	eGlnLeuValAla ::::: TTCCTTTGTTGAA	Θ ή
343 800	26 pGlnAlaProAspGlnSerProCysGlnProLeuValProProValProG :	7 9
326 756	10 TrpGlnLeuAspAlaProCysCysLeuProGlyLysValThicLeuCysTr :	2 u
309 706	erProGlyVal :: CCCTGCAGAGC	<u>ი</u> ა
293 657	76 oAspSerGluArgValGluPheCysProPheArgGluAspProGlyAlaH	ວັກ່
276 607	.spLeuVal.ProCysLeuCysIleGlnValTrpSerLeuGluPr 	u ν
260 557	43 sSerLeuTrpTyrLysAsnLeuThrGlyProGlnAsnIleThrLeuAsnH	s N
243 520	27 GlnAspPheSerPheLeuLeuTyrLeuArgProValProAspAlaLeuLy	<u>,</u> 4 2
226 496	10 alSerThrAspGlyAspAsnValLeuLeuThrLeuAspValSerGluGlu	A 2
210 446	93 uGluValArgAspSerIleGlnSerCysTrpValLeuProTrpLeuAsnV	٠ 🚣 🛏
193 433	77 TyrGlnLysGluLeuAsnLeuThrGlnGlnLeuProAspCysArgGlyLe :: 93 TACGAGAAGGAACTCAACCACACACAGCTGCCTGCCCT	ωμ
176 392	0 luAlaSerLeuGlyAlaGluValGlnIleTrpSerTyrThrLysProArg ::: ::: :::	ωµ
160 342	43 pLeuvalGlnProGlyGlnSerValGlySerAlaValPheAspCysPheG 	2 1
143 292	27 AlaTyrProIle 43 GCCTACCCTACT	2 1
126 242	SerArgAsnAlaSerLeuGlnAlaGlnValValLeuSerP 	2 1
206	06	N
\vdash	GlyHisTrpAlaGluProGluGluAlaGlyLysSerAspSerGluLeu	
93	77 LysThrAspCysAlaLeuArgValArgValValValHisLeuAlaValHi:::	<u> </u>
76 159	60 alLeuvalProThrArgLeuGlnThrGluLeuValLeuArgCysProGln ::: :::	ш
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359 GlyHisproAsnLeuCysValGlnValSer 368

851

GGGCACCCTAACCTCTGTGTTCGGTTGAAC

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BASE COUNT
ORIGIN
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lignment_block:
US-09-09-471-5 x BI282622/rev
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MEDLINE
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ercent Similarity:
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                                                                                                                                                                              ignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence contained an oligo-dr track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dr track served to identify it as a clone from the non-normalized rat aorta pool library CDNA Library Preparation: M.B. Soares Lab Clone distribution: Clones will be available through Research Genetics (www.resgen.com)
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619 bp mRNA linear EST 19-JUL-200U1-R-CW0s-ccd-b-11-0-UI.sl UI-R-CW0s Rattus norvegicus cDNA clone U1-R-CW0s-ccd-b-11-0-UI 3', mRNA sequence.
                                                                                                                                                    Quality:
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Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 619)
Bonaldo, M.F., Lennor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukáryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BI282622.1 GI:14933575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: msoares@blue.weeg.uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome Res. 6 (9), 791-806 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eckstein Medical Research Building Iowa City, IA 52242, : 319 335 8250 : 319 335 9565
                                                                                                                                                                                                                                                                                 105
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                                                                                                                                                                                                                                                                               TAG_TISSUE=rat aorta pool
TAG_SEQ=CTGTAGGATC"
197 c 211 g 106
                                                                                                                                                                                                                                                                                                                                                                                                                         library is a non-normalized library constructed from the following rat aorta tissues: embryonic day 19, embryonic day 21, adult day 17, adult day 12, adult day 75, adult day 200. For a detailed description of the library from which this clone was derived, please visit our web site at ratest enguineach. The subtraction has been previously
                                                                                                   893.00
4.907
94.301
                                                                                                                                                                                                                                                                                                                                                        TAG_LIB-UI-R-CWOS
                                                                                                                                                                                                                                                                                                                                                                                  described in (Bonaldo, Lennon and Soares, 6:791-806, 1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="DH10B (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-CW0s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="UI-R-CW0s-ccd-b-11-0-UI"
/clone_lib="UI-R-CW0s"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dev_stage="ADULT"
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                                                                                             Length: 193
Gaps: 0
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Align seg 1/1
689 rpAspLeuGlyProCysThrThrLeuGlu 698
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                                                                                                                                               656 GlyArgProAlaAspArgValGluArgValThrGlnAlaLeuArgSerAl
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|:::||||||:::|
269 CACTGTACCCGCCCTGTTCCGCGTCGCGCCCCTCTTCTCCCCTGCCCTCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 506 AspGlyAlaGlyTyrGluArgLeuValGlyAlaLeuAlaSerAlaLeuSe
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                                                                                                                                                                                                                                                                                                                                                                                        aLeuAspSerCysThrSerSerSerGluAlaProGlyCysCysGluGluT
                                                                                                                                                                                                               lnLeuProAlaPheLeuAspAlaLeuGlnGlyGlyCysSerThrSerAla
                                                                                                                                                                                                                                                                                                                        CAGGAGGATGGCGTGGTCATACTTCTCTCTCACCCGCGGCCGTGGCGCA
                                                                                                                               GGGCGACCTGCGGACAGGCCGGAACGAGTGGCCCAGGCGCTGCTGTCCGC
                                                                                                                                                                                              AGCTGCCGGCCTTCCTGGATGCACTGCAGGGAAGCAGCTCCCAGTCCCCC
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